

# **R: A Language and Environment for Statistical Computing**

## **Reference Index**

The R Development Core Team

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# **Part I**





# Chapter 1

## The base package

---

base-package

*The R Base Package*

---

### Description

Base R functions

### Details

This package contains the basic functions which let R function as a language: arithmetic, input/output, basic programming support, etc. Its contents are available through inheritance from any environment.

For a complete list of functions, use `library(help="base")`.

---

.Device

*Lists of Open/Active Graphics Devices*

---

### Description

A pairlist of the names of open graphics devices is stored in `.Devices`. The name of the active device (see `dev.cur`) is stored in `.Device`. Both are symbols and so appear in the base name space.

### Value

`.Device` is a length-one character vector.

`.Devices` is a [pairlist](#) of length-one character vectors. The first entry is always "null device", and there are as many entries as the maximal number of graphics devices which have been simultaneously active. If a device has been removed, its entry will be "" until the device number is reused.

.Machine

*Numerical Characteristics of the Machine***Description**

.Machine is a variable holding information on the numerical characteristics of the machine R is running on, such as the largest double or integer and the machine's precision.

**Usage**

.Machine

**Details**

The algorithm is based on Cody's (1988) subroutine MACHAR. As all current implementations of R use 32-bit integers and almost all use IEC 60059 floating-point (double precision) arithmetic, all but the last two values are the same for almost all R builds.

Note that on most platforms smaller positive values than .Machine\$double.xmin can occur. On a typical R platform the smallest positive double is about  $5e-324$ .

**Value**

A list with components

- `double.eps` the smallest positive floating-point number  $x$  such that  $1 + x \neq 1$ . It equals  $\text{double.base}^{\text{ulp.digits}}$  if either `double.base` is 2 or `double.rounding` is 0; otherwise, it is  $(\text{double.base}^{\text{double.ulp.digits}}) / 2$ . Normally  $2.220446e-16$ .
- `double.neg.eps` a small positive floating-point number  $x$  such that  $1 - x \neq 1$ . It equals  $\text{double.base}^{\text{double.neg.ulp.digits}}$  if `double.base` is 2 or `double.rounding` is 0; otherwise, it is  $(\text{double.base}^{\text{double.neg.ulp.digits}}) / 2$ . Normally  $1.110223e-16$ . As `double.neg.ulp.digits` is bounded below by  $-(\text{double.digits} + 3)$ , `double.neg.eps` may not be the smallest number that can alter 1 by subtraction.
- `double.xmin` the smallest non-zero normalized floating-point number, a power of the radix, i.e.,  $\text{double.base}^{\text{double.min.exp}}$ . Normally  $2.225074e-308$ .
- `double.xmax` the largest normalized floating-point number. Typically, it is equal to  $(1 - \text{double.neg.eps}) * \text{double.base}^{\text{double.max.exp}}$ , but on some machines it is only the second or third largest such number, being too small by 1 or 2 units in the last digit of the significand. Normally  $1.797693e+308$ . Note that larger unnormalized numbers can occur.
- `double.base` the radix for the floating-point representation: normally 2.
- `double.digits` the number of base digits in the floating-point significand: normally 53.
- `double.rounding` the rounding action, one of.  
 0 if floating-point addition chops;  
 1 if floating-point addition rounds, but not in the IEEE style;

2 if floating-point addition rounds in the IEEE style;  
3 if floating-point addition chops, and there is partial underflow;  
4 if floating-point addition rounds, but not in the IEEE style, and there is partial underflow;  
5 if floating-point addition rounds in the IEEE style, and there is partial underflow.  
Normally 5.

`double.guard` the number of guard digits for multiplication with truncating arithmetic. It is 1 if floating-point arithmetic truncates and more than `double.digits` `double.base` digits participate in the post-normalization shift of the floating-point significand in multiplication, and 0 otherwise.

`double.ulp.digits` the largest negative integer `i` such that  $1 + \text{double.base}^i \neq 1$ , except that it is bounded below by  $-(\text{double.digits} + 3)$ . Normally -52.

`double.neg.ulp.digits` the largest negative integer `i` such that  $1 - \text{double.base}^i \neq 1$ , except that it is bounded below by  $-(\text{double.digits} + 3)$ . Normally -53.

`double.exponent` the number of bits (decimal places if `double.base` is 10) reserved for the representation of the exponent (including the bias or sign) of a floating-point number. Normally 11.

`double.min.exp` the largest in magnitude negative integer `i` such that `double.base` <sup>`i`</sup> is positive and normalized. Normally -1022.

`double.max.exp` the smallest positive power of `double.base` that overflows. Normally 1024.

`integer.max` the largest integer which can be represented. Always 2147483647.

`sizeof.long` the number of bytes in a C `long` type: 4 or 8 (most 64-bit systems, but not Windows).

`sizeof.longlong` the number of bytes in a C `long long` type. Will be zero if there is no such type, otherwise usually 8.

`sizeof.longdouble` the number of bytes in a C `long double` type. Will be zero if there is no such type, otherwise possibly 12 (most 32-bit builds) or 16 (most 64-bit builds).

`sizeof.pointer` the number of bytes in a C `SEXP` type. Will be 4 on 32-bit builds and 8 on 64-bit builds of R.

**Note**

`sizeof.longdouble` only tells you the amount of storage allocated for a long double (which are used internally by R for accumulators in e.g. `sum`, and can be read by `readBin`). Often what is stored is the 80-bit extended double type of IEC 60059, padded to the double alignment used on the platform — this seems to be the case for the common R platforms using ix86 and x86\_64 chips.

**References**

Cody, W. J. (1988) MACHAR: A subroutine to dynamically determine machine parameters. *Transactions on Mathematical Software*, **14**, 4, 303–311.

**See Also**

[.Platform](#) for details of the platform.

**Examples**

```
.Machine
## or for a neat printout
noquote(unlist(format(.Machine)))
```

---

.Platform                      *Platform Specific Variables*

---

**Description**

.Platform is a list with some details of the platform under which R was built. This provides means to write OS-portable R code.

**Usage**

```
.Platform
```

**Value**

A list with at least the following components:

OS.type	character string, giving the <b>Operating System</b> (family) of the computer. One of "unix" or "windows".
file.sep	character string, giving the <b>file separator</b> used on your platform: "/" on both Unix-alikes <i>and</i> on Windows (but not on the once port to Classic Mac OS).
dynlib.ext	character string, giving the file name <b>extension</b> of <b>dynamically loadable libraries</b> , e.g., ".dll" on Windows and ".so" or ".sl" on Unix-alikes. (Note for Mac OS X users: these are shared objects as loaded by <a href="#">dyn.load</a> and not dylibs: see <a href="#">dyn.load</a> .)
GUI	character string, giving the type of GUI in use, or "unknown" if no GUI can be assumed. Possible values are for Unix-alikes the values given via the '-g' command-line flag ("X11", "Tk"), "AQUA" (running under R.app on Mac OS X), "Rgui" and "RTerm" (Windows) and perhaps others under alternative front-ends or embedded R.
endian	character string, "big" or "little", giving the endianness of the processor in use. This is relevant when it is necessary to know the order to read/write bytes of e.g. an integer or double from/to a connection: see <a href="#">readBin</a> .
pkgType	character string, the preferred setting for <a href="#">options("pkgType")</a> . Values "source", "mac.binary", "mac.binary.leopard" and "win.binary" are currently in use.
path.sep	character string, giving the <b>path separator</b> , used on your platform, e.g., ":" on Unix-alikes and ";" on Windows. Used to separate paths in environment variables such as PATH and TEXINPUTS.
r_arch	character string, possibly "". The name of the architecture-specific directory used in this build of R.

## AQUA

`.Platform$GUI` is set to "AQUA" under the Mac OS X GUI, R.app. This has a number of consequences:

- the `DISPLAY` environment variable is set.
- appends `‘/usr/local/bin’` to the `PATH` environment variable.
- the default graphics device is set to `quartz`.
- selects native (rather than Tk) widgets for the `graphics = TRUE` options of `menu` and `select.list`.
- HTML help is displayed in the internal browser.
- The spreadsheet-like data editor/viewer uses a Quartz version rather than the X11 one.

## See Also

`R.version` and `Sys.info` give more details about the OS. In particular, `R.version$platform` is the canonical name of the platform under which R was compiled.

`.Machine` for details of the arithmetic used, and `system` for invoking platform-specific system commands.

## Examples

```
## Note: this can be done in a system-independent way
## by file.info()$isdir
if(.Platform$OS.type == "unix") {
  system.test <- function(...) { system(paste("test", ...)) == 0 }
  dir.exists <- function(dir)
    sapply(dir, function(d) system.test("-d", d))
  dir.exists(c(R.home(), "/tmp", "~", "/NO"))# > T T T F
}
```

---

abbreviate

*Abbreviate Strings*

---

## Description

Abbreviate strings to at least `minlength` characters, such that they remain *unique* (if they were), unless `strict=TRUE`.

## Usage

```
abbreviate(names.arg, minlength = 4, use.classes = TRUE,
           dot = FALSE, strict = FALSE,
           method = c("left.kept", "both.sides"))
```

**Arguments**

<code>names.arg</code>	a character vector of names to be abbreviated, or an object to be coerced to a character vector by <code>as.character</code> .
<code>minlength</code>	the minimum length of the abbreviations.
<code>use.classes</code>	logical (currently ignored by R).
<code>dot</code>	logical: should a dot (" . ") be appended?
<code>strict</code>	logical: should <code>minlength</code> be observed strictly? Note that setting <code>strict=TRUE</code> may return <i>non-unique</i> strings.
<code>method</code>	a string specifying the method used with default <code>"left.kept"</code> , see ‘Details’ below.

**Details**

The algorithm (`method = "left.kept"`) used is similar to that of `S`. For a single string it works as follows. First all spaces at the beginning of the string are stripped. Then (if necessary) any other spaces are stripped. Next, lower case vowels are removed (starting at the right) followed by lower case consonants. Finally if the abbreviation is still longer than `minlength` upper case letters are stripped.

Characters are always stripped from the end of the word first. If an element of `names.arg` contains more than one word (words are separated by space) then at least one letter from each word will be retained.

Missing (NA) values are unaltered.

If `use.classes` is `FALSE` then the only distinction is to be between letters and space. This has NOT been implemented.

**Value**

A character vector containing abbreviations for the strings in its first argument. Duplicates in the original `names.arg` will be given identical abbreviations. If any non-duplicated elements have the same `minlength` abbreviations then, if `method = "both.sides"` the basic internal `abbreviate()` algorithm is applied to the characterwise *reversed* strings; if there are still duplicated abbreviations and if `strict=FALSE` as by default, `minlength` is incremented by one and new abbreviations are found for those elements only. This process is repeated until all unique elements of `names.arg` have unique abbreviations.

The character version of `names.arg` is attached to the returned value as a `names` argument: no other attributes are retained.

**Warning**

This is really only suitable for English, and does not work correctly with non-ASCII characters in multibyte locales. It will warn if used with non-ASCII characters.

**See Also**

`substr`.

**Examples**

```
x <- c("abcd", "efgh", "abce")
abbreviate(x, 2)
abbreviate(x, 2, strict=TRUE)# >> 1st and 3rd are == "ab"

(st.abb <- abbreviate(state.name, 2))
table(nchar(st.abb))# out of 50, 3 need 4 letters :
as <- abbreviate(state.name, 3, strict=TRUE)
as[which(as == "Mss")]

## method="both.sides" helps: no 4-letters, and only 4 3-letters:
st.ab2 <- abbreviate(state.name, 2, method="both")
table(nchar(st.ab2))
## Compare the two methods:
cbind(st.abb, st.ab2)
```

agrep

*Approximate String Matching (Fuzzy Matching)***Description**

Searches for approximate matches to *pattern* (the first argument) within the string *x* (the second argument) using the Levenshtein edit distance.

**Usage**

```
agrep(pattern, x, ignore.case = FALSE, value = FALSE,
       max.distance = 0.1, useBytes = FALSE)
```

**Arguments**

<code>pattern</code>	a non-empty character string to be matched ( <i>not</i> a regular expression!). Coerced by <code>as.character</code> to a string if possible.
<code>x</code>	character vector where matches are sought. Coerced by <code>as.character</code> to a character vector if possible.
<code>ignore.case</code>	if <code>FALSE</code> , the pattern matching is <i>case sensitive</i> and if <code>TRUE</code> , case is ignored during matching.
<code>value</code>	if <code>FALSE</code> , a vector containing the (integer) indices of the matches determined is returned and if <code>TRUE</code> , a vector containing the matching elements themselves is returned.
<code>max.distance</code>	Maximum distance allowed for a match. Expressed either as integer, or as a fraction of the <i>pattern</i> length (will be replaced by the smallest integer not less than the corresponding fraction of the pattern length), or a list with possible components <ul style="list-style-type: none"> <li><code>all</code>: maximal (overall) distance</li> <li><code>insertions</code>: maximum number/fraction of insertions</li> <li><code>deletions</code>: maximum number/fraction of deletions</li> <li><code>substitutions</code>: maximum number/fraction of substitutions</li> </ul> If <code>all</code> is missing, it is set to 10%, the other components default to <code>all</code> . The component names can be abbreviated.



`useBytes` logical. in a multibyte locale, should the comparison be character-by-character (the default) or byte-by-byte.

### Details

The Levenshtein edit distance is used as measure of approximateness: it is the total number of insertions, deletions and substitutions required to transform one string into another.

As from R 2.10.0 this uses `tre` by Ville Laurikari (<http://http://laurikari.net/tre/>), which supports MBCS character matching much better than the previous version.

### Value

Either a vector giving the indices of the elements that yielded a match, or, if `value` is `TRUE`, the matched elements (after coercion, preserving names but no other attributes).

### Author(s)

Original version by David Meyer. Current version by Brian Ripley.

### See Also

[grep](#)

### Examples

```
agrep("lasy", "1 lazy 2")
agrep("lasy", c("1 lazy 2", "1 lasy 2"), max = list(sub = 0))
agrep("laysy", c("1 lazy", "1", "1 LAZY"), max = 2)
agrep("laysy", c("1 lazy", "1", "1 LAZY"), max = 2, value = TRUE)
agrep("laysy", c("1 lazy", "1", "1 LAZY"), max = 2, ignore.case = TRUE)
```

---

all

*Are All Values True?*

---

### Description

Given a set of logical vectors, are all of the values true?

### Usage

```
all(..., na.rm = FALSE)
```

### Arguments

`...` zero or more logical vectors. Other objects of zero length are ignored, and the rest are coerced to logical ignoring any class.

`na.rm` logical. If true NA values are removed before the result is computed.

## Details

This is a generic function: methods can be defined for it directly or via the [Summary](#) group generic. For this to work properly, the arguments `...` should be unnamed, and dispatch is on the first argument.

Coercion of types other than integer (raw, double, complex, character, list) gives a warning as this is often unintentional.

This is a [primitive](#) function.

## Value

The value is a logical vector of length one.

Let `x` denote the concatenation of all the logical vectors in `...` (after coercion), after removing NAs if requested by `na.rm = TRUE`.

The value returned is `TRUE` if all of the values in `x` are `TRUE` (including if there are no values), and `FALSE` if at least one of the values in `x` is `FALSE`. Otherwise the value is `NA` (which can only occur if `na.rm = FALSE` and `...` contains no `FALSE` values and at least one `NA` value).

## S4 methods

This is part of the S4 [Summary](#) group generic. Methods for it must use the signature `x, ..., na.rm`.

## Note

That `all(logical(0))` is `true` is a useful convention: it ensures that

```
all(all(x), all(y)) == all(x,y)
```

even if `x` has length zero.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[any](#), the ‘complement’ of `all`, and [stopifnot](#)(\*) which is an `all`(\*) ‘insurance’.

## Examples

```
range(x <- sort(round(stats::rnorm(10) - 1.2, 1)))
if(all(x < 0)) cat("all x values are negative\n")

all(logical(0)) # true, as all zero of the elements are true.
```

---

<code>all.equal</code>	<i>Test if Two Objects are (Nearly) Equal</i>
------------------------	---

---

### Description

`all.equal(x, y)` is a utility to compare R objects `x` and `y` testing ‘near equality’. If they are different, comparison is still made to some extent, and a report of the differences is returned. Don’t use `all.equal` directly in `if` expressions—either use `isTRUE(all.equal(...))` or `identical` if appropriate.

### Usage

```
all.equal(target, current, ...)

## S3 method for class 'numeric':
all.equal(target, current,
          tolerance = .Machine$double.eps ^ 0.5,
          scale = NULL, check.attributes = TRUE, ...)

attr.all.equal(target, current,
               check.attributes = TRUE, check.names = TRUE, ...)
```

### Arguments

<code>target</code>	R object.
<code>current</code>	other R object, to be compared with <code>target</code> .
<code>...</code>	Further arguments for different methods, notably the following two, for numerical comparison:
<code>tolerance</code>	numeric $\geq 0$ . Differences smaller than <code>tolerance</code> are not considered.
<code>scale</code>	numeric scalar $> 0$ (or <code>NULL</code> ). See ‘Details’.
<code>check.attributes</code>	logical indicating if the <code>attributes(.)</code> of <code>target</code> and <code>current</code> should be compared as well.
<code>check.names</code>	logical indicating if the <code>names(.)</code> of <code>target</code> and <code>current</code> should be compared as well (and separately from the <code>attributes</code> ).

### Details

There are several methods available, most of which are dispatched by the default method, see `methods("all.equal")`. `all.equal.list` and `all.equal.language` provide comparison of recursive objects.

Numerical comparisons for `scale = NULL` (the default) are done by first computing the mean absolute difference of the two numerical vectors. If this is smaller than `tolerance` or not finite, absolute differences are used, otherwise relative differences scaled by the mean absolute difference.

If `scale` is positive, absolute comparisons are made after scaling (dividing) by `scale`.

For complex arguments, the modulus `Mod` of the difference is used: `all.equal.numeric` is called so arguments `tolerance` and `scale` are available.

`attr.all.equal` is used for comparing `attributes`, returning `NULL` or a character vector.

**Value**

Either TRUE (NULL for attr.all.equal) or a vector of mode "character" describing the differences between target and current.

**References**

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer (for =).

**See Also**

identical, isTRUE, ==, and all for exact equality testing.

**Examples**

```
all.equal(pi, 355/113)
# not precise enough (default tol) > relative error

d45 <- pi*(1/4 + 1:10)
stopifnot(
  all.equal(tan(d45), rep(1,10))      # TRUE, but
  all      (tan(d45) == rep(1,10))    # FALSE, since not exactly
  all.equal(tan(d45), rep(1,10), tol=0) # to see difference
```

---

all.names

*Find All Names in an Expression*


---

**Description**

Return a character vector containing all the names which occur in an expression or call.

**Usage**

```
all.names(expr, functions = TRUE, max.names = -1L, unique = FALSE)
all.vars(expr, functions = FALSE, max.names = -1L, unique = TRUE)
```

**Arguments**

expr	an expression or call from which the names are to be extracted.
functions	a logical value indicating whether function names should be included in the result.
max.names	the maximum number of names to be returned. -1 indicates no limit (other than vector size limits).
unique	a logical value which indicates whether duplicate names should be removed from the value.

**Details**

These functions differ only in the default values for their arguments.

**Value**

A character vector with the extracted names.

**Examples**

```
all.names(expression(sin(x+y)))
all.vars(expression(sin(x+y)))
```

---

any

*Are Some Values True?*


---

**Description**

Given a set of logical vectors, is at least one of the values true?

**Usage**

```
any(..., na.rm = FALSE)
```

**Arguments**

`...` zero or more logical vectors. Other objects of zero length are ignored, and the rest are coerced to logical ignoring any class.

`na.rm` logical. If true NA values are removed before the result is computed.

**Details**

This is a generic function: methods can be defined for it directly or via the [Summary](#) group generic. For this to work properly, the arguments `...` should be unnamed, and dispatch is on the first argument.

Coercion of types other than integer (raw, double, complex, character, list) gives a warning as this is often unintentional.

This is a [primitive](#) function.

**Value**

The value is a logical vector of length one.

Let `x` denote the concatenation of all the logical vectors in `...` (after coercion), after removing NAs if requested by `na.rm = TRUE`.

The value returned is `TRUE` if at least one of the values in `x` is `TRUE`, and `FALSE` if all of the values in `x` are `FALSE` (including if there are no values). Otherwise the value is `NA` (which can only occur if `na.rm = FALSE` and `...` contains no `TRUE` values and at least one `NA` value).

**S4 methods**

This is part of the S4 [Summary](#) group generic. Methods for it must use the signature `x, ..., na.rm`.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[all](#), the ‘complement’ of [any](#).

**Examples**

```
range(x <- sort(round(stats::rnorm(10) - 1.2,1)))
if(any(x < 0)) cat("x contains negative values\n")
```

aperm

*Array Transposition***Description**

Transpose an array by permuting its dimensions and optionally resizing it.

**Usage**

```
aperm(a, perm, resize = TRUE)
```

**Arguments**

<code>a</code>	the array to be transposed.
<code>perm</code>	the subscript permutation vector, which must be a permutation of the integers <code>1:n</code> , where <code>n</code> is the number of dimensions of <code>a</code> . The default is to reverse the order of the dimensions.
<code>resize</code>	a flag indicating whether the vector should be resized as well as having its elements reordered (default <code>TRUE</code> ).

**Value**

A transposed version of array `a`, with subscripts permuted as indicated by the array `perm`. If `resize` is `TRUE`, the array is reshaped as well as having its elements permuted, the `dimnames` are also permuted; if `resize = FALSE` then the returned object has the same dimensions as `a`, and the `dimnames` are dropped. In each case other attributes are copied from `a`.

The function `t` provides a faster and more convenient way of transposing matrices.

**Author(s)**

Jonathan Rougier, <J.C.Rougier@durham.ac.uk> did the faster C implementation.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`t`, to transpose matrices.

**Examples**

```
# interchange the first two subscripts on a 3-way array x
x <- array(1:24, 2:4)
xt <- aperm(x, c(2,1,3))
stopifnot(t(xt[, ,2]) == x[, ,2],
           t(xt[, ,3]) == x[, ,3],
           t(xt[, ,4]) == x[, ,4])
```

---

 append

*Vector Merging*


---

**Description**

Add elements to a vector.

**Usage**

```
append(x, values, after = length(x))
```

**Arguments**

<code>x</code>	the vector to be modified.
<code>values</code>	to be included in the modified vector.
<code>after</code>	a subscript, after which the values are to be appended.

**Value**

A vector containing the values in `x` with the elements of `values` appended after the specified element of `x`.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**Examples**

```
append(1:5, 0:1, after=3)
```

---

`apply`*Apply Functions Over Array Margins*

---

### Description

Returns a vector or array or list of values obtained by applying a function to margins of an array or matrix.

### Usage

```
apply(X, MARGIN, FUN, ...)
```

### Arguments

<code>X</code>	an array, including a matrix.
<code>MARGIN</code>	a vector giving the subscripts which the function will be applied over. 1 indicates rows, 2 indicates columns, <code>c(1, 2)</code> indicates rows and columns.
<code>FUN</code>	the function to be applied: see ‘Details’. In the case of functions like <code>+</code> , <code>%*%</code> , etc., the function name must be backquoted or quoted.
<code>...</code>	optional arguments to <code>FUN</code> .

### Details

If `X` is not an array but has a non-null `dim` value, `apply` attempts to coerce it to an array via `as.matrix` if it is two-dimensional (e.g., data frames) or via `as.array`.

`FUN` is found by a call to `match.fun` and typically is either a function or a symbol (e.g. a backquoted name) or a character string specifying a function to be searched for from the environment of the call to `apply`.

### Value

If each call to `FUN` returns a vector of length `n`, then `apply` returns an array of dimension `c(n, dim(X)[MARGIN])` if `n > 1`. If `n` equals 1, `apply` returns a vector if `MARGIN` has length 1 and an array of dimension `dim(X)[MARGIN]` otherwise. If `n` is 0, the result has length 0 but not necessarily the ‘correct’ dimension.

If the calls to `FUN` return vectors of different lengths, `apply` returns a list of length `prod(dim(X)[MARGIN])` with `dim` set to `MARGIN` if this has length greater than one.

In all cases the result is coerced by `as.vector` to one of the basic vector types before the dimensions are set, so that (for example) factor results will be coerced to a character array.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[lapply](#), [tapply](#), and convenience functions [sweep](#) and [aggregate](#).



**Examples**

```
## Compute row and column sums for a matrix:
x <- cbind(x1 = 3, x2 = c(4:1, 2:5))
dimnames(x)[[1]] <- letters[1:8]
apply(x, 2, mean, trim = .2)
col.sums <- apply(x, 2, sum)
row.sums <- apply(x, 1, sum)
rbind(cbind(x, Rtot = row.sums), Ctot = c(col.sums, sum(col.sums)))

stopifnot( apply(x, 2, is.vector) )

## Sort the columns of a matrix
apply(x, 2, sort)

##- function with extra args:
cave <- function(x, c1, c2) c(mean(x[c1]), mean(x[c2]))
apply(x,1, cave, c1="x1", c2=c("x1","x2"))

ma <- matrix(c(1:4, 1, 6:8), nrow = 2)
ma
apply(ma, 1, table) #--> a list of length 2
apply(ma, 1, stats::quantile)# 5 x n matrix with rownames

stopifnot(dim(ma) == dim(apply(ma, 1:2, sum)))

## Example with different lengths for each call
z <- array(1:24, dim=2:4)
zseq <- apply(z, 1:2, function(x) seq_len(max(x)))
zseq ## a 2 x 3 matrix
typeof(zseq) ## list
dim(zseq) ## 2 3
zseq[1,]
apply(z, 3, function(x) seq_len(max(x)))
# a list without a dim attribute
```

---

args

*Argument List of a Function*

---

**Description**

Displays the argument names and corresponding default values of a function or primitive.

**Usage**

```
args(name)
```

**Arguments**

name                    a function (a closure or a primitive). If name is a character string then the function with that name is found and used.

**Details**

This function is mainly used interactively to print the argument list of a function. For programming, consider using [formals](#) instead.

**Value**

For a closure, a closure with identical formal argument list but an empty (NULL) body.

For a primitive, a closure with the documented usage and NULL body. Note that some primitives do not make use of named arguments and match by position rather than name.

NULL in case of a non-function.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[formals](#), [help](#).

**Examples**

```
args(c)
args(graphics::plot.default)
```

---

Arithmetic

*Arithmetic Operators*

---

**Description**

These binary operators perform arithmetic on numeric or complex vectors (or objects which can be coerced to them).

**Usage**

```
x + y
x - y
x * y
x / y
x ^ y
x %% y
x %/% y
```

**Arguments**

*x*, *y*            numeric or complex vectors or objects which can be coerced to such, or other objects for which methods have been written.

**Details**

The binary arithmetic operators are generic functions: methods can be written for them individually or via the [Ops](#) group generic function. (See [Ops](#) for how dispatch is computed.)

If applied to arrays the result will be an array if this is sensible (for example it will not if the recycling rule has been invoked).

Logical vectors will be coerced to integer or numeric vectors, FALSE having value zero and TRUE having value one.

$1 \wedge y$  and  $y \wedge 0$  are 1, *always*.  $x \wedge y$  should also give the proper limit result when either argument is infinite (i.e., +- `Inf`).

Objects such as arrays or time-series can be operated on this way provided they are conformable.

For real arguments, `%%` can be subject to catastrophic loss of accuracy if  $x$  is much larger than  $y$ , and a warning is given if this is detected.

`%%` and  $x \% \% y$  can be used for non-integer  $y$ , e.g.  $1 \% \% 0.2$ , but the results are subject to rounding error and so may be platform-dependent. Because the IEC 60059 representation of  $0.2$  is a binary fraction slightly larger than  $0.2$ , the answer to  $1 \% \% 0.2$  should be 4 but most platforms give 5.

## Value

These operators return vectors containing the result of the element by element operations. The elements of shorter vectors are recycled as necessary (with a `warning` when they are recycled only *fractionally*). The operators are `+` for addition, `-` for subtraction, `*` for multiplication, `/` for division and `^` for exponentiation.

`%%` indicates  $x \bmod y$  and `%%` indicates integer division. It is guaranteed that  $x == (x \% \% y) + y * (x \% \% y)$  (up to rounding error) unless  $y == 0$  where the result is `NA_integer_` or `NaN` (depending on the `typeof` of the arguments). See [http://en.wikipedia.org/wiki/Modulo\\_operation](http://en.wikipedia.org/wiki/Modulo_operation) for the rationale.

If either argument is complex the result will be complex, and if one or both arguments are numeric, the result will be numeric. If both arguments are integer, the result of `/` and `^` is numeric and of the other operators integer (with overflow returned as `NA` with a warning).

The rules for determining the attributes of the result are rather complicated. Most attributes are taken from the longer argument, the first if they are of the same length. Names will be copied from the first if it is the same length as the answer, otherwise from the second if that is. For time series, these operations are allowed only if the series are compatible, when the class and `tsp` attribute of whichever is a time series (the same, if both are) are used. For arrays (and an array result) the dimensions and dimnames are taken from first argument if it is an array, otherwise the second.

## S4 methods

These operators are members of the S4 `Arith` group generic, and so methods can be written for them individually as well as for the group generic (or the `Ops` group generic), with arguments `c(e1, e2)`.

## Note

`**` is translated in the parser to `^`, but this was undocumented for many years. It appears as an index entry in Becker *et al* (1988), pointing to the help for `Deprecated` but is not actually mentioned on that page. Even though it has been deprecated in S for 20 years, it was still accepted in 2008.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

`sqrt` for miscellaneous and `Special` for special mathematical functions.

`Syntax` for operator precedence.

`%%*` for matrix multiplication.

**Examples**

```
x <- -1:12
x + 1
2 * x + 3
x %% 2 #-- is periodic
x %/% 5
```

array

*Multi-way Arrays***Description**

Creates or tests for arrays.

**Usage**

```
array(data = NA, dim = length(data), dimnames = NULL)
as.array(x, ...)
is.array(x)
```

**Arguments**

<code>data</code>	a vector (including a list) giving data to fill the array.
<code>dim</code>	the <code>dim</code> attribute for the array to be created, that is a vector of length one or more giving the maximal indices in each dimension.
<code>dimnames</code>	either <code>NULL</code> or the names for the dimensions. This is a list with one component for each dimension, either <code>NULL</code> or a character vector of the length given by <code>dim</code> for that dimension. The list can be named, and the list names will be used as names for the dimensions. If the list is shorter than the number of dimensions, it is extended by <code>NULL</code> s to the length required
<code>x</code>	an R object.
<code>...</code>	additional arguments to be passed to or from methods.

**Details**

An array in R can have one, two or more dimensions. It is simply a vector which is stored with additional [attributes](#) giving the dimensions (attribute "`dim`") and optionally names for those dimensions (attribute "`dimnames`").

A two-dimensional array is the same thing as a [matrix](#).

One-dimensional arrays often look like vectors, but may be handled differently by some functions: [str](#) does distinguish them in recent versions of R.

The "`dim`" attribute is an integer vector of length one or more containing non-negative values: the product of the values must match the length of the array.

The "`dimnames`" attribute is optional: if present it is a list with one component for each dimension, either `NULL` or a character vector of the length given by the element of the "`dim`" attribute for that dimension.

`is.array` is a [primitive](#) function.

**Value**

`array` returns an array with the extents specified in `dim` and naming information in `dimnames`. The values in `data` are taken to be those in the array with the leftmost subscript moving fastest. If there are too few elements in `data` to fill the array, then the elements in `data` are recycled. If `data` has length zero, NA of an appropriate type is used for atomic vectors (0 for raw vectors) and NULL for lists.

`as.array` is a generic function for coercing to arrays. The default method does so by attaching a `dim` attribute to it. It also attaches `dimnames` if `x` has `names`. The sole purpose of this is to make it possible to access the `dim[names]` attribute at a later time.

`is.array` returns TRUE or FALSE depending on whether its argument is an array (i.e., has a `dim` attribute of positive length) or not. It is generic: you can write methods to handle specific classes of objects, see [InternalMethods](#).

**Note**

`is.array` is a [primitive](#) function.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[aperm](#), [matrix](#), [dim](#), [dimnames](#).

**Examples**

```
dim(as.array(letters))
array(1:3, c(2,4)) # recycle 1:3 "2 2/3 times"
#      [,1] [,2] [,3] [,4]
#[1,]  1   3   2   1
#[2,]  2   1   3   2
```

---

as.data.frame                    *Coerce to a Data Frame*

---

**Description**

Functions to check if an object is a data frame, or coerce it if possible.

**Usage**

```
as.data.frame(x, row.names = NULL, optional = FALSE, ...)

## S3 method for class 'character':
as.data.frame(x, ...,
              stringsAsFactors = default.stringsAsFactors())

## S3 method for class 'matrix':
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

```
stringsAsFactors = default.stringsAsFactors())

is.data.frame(x)
```

### Arguments

<code>x</code>	any R object.
<code>row.names</code>	NULL or a character vector giving the row names for the data frame. Missing values are not allowed.
<code>optional</code>	logical. If TRUE, setting row names and converting column names (to syntactic names: see <a href="#">make.names</a> ) is optional.
<code>...</code>	additional arguments to be passed to or from methods.
<code>stringsAsFactors</code>	logical: should the character vector be converted to a factor?

### Details

`as.data.frame` is a generic function with many methods, and users and packages can supply further methods.

If a list is supplied, each element is converted to a column in the data frame. Similarly, each column of a matrix is converted separately. This can be overridden if the object has a class which has a method for `as.data.frame`: two examples are matrices of class `"model.matrix"` (which are included as a single column) and list objects of class `"POSIXlt"` which are coerced to class `"POSIXct"`.

Arrays can be converted to data frames. One-dimensional arrays are treated like vectors and two-dimensional arrays like matrices. Arrays with more than two dimensions are converted to matrices by ‘flattening’ all dimensions after the first and creating suitable column labels.

Character variables are converted to factor columns unless protected by [I](#).

If a data frame is supplied, all classes preceding `"data.frame"` are stripped, and the row names are changed if that argument is supplied.

If `row.names = NULL`, row names are constructed from the names or `dimnames` of `x`, otherwise are the integer sequence starting at one. Few of the methods check for duplicated row names. Names are removed from vector columns unless [I](#).

### Value

`as.data.frame` returns a data frame, normally with all row names `" "` if `optional = TRUE`.

`is.data.frame` returns TRUE if its argument is a data frame (that is, has `"data.frame"` amongst its classes) and FALSE otherwise.

### References

Chambers, J. M. (1992) *Data for models*. Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

### See Also

[data.frame](#), [as.data.frame.table](#) for the `table` method (which has additional arguments if called directly).

---

as.environment      *Coerce to an Environment Object*

---

### Description

Converts a number or a character string to the corresponding environment on the search path.

### Usage

```
as.environment(object)
```

### Arguments

`object`      the object to convert. If it is already an environment, just return it. If it is a number, return the environment corresponding to that position on the search list. If it is a character string, match the string to the names on the search list.

### Value

The corresponding environment object.

### Note

This is a [primitive](#) function.

### Author(s)

John Chambers

### See Also

[environment](#) for creation and manipulation, [search](#).

### Examples

```
as.environment(1) ## the global environment
identical(globalenv(), as.environment(1)) ## is TRUE
try(as.environment("package:stats"))      ## stats need not be loaded
```

---

as.function      *Convert Object to Function*

---

### Description

`as.function` is a generic function which is used to convert objects to functions.

`as.function.default` works on a list `x`, which should contain the concatenation of a formal argument list and an expression or an object of mode "[call](#)" which will become the function body. The function will be defined in a specified environment, by default that of the caller.

## Usage

```
as.function(x, ...)  
  
## Default S3 method:  
as.function(x, envir = parent.frame(), ...)
```

## Arguments

x	object to convert, a list for the default method.
...	additional arguments, depending on object
envir	environment in which the function should be defined

## Value

The desired function.

## Note

For ancient historical reasons, `envir = NULL` uses the global environment rather than the base environment. Please use `envir = globalenv\(\)` instead if this is what you want, as the special handling of `NULL` may change in a future release.

## Author(s)

Peter Dalgaard

## See Also

[function](#); [alist](#) which is handy for the construction of argument lists, etc.

## Examples

```
as.function(alist(a=,b=2,a+b))  
as.function(alist(a=,b=2,a+b))(3)
```

## Description

Functions to manipulate objects of classes "POSIXlt" and "POSIXct" representing calendar dates and times.



**Usage**

```

as.POSIXct(x, tz = "", ...)
as.POSIXlt(x, tz = "", ...)

## S3 method for class 'character':
as.POSIXlt(x, tz = "", format, ...)

## S3 method for class 'numeric':
as.POSIXlt(x, tz = "", origin, ...)

## S3 method for class 'POSIXlt':
as.double(x, ...)

```

**Arguments**

x	An object to be converted.
tz	A timezone specification to be used for the conversion, <i>if one is required</i> . System-specific (see <a href="#">time zones</a> ), but "" is the current timezone, and "GMT" is UTC (Universal Time, Coordinated).
...	further arguments to be passed to or from other methods.
format	character string giving a date-time format as used by <a href="#">strptime</a> .
origin	a date-time object, or something which can be coerced by <code>as.POSIXct(tz="GMT")</code> to such an object.

**Details**

The `as.POSIX*` functions convert an object to one of the two classes used to represent date/times (calendar dates plus time to the nearest second). They can convert a wide variety of objects, including objects of the other class and of classes "Date", "date" (from package [date](#)), "chron" and "dates" (from package [chron](#)) to these classes. Dates without times are treated as being at midnight UTC.

They can also convert character strings of the formats "2001-02-03" and "2001/02/03" optionally followed by white space and a time in the format "14:52" or "14:52:03". (Formats such as "01/02/03" are ambiguous but can be converted via a format specification by [strptime](#).) Fractional seconds are allowed. Alternatively, `format` can be specified for character vectors or factors: if it is not specified and no standard format works for the first non-NA input an error is thrown.

Logical NAs can be converted to either of the classes, but no other logical vectors can be.

The `as.double` method converts "POSIXlt" objects to "POSIXct".

If you are given a numeric time as the number of seconds since an epoch, see the examples.

**Value**

`as.POSIXct` and `as.POSIXlt` return an object of the appropriate class. If `tz` was specified, `as.POSIXlt` will give an appropriate "tzone" attribute.

**Note**

If you want to extract specific aspects of a time (such as the day of the week) just convert it to class "POSIXlt" and extract the relevant component(s) of the list, or if you want a character representation (such as a named day of the week) use `format.POSIXlt` or `format.POSIXct`.

If a timezone is needed and that specified is invalid on your system, what happens is system-specific but it will probably be ignored.

### See Also

[DateTimeClasses](#) for details of the classes; [strptime](#) for conversion to and from character representations. [Sys.timezone](#) for details of the (system-specific)naming of time zones.

### Examples

```
(z <- Sys.time())           # the current datetime, as class "POSIXct"
unclass(z)                  # a large integer
floor(unclass(z)/86400)     # the number of days since 1970-01-01 (UTC)
(z <- as.POSIXlt(Sys.time())) # the current datetime, as class "POSIXlt"
unlist(unclass(z))         # a list shown as a named vector

## suppose we have a time in seconds since 1960-01-01 00:00:00 GMT
z <- 1472562988
# ways to convert this
as.POSIXct(z, origin="1960-01-01")           # local
as.POSIXct(z, origin="1960-01-01", tz="GMT") # in UTC
as.POSIXct(z, origin=ISOdatetime(1960,1,1,0,0,0)) # local
ISOdatetime(1960,1,1,0,0,0) + z              # local

## SPSS dates (R-help 2006-02-16)
z <- c(10485849600, 10477641600, 10561104000, 10562745600)
as.Date(as.POSIXct(z, origin="1582-10-14", tz="GMT"))

as.POSIXlt(Sys.time(), "GMT") # the current time in UTC
## Not run: ## These may not be correct names on your system
as.POSIXlt(Sys.time(), "America/New_York") # in New York
as.POSIXlt(Sys.time(), "EST5EDT")         # alternative.
as.POSIXlt(Sys.time(), "EST" )           # somewhere in Eastern Canada
as.POSIXlt(Sys.time(), "HST")            # in Hawaii
as.POSIXlt(Sys.time(), "Australia/Darwin")

## End(Not run)
```

### Description

Change the class of an object to indicate that it should be treated 'as is'.

### Usage

```
I(x)
```

### Arguments

x                    an object

## Details

Function `I` has two main uses.

- In function `data.frame`. Protecting an object by enclosing it in `I()` in a call to `data.frame` inhibits the conversion of character vectors to factors and the dropping of names, and ensures that matrices are inserted as single columns. `I` can also be used to protect objects which are to be added to a data frame, or converted to a data frame via `as.data.frame`.  
It achieves this by prepending the class "AsIs" to the object's classes. Class "AsIs" has a few of its own methods, including for `[], as.data.frame, print` and `format`.
- In function `formula`. There it is used to inhibit the interpretation of operators such as "+", "-", "\*" and "^" as formula operators, so they are used as arithmetical operators. This is interpreted as a symbol by `terms.formula`.

## Value

A copy of the object with class "AsIs" prepended to the class(es).

## References

Chambers, J. M. (1992) *Linear models*. Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

## See Also

`data.frame`, `formula`

---

assign

*Assign a Value to a Name*

---

## Description

Assign a value to a name in an environment.

## Usage

```
assign(x, value, pos = -1, envir = as.environment(pos),
       inherits = FALSE, immediate = TRUE)
```

## Arguments

<code>x</code>	a variable name, given as a character string. No coercion is done, and the first element of a character vector of length greater than one will be used, with a warning.
<code>value</code>	a value to be assigned to <code>x</code> .
<code>pos</code>	where to do the assignment. By default, assigns into the current environment. See the details for other possibilities.
<code>envir</code>	the <code>environment</code> to use. See the details section.
<code>inherits</code>	should the enclosing frames of the environment be inspected?
<code>immediate</code>	an ignored compatibility feature.

## Details

There are no restrictions on name: it can be a non-syntactic name (see [make.names](#)).

The `pos` argument can specify the environment in which to assign the object in any of several ways: as an integer (the position in the `search` list); as the character string name of an element in the search list; or as an `environment` (including using `sys.frame` to access the currently active function calls). The `envir` argument is an alternative way to specify an environment, but is primarily there for back compatibility.

`assign` does not dispatch assignment methods, so it cannot be used to set elements of vectors, names, attributes, etc.

Note that assignment to an attached list or data frame changes the attached copy and not the original object: see [attach](#) and [with](#).

## Value

This function is invoked for its side effect, which is assigning `value` to the variable `x`. If no `envir` is specified, then the assignment takes place in the currently active environment.

If `inherits` is `TRUE`, enclosing environments of the supplied environment are searched until the variable `x` is encountered. The value is then assigned in the environment in which the variable is encountered (provided that the binding is not locked: see [lockBinding](#): if it is, an error is signaled). If the symbol is not encountered then assignment takes place in the user's workspace (the global environment).

If `inherits` is `FALSE`, assignment takes place in the initial frame of `envir`, unless an existing binding is locked or there is no existing binding and the environment is locked.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[<-](#), [get](#), [exists](#), [environment](#).

## Examples

```
for(i in 1:6) { #-- Create objects 'r.1', 'r.2', ... 'r.6' --
  nam <- paste("r",i, sep=".")
  assign(nam, 1:i)
}
ls(pattern = "^r..$")

##-- Global assignment within a function:
myf <- function(x) {
  innerf <- function(x) assign("Global.res", x^2, envir = .GlobalEnv)
  innerf(x+1)
}
myf(3)
Global.res # 16

a <- 1:4
assign("a[1]", 2)
a[1] == 2 #FALSE
get("a[1]") == 2 #TRUE
```

---

`assignOps`*Assignment Operators*

---

**Description**

Assign a value to a name.

**Usage**

```
x <- value
x <<- value
value -> x
value ->> x
```

```
x = value
```

**Arguments**

<code>x</code>	a variable name (possibly quoted).
<code>value</code>	a value to be assigned to <code>x</code> .

**Details**

There are three different assignment operators: two of them have leftwards and rightwards forms.

The operators `<-` and `=` assign into the environment in which they are evaluated. The operator `<-` can be used anywhere, whereas the operator `=` is only allowed at the top level (e.g., in the complete expression typed at the command prompt) or as one of the subexpressions in a braced list of expressions.

The operators `<<-` and `->>` cause a search to be made through the environment for an existing definition of the variable being assigned. If such a variable is found (and its binding is not locked) then its value is redefined, otherwise assignment takes place in the global environment. Note that their semantics differ from that in the S language, but are useful in conjunction with the scoping rules of R. See ‘The R Language Definition’ manual for further details and examples.

In all the assignment operator expressions, `x` can be a name or an expression defining a part of an object to be replaced (e.g., `z[[1]]`). A syntactic name does not need to be quoted, though it can be (preferably by [backticks](#)).

The leftwards forms of assignment `<- = <<-` group right to left, the other from left to right.

**Value**

value. Thus one can use `a <- b <- c <- 6`.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Chamber, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer (for `=`).

**See Also**

[assign](#), [environment](#).

---

attach

*Attach Set of R Objects to Search Path*

---

**Description**

The database is attached to the R search path. This means that the database is searched by R when evaluating a variable, so objects in the database can be accessed by simply giving their names.

**Usage**

```
attach(what, pos = 2, name = deparse(substitute(what)),
       warn.conflicts = TRUE)
```

**Arguments**

`what` 'database'. This can be a `data.frame` or a `list` or a R data file created with [save](#) or `NULL` or an environment. See also 'Details'.

`pos` integer specifying position in [search\(\)](#) where to attach.

`name` name to use for the attached database.

`warn.conflicts` logical. If `TRUE`, warnings are printed about [conflicts](#) from attaching the database, unless that database contains an object `.conflicts.OK`. A conflict is a function masking a function, or a non-function masking a non-function.

**Details**

When evaluating a variable or function name R searches for that name in the databases listed by [search](#). The first name of the appropriate type is used.

By attaching a data frame (or list) to the search path it is possible to refer to the variables in the data frame by their names alone, rather than as components of the data frame (e.g. in the example below, `height` rather than `women$height`).

By default the database is attached in position 2 in the search path, immediately after the user's workspace and before all previously loaded packages and previously attached databases. This can be altered to attach later in the search path with the `pos` option, but you cannot attach at `pos=1`.

The database is not actually attached. Rather, a new environment is created on the search path and the elements of a list (including columns of a data frame) or objects in a save file or an environment are *copied* into the new environment. If you use `<<-` or [assign](#) to assign to an attached database, you only alter the attached copy, not the original object. (Normal assignment will place a modified version in the user's workspace: see the examples.) For this reason `attach` can lead to confusion.

One useful 'trick' is to use `what = NULL` (or equivalently a length-zero list) to create a new environment on the search path into which objects can be assigned by [assign](#) or [load](#) or [sys.source](#).

Names starting "package:" are reserved for [library](#) and should not be used by end users. The name given for the attached environment will be used by [search](#) and can be used as the argument to [as.environment](#).

There are hooks to attach user-defined table objects of class "UserDefinedDatabase", supported by the Omegahat package **RObjectTables**. See <http://www.omegahat.org/RObjectTables/>.

### Value

The `environment` is returned invisibly with a "name" attribute.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

`library`, `detach`, `search`, `objects`, `environment`, `with`.

### Examples

```
require(utils)

summary(women$height) # refers to variable 'height' in the data frame
attach(women)
summary(height)      # The same variable now available by name
height <- height*2.54 # Don't do this. It creates a new variable
                    # in the user's workspace

find("height")
summary(height)      # The new variable in the workspace
rm(height)
summary(height)      # The original variable.
height <-<- height*25.4 # Change the copy in the attached environment
find("height")
summary(height)      # The changed copy
detach("women")
summary(women$height) # unchanged

## Not run: ## create an environment on the search path and populate it
sys.source("myfuns.R", envir=attach(NULL, name="myfuns"))

## End(Not run)
```

---

attr

*Object Attributes*

---

### Description

Get or set specific attributes of an object.

### Usage

```
attr(x, which, exact = FALSE)
attr(x, which) <- value
```

## Arguments

<code>x</code>	an object whose attributes are to be accessed.
<code>which</code>	a non-empty character string specifying which attribute is to be accessed.
<code>exact</code>	logical: should <code>which</code> be matched exactly?
<code>value</code>	an object, the new value of the attribute, or <code>NULL</code> to remove the attribute.

## Details

These functions provide access to a single attribute of an object. The replacement form causes the named attribute to take the value specified (or create a new attribute with the value given).

The extraction function first looks for an exact match to `which` amongst the attributes of `x`, then (unless `exact = TRUE`) a unique partial match. (Setting `options(warnPartialMatchAttr=TRUE)` causes partial matches to give warnings.)

The replacement function only uses exact matches.

Note that some attributes (namely `class`, `comment`, `dim`, `dimnames`, `names`, `row.names` and `tsp`) are treated specially and have restrictions on the values which can be set. (Note that this is not true of `levels` which should be set for factors via the `levels` replacement function.)

The extractor function allows (and does not match) empty and missing values of `which`: the replacement function does not.

Both are [primitive](#) functions.

## Value

For the extractor, the value of the attribute matched, or `NULL` if no exact match is found and no or more than one partial match is found.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[attributes](#)

## Examples

```
# create a 2 by 5 matrix
x <- 1:10
attr(x, "dim") <- c(2, 5)
```



---

`attributes`*Object Attribute Lists*

---

### Description

These functions access an object's attributes. The first form below returns the object's attribute list. The replacement forms uses the list on the right-hand side of the assignment as the object's attributes (if appropriate).

### Usage

```
attributes(obj)
attributes(obj) <- value
mostattributes(obj) <- value
```

### Arguments

<code>obj</code>	an object
<code>value</code>	an appropriate named list of attributes, or <code>NULL</code> .

### Details

Unlike `attr` it is possible to set attributes on a `NULL` object: it will first be coerced to an empty list.

Note that some attributes (namely `class`, `comment`, `dim`, `dimnames`, `names`, `row.names` and `tsp`) are treated specially and have restrictions on the values which can be set. (Note that this is not true of `levels` which should be set for factors via the `levels` replacement function.)

Attributes are not stored internally as a list and should be thought of as a set and not a vector. They must have unique names (and `NA` is taken as "NA", not a missing value).

Assigning attributes first removes all attributes, then sets any `dim` attribute and then the remaining attributes in the order given: this ensures that setting a `dim` attribute always precedes the `dimnames` attribute.

The `mostattributes` assignment takes special care for the `dim`, `names` and `dimnames` attributes, and assigns them only when valid whereas an `attributes` assignment would give an error if any are not.

The names of a pairlist are not stored as attributes, but are reported as if they were (and can be set by the replacement method for attributes).

Both forms of `attributes` are **primitive** functions.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

`attr`.

## Examples

```
x <- cbind(a=1:3, pi=pi) # simple matrix w/ dimnames
attributes(x)

## strip an object's attributes:
attributes(x) <- NULL
x # now just a vector of length 6

mostattributes(x) <- list(mycomment = "really special", dim = 3:2,
  dimnames = list(LETTERS[1:3], letters[1:5]), names = paste(1:6))
x # dim(), but not {dim}names
```

---

autoload

*On-demand Loading of Packages*

---

## Description

`autoload` creates a promise-to-evaluate autoloader and stores it with name `name` in `.AutoloadEnv` environment. When R attempts to evaluate `name`, `autoloader` is run, the package is loaded and `name` is re-evaluated in the new package's environment. The result is that R behaves as if `file` was loaded but it does not occupy memory.

`.Autoloaded` contains the names of the packages for which autoloading has been promised.

## Usage

```
autoload(name, package, reset = FALSE, ...)
autoloader(name, package, ...)

.AutoloadEnv
.Autoloaded
```

## Arguments

<code>name</code>	string giving the name of an object.
<code>package</code>	string giving the name of a package containing the object.
<code>reset</code>	logical: for internal use by autoloader.
<code>...</code>	other arguments to <code>library</code> .

## Value

This function is invoked for its side-effect. It has no return value.

## See Also

[delayedAssign](#), [library](#)

**Examples**

```

require(stats)
autoload("interpSpline", "splines")
search()
ls("Autoloads")
.Autoloaded

x <- sort(stats::rnorm(12))
y <- x^2
is <- interpSpline(x,y)
search() ## now has splines
detach("package:splines")
search()
is2 <- interpSpline(x,y+x)
search() ## and again
detach("package:splines")

```

backsolve

*Solve an Upper or Lower Triangular System***Description**

Solves a system of linear equations where the coefficient matrix is upper (or ‘right’, ‘R’) or lower (‘left’, ‘L’) triangular.

```

x <- backsolve (R, b) solves  $Rx = b$ , and
x <- forwardsolve (L, b) solves  $Lx = b$ , respectively.

```

**Usage**

```

backsolve(r, x, k=ncol(r), upper.tri=TRUE, transpose=FALSE)
forwardsolve(l, x, k=ncol(l), upper.tri=FALSE, transpose=FALSE)

```

**Arguments**

<code>r, l</code>	an upper (or lower) triangular matrix giving the coefficients for the system to be solved. Values below (above) the diagonal are ignored.
<code>x</code>	a matrix whose columns give the right-hand sides for the equations.
<code>k</code>	The number of columns of <code>r</code> and rows of <code>x</code> to use.
<code>upper.tri</code>	logical; if TRUE (default), the <i>upper triangular</i> part of <code>r</code> is used. Otherwise, the lower one.
<code>transpose</code>	logical; if TRUE, solve $r' * y = x$ for $y$ , i.e., <code>t(r) %*% y == x</code> .

**Value**

The solution of the triangular system. The result will be a vector if `x` is a vector and a matrix if `x` is a matrix.

Note that `forwardsolve(L, b)` is just a wrapper for `backsolve(L, b, upper.tri=FALSE)`.

## References

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- Dongarra, J. J., Bunch, J. R., Moler, C. B. and Stewart, G. W. (1978) *LINPACK Users Guide*. Philadelphia: SIAM Publications.

## See Also

[chol](#), [qr](#), [solve](#).

## Examples

```
## upper triangular matrix 'r':
r <- rbind(c(1,2,3),
           c(0,1,1),
           c(0,0,2))
( y <- backsolve(r, x <- c(8,4,2)) ) # -1 3 1
r %*% y # == x = (8,4,2)
backsolve(r, x, transpose = TRUE) # 8 -12 -5
```

---

basename	<i>Manipulate File Paths</i>
----------	------------------------------

---

## Description

`basename` removes all of the path up to and including the last path separator (if any).

`dirname` returns the part of the path up to but excluding the last path separator, or "." if there is no path separator.

## Usage

```
basename(path)
dirname(path)
```

## Arguments

`path` character vector, containing path names.

## Details

For `dirname` tilde expansion is done: see the description of [path.expand](#).

Trailing path separators are removed before dissecting the path, and for `dirname` any trailing file separators are removed from the result.

On Windows this will accept either `\` or `/` as the path separator, but `dirname` will return a path using `/` (except if a network share, when the leading `\\` will be preserved). Only expect these to be able to handle complete paths, and not for example just a share or a drive.

## Value

A character vector of the same length as `path`. A zero-length input will give a zero-length output with no error.

If an element of `path` is `NA`, so is the result.

**Note**

These are not wrappers for the POSIX system functions of the same names: in particular they do **not** have the special handling of the path "/" and of returning "." for empty strings in `basename`.

**See Also**

`file.path`, `path.expand`.

**Examples**

```
basename(file.path("", "p1", "p2", "p3", c("file1", "file2")))
dirname(file.path("", "p1", "p2", "p3", "filename"))
```

---

Bessel

*Bessel Functions*

---

**Description**

Bessel Functions of integer and fractional order, of first and second kind,  $J_\nu$  and  $Y_\nu$ , and Modified Bessel functions (of first and third kind),  $I_\nu$  and  $K_\nu$ .

**Usage**

```
besselI(x, nu, expon.scaled = FALSE)
besselK(x, nu, expon.scaled = FALSE)
besselJ(x, nu)
besselY(x, nu)
```

**Arguments**

`x` numeric,  $\geq 0$ .

`nu` numeric; The *order* (maybe fractional!) of the corresponding Bessel function.

`expon.scaled` logical; if TRUE, the results are exponentially scaled in order to avoid overflow ( $I_\nu$ ) or underflow ( $K_\nu$ ), respectively.

**Details**

If `expon.scaled = TRUE`,  $e^{-x}I_\nu(x)$ , or  $e^xK_\nu(x)$  are returned.

For  $\nu < 0$ , formulae 9.1.2 and 9.6.2 from Abramowitz & Stegun are applied (which is probably suboptimal), except for `besselK` which is symmetric in `nu`.

**Value**

Numeric vector of the same length of `x` with the (scaled, if `expon.scale=TRUE`) values of the corresponding Bessel function.

**Author(s)**

Original Fortran code: W. J. Cody, Argonne National Laboratory  
 Translation to C and adaption to R: Martin Maechler <maechler@stat.math.ethz.ch.>

**Source**

The C code is a translation of Fortran routines from [http://www.netlib.org/specfun/r\[ijky\]besl](http://www.netlib.org/specfun/r[ijky]besl).

**References**

Abramowitz, M. and Stegun, I. A. (1972) *Handbook of Mathematical Functions*. Dover, New York; Chapter 9: Bessel Functions of Integer Order.

**See Also**

Other special mathematical functions, such as [gamma](#),  $\Gamma(x)$ , and [beta](#),  $B(x)$ .

**Examples**

```
require(graphics)

nus <- c(0:5, 10, 20)

x <- seq(0, 4, length.out = 501)
plot(x, x, ylim = c(0, 6), ylab = "", type = "n",
     main = "Bessel Functions I_nu(x)")
for(nu in nus) lines(x, besselI(x, nu=nu), col = nu+2)
legend(0, 6, legend = paste("nu=", nus), col = nus+2, lwd = 1)

x <- seq(0, 40, length.out = 801); yl <- c(-.8, .8)
plot(x, x, ylim = yl, ylab = "", type = "n",
     main = "Bessel Functions J_nu(x)")
for(nu in nus) lines(x, besselJ(x, nu=nu), col = nu+2)
legend(32, -.18, legend = paste("nu=", nus), col = nus+2, lwd = 1)

## Negative nu's :
xx <- 2:7
nu <- seq(-10, 9, length.out = 2001)
op <- par(lab = c(16, 5, 7))
matplot(nu, t(outer(xx, nu, besselI)), type = "l", ylim = c(-50, 200),
        main = expression(paste("Bessel ", I[nu](x), " for fixed ", x,
                                ", as ", f(nu))),
        xlab = expression(nu))
abline(v=0, col = "light gray", lty = 3)
legend(5, 200, legend = paste("x=", xx), col=seq(xx), lty=seq(xx))
par(op)

x0 <- 2^(-20:10)
plot(x0, x0^-8, log="xy", ylab="", type="n",
     main = "Bessel Functions J_nu(x) near 0\n log - log scale")
for(nu in sort(c(nus, nus+.5)))
  lines(x0, besselJ(x0, nu=nu), col = nu+2)
legend(3, 1e50, legend = paste("nu=", paste(nus, nus+.5, sep=",")),
      col = nus + 2, lwd = 1)

plot(x0, x0^-8, log="xy", ylab="", type="n",
     main = "Bessel Functions K_nu(x) near 0\n log - log scale")
for(nu in sort(c(nus, nus+.5)))
  lines(x0, besselK(x0, nu=nu), col = nu+2)
legend(3, 1e50, legend = paste("nu=", paste(nus, nus+.5, sep=",")),
```

```

        col = nus + 2, lwd = 1)

x <- x[x > 0]
plot(x, x, ylim=c(1e-18, 1e11), log = "y", ylab = "", type = "n",
     main = "Bessel Functions K_nu(x)")
for(nu in nus) lines(x, besselK(x, nu=nu), col = nu+2)
legend(0, 1e-5, legend=paste("nu=", nus), col = nus+2, lwd = 1)

yl <- c(-1.6, .6)
plot(x, x, ylim = yl, ylab = "", type = "n",
     main = "Bessel Functions Y_nu(x)")
for(nu in nus){
  xx <- x[x > .6*nu]
  lines(xx, besselY(xx, nu=nu), col = nu+2)
}
legend(25, -.5, legend = paste("nu=", nus), col = nus+2, lwd = 1)

## negative nu in bessel_Y -- was bogus for a long time
curve(besselY(x, -0.1), 0, 10, ylim = c(-3,1), ylab = '')
for(nu in c(seq(-0.2, -2, by = -0.1)))
  curve(besselY(x, nu), add = TRUE)
title(expression(besselY(x, nu) * " " *
                {nu == list(-0.1, -0.2, ..., -2)}))

```

---

bindenv

*Binding and Environment Adjustments*


---

## Description

These functions represent an experimental interface for adjustments to environments and bindings within environments. They allow for locking environments as well as individual bindings, and for linking a variable to a function.

## Usage

```

lockEnvironment(env, bindings = FALSE)
environmentIsLocked(env)
lockBinding(sym, env)
unlockBinding(sym, env)
bindingIsLocked(sym, env)
makeActiveBinding(sym, fun, env)
bindingIsActive(sym, env)

```

## Arguments

env	an environment.
bindings	logical specifying whether bindings should be locked.
sym	a name object or character string
fun	a function taking zero or one arguments

## Details

The function `lockEnvironment` locks its environment argument, which must be a normal environment (not base). (Locking the base environment and name space may be supported later.) Locking the environment prevents adding or removing variable bindings from the environment. Changing the value of a variable is still possible unless the binding has been locked. The name space environments of packages with name spaces are locked when loaded.

`lockBinding` locks individual bindings in the specified environment. The value of a locked binding cannot be changed. Locked bindings may be removed from an environment unless the environment is locked.

`makeActiveBinding` installs `fun` so that getting the value of `sym` calls `fun` with no arguments, and assigning to `sym` calls `fun` with one argument, the value to be assigned. This allows the implementation of things like C variables linked to R variables and variables linked to databases. It may also be useful for making thread-safe versions of some system globals.

## Value

The `*isLocked` functions return a length-one logical vector. The remaining functions return `NULL`, invisibly.

## Author(s)

Luke Tierney

## Examples

```
# locking environments
e <- new.env()
assign("x", 1, envir = e)
get("x", envir = e)
lockEnvironment(e)
get("x", envir = e)
assign("x", 2, envir = e)
try(assign("y", 2, envir = e)) # error

# locking bindings
e <- new.env()
assign("x", 1, envir = e)
get("x", envir = e)
lockBinding("x", e)
try(assign("x", 2, envir = e)) # error
unlockBinding("x", e)
assign("x", 2, envir = e)
get("x", envir = e)

# active bindings
f <- local( {
  x <- 1
  function(v) {
    if (missing(v))
      cat("get\n")
    else {
      cat("set\n")
      x <<- v
    }
  }
}
```



```

        x
    }
})
makeActiveBinding("fred", f, .GlobalEnv)
bindingIsActive("fred", .GlobalEnv)
fred
fred <- 2
fred

```

---

body

*Access to and Manipulation of the Body of a Function*


---

## Description

Get or set the body of a function.

## Usage

```

body(fun = sys.function(sys.parent()))
body(fun, envir = environment(fun)) <- value

```

## Arguments

<code>fun</code>	a function object, or see ‘Details’.
<code>envir</code>	environment in which the function should be defined.
<code>value</code>	an object, usually a language object: see section ‘Value’.

## Details

For the first form, `fun` can be a character string naming the function to be manipulated, which is searched for from the parent environment. If it is not specified, the function calling `body` is used.

The bodies of all but the simplest are braced expressions, that is calls to `{`: see the ‘Examples’ section for how to create such a call.

## Value

`body` returns the body of the function specified. This is normally a language object, most often a call to `{`, but it can also be an object (e.g. `pi`) to be the return value of the function.

The replacement form sets the body of a function to the object on the right hand side, and (potentially) resets the environment of the function. If `value` is of class `"expression"` the first element is used as the body: any additional elements are ignored, with a warning.

## Note

Prior to R 2.9.0, list values of `value` needed to be supplied as a single-element list of the list: this was undocumented prior to R 2.8.1 so is unlikely to actually occur.

## See Also

[alist](#), [args](#), [function](#).

**Examples**

```
body(body)
f <- function(x) x^5
body(f) <- quote(5^x)
## or equivalently body(f) <- expression(5^x)
f(3) # = 125
body(f)

## creating a multi-expression body
e <- expression(y <- x^2, return(y)) # or a list
body(f) <- as.call(c(as.name("{}"), e))
f
f(8)
```

---

bquote

*Partial substitution in expressions*

---

**Description**

An analogue of the LISP backquote macro. `bquote` quotes its argument except that terms wrapped in `.()` are evaluated in the specified `where` environment.

**Usage**

```
bquote(expr, where = parent.frame())
```

**Arguments**

<code>expr</code>	A language object.
<code>where</code>	An environment.

**Value**

A language object.

**See Also**

[quote](#), [substitute](#)

**Examples**

```
require(graphics)

a <- 2

bquote(a == a)
quote(a == a)

bquote(a == .(a))
substitute(a == A, list(A = a))

plot(1:10, a*(1:10), main = bquote(a == .(a)))
```

```
## to set a function default arg
default <- 1
bquote( function(x, y = .(default)) x+y )
```

---

 browser

*Environment Browser*


---

## Description

Interrupt the execution of an expression and allow the inspection of the environment where `browser` was called from.

## Usage

```
browser(text="", condition=NULL, expr=TRUE, skipCalls=0L)
```

## Arguments

<code>text</code>	a text string that can be retrieved once the browser is invoked.
<code>condition</code>	a condition that can be retrieved once the browser is invoked.
<code>expr</code>	An expression, which if it evaluates to <code>TRUE</code> the debugger will be invoked, otherwise control is returned directly.
<code>skipCalls</code>	how many previous calls to skip when reporting the calling context.

## Details

A call to `browser` can be included in the body of a function. When reached, this causes a pause in the execution of the current expression and allows access to the R interpreter.

The purpose of the `text` and `condition` arguments are to allow helper programs (e.g. external debuggers) to insert specific values here, so that the specific call to `browser` (perhaps its location in a source file) can be identified and special processing can be achieved. The values can be retrieved by calling `browserText` and `browserCondition`.

The purpose of the `expr` argument is to allow for the illusion of conditional debugging. It is an illusion, because execution is always paused at the call to `browser`, but control is only passed to the evaluator described below if `expr` evaluates to `TRUE`. In most cases it is going to be more efficient to use an `if` statement in the calling program, but in some cases using this argument will be simpler.

The `skipCalls` argument should be used when the `browser()` call is nested within another debugging function: it will look further up the call stack to report its location.

At the browser prompt the user can enter commands or R expressions. The commands are

`c` (or just return) exit the browser and continue execution at the next statement.

`cont` synonym for `c`.

`n` enter the step-through debugger. This changes the meaning of `c`: see the documentation for `debug`.

`where` print a stack trace of all active function calls.

`Q` exit the browser and the current evaluation and return to the top-level prompt.

(Leading and trailing whitespace is ignored, except for return).

Anything else entered at the browser prompt is interpreted as an R expression to be evaluated in the calling environment: in particular typing an object name will cause the object to be printed, and `ls()` lists the objects in the calling frame. (If you want to look at an object with a name such as `n`, print it explicitly.)

The number of lines printed for the deparsed call can be limited by setting `options(deparse.max.lines)`.

This is a primitive function but does argument matching in the standard way.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

## See Also

`debug`, and `traceback` for the stack on error. `browserText` for how to retrieve the text and condition.

---

browserText

*Functions to Retrieve Values Supplied by Calls to the Browser*

---

## Description

A call to `browser` can provide context by supplying either a text argument or a condition argument. These functions can be used to retrieve either of these arguments.

## Usage

```
browserText(n=1)
browserCondition(n=1)
browserSetDebug(n=1)
```

## Arguments

`n` The number of contexts to skip over, it must be non-negative.

## Details

Each call to `browser` can supply either a text string or a condition. The functions `browserText` and `browserCondition` provide ways to retrieve those values. Since there can be multiple `browser` contexts active at any time we also support retrieving values from the different contexts. The innermost (most recently initiated) `browser` context is numbered 1 other contexts are numbered sequentially.

`browserSetDebug` provides a mechanism for initiating the browser in one of the calling functions. See `sys.frame` for a more complete discussion of the calling stack. To use `browserSetDebug` you select some calling function, determine how far back it is in the call stack and call `browserSetDebug` with `n` set to that value. Then, by typing `c` at the browser prompt you will cause evaluation to continue, and provided there are no intervening calls to `browser` or other interrupts, control will halt again once evaluation has returned to the closure specified. This is similar to the `up` functionality in `gdb` or the "step out" functionality in other debuggers.

**Value**

`browserText` returns the text, while `browserCondition` returns the condition from the specified browser context.

`browserSetDebug` returns NULL, invisibly.

**Note**

It may be of interest to allow for querying further up the set of browser contexts and this functionality may be added at a later date.

**Author(s)**

R. Gentleman

**See Also**

[browser](#)

---

`builtins`

*Returns the Names of All Built-in Objects*

---

**Description**

Return the names of all the built-in objects. These are fetched directly from the symbol table of the R interpreter.

**Usage**

```
builtins(internal = FALSE)
```

**Arguments**

`internal` a logical indicating whether only 'internal' functions (which can be called via `.Internal`) should be returned.

**Details**

`builtins()` returns an unsorted list of the objects in the symbol table, that is all the objects in the base environment. These are the built-in objects plus any that have been added subsequently when the base package was loaded. It is less confusing to use `ls(baseenv(), all=TRUE)`.

`builtins(TRUE)` returns an unsorted list of the names of internal functions, that is those which can be accessed as `.Internal(foo(args ...))` for `foo` in the list.

**Value**

A character vector.

## Description

Function `by` is an object-oriented wrapper for `tapply` applied to data frames.

## Usage

```
by(data, INDICES, FUN, ..., simplify = TRUE)
```

## Arguments

<code>data</code>	an R object, normally a data frame, possibly a matrix.
<code>INDICES</code>	a factor or a list of factors, each of length <code>nrow(data)</code> .
<code>FUN</code>	a function to be applied to data frame subsets of <code>data</code> .
<code>...</code>	further arguments to <code>FUN</code> .
<code>simplify</code>	logical: see <code>tapply</code> .

## Details

A data frame is split by row into data frames subsetted by the values of one or more factors, and function `FUN` is applied to each subset in turn.

Object `data` will be coerced to a data frame by the default method, *but* if this results in a 1-column data frame, the objects passed to `FUN` are dropped to a subsets of that column. (This was the long-term behaviour, but only documented since R 2.7.0.)

## Value

An object of class "by", giving the results for each subset. This is always a list if `simplify` is false, otherwise a list or array (see `tapply`).

## See Also

`tapply`

## Examples

```
require(stats)
attach(warpbreaks)
by(warpbreaks[, 1:2], tension, summary)
by(warpbreaks[, 1], list(wool = wool, tension = tension), summary)
by(warpbreaks, tension, function(x) lm(breaks ~ wool, data = x))

## now suppose we want to extract the coefficients by group
tmp <- by(warpbreaks, tension, function(x) lm(breaks ~ wool, data = x))
sapply(tmp, coef)

detach("warpbreaks")
```

c

*Combine Values into a Vector or List***Description**

This is a generic function which combines its arguments.

The default method combines its arguments to form a vector. All arguments are coerced to a common type which is the type of the returned value, and all attributes except names are removed.

**Usage**

```
c(..., recursive=FALSE)
```

**Arguments**

<code>...</code>	objects to be concatenated.
<code>recursive</code>	logical. If <code>recursive = TRUE</code> , the function recursively descends through lists (and pairlists) combining all their elements into a vector.

**Details**

The output type is determined from the highest type of the components in the hierarchy `NULL < raw < logical < integer < real < complex < character < list < expression`. Pairlists are treated as lists, but non-vector components (such names and calls) are treated as one-element lists which cannot be unlisted even if `recursive = TRUE`.

`c` is sometimes used for its side effect of removing attributes except names, for example to turn an array into a vector. `as.vector` is a more intuitive way to do this, but also drops names. Note too that methods other than the default are not required to do this (and they will almost certainly preserve a class attribute).

This is a [primitive](#) function.

**Value**

NULL or an expression or a vector of an appropriate mode. (With no arguments the value is NULL.)

**S4 methods**

This function is S4 generic, but with argument list `(x, ..., recursive = FALSE)`.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[unlist](#) and [as.vector](#) to produce attribute-free vectors.

**Examples**

```

c(1,7:9)
c(1:5, 10.5, "next")

## uses with a single argument to drop attributes
x <- 1:4
names(x) <- letters[1:4]
x
c(x)          # has names
as.vector(x) # no names
dim(x) <- c(2,2)
x
c(x)
as.vector(x)

## append to a list:
ll <- list(A = 1, c="C")
## do *not* use
c(ll, d = 1:3) # which is == c(ll, as.list(c(d=1:3)))
## but rather
c(ll, d = list(1:3)) # c() combining two lists

c(list(A=c(B=1)), recursive=TRUE)

c(options(), recursive=TRUE)
c(list(A=c(B=1,C=2), B=c(E=7)), recursive=TRUE)

```

---

call

*Function Calls*


---

**Description**

Create or test for objects of mode "call".

**Usage**

```

call(name, ...)
is.call(x)
as.call(x)

```

**Arguments**

name	a non-empty character string naming the function to be called.
...	arguments to be part of the call.
x	an arbitrary R object.

**Details**

`call` returns an unevaluated function call, that is, an unevaluated expression which consists of the named function applied to the given arguments (`name` must be a quoted string which gives the name of a function to be called). Note that although the call is unevaluated, the arguments ... are evaluated.



call is a primitive, so the first argument is taken as name and the remaining arguments as arguments for the constructed call: if the first argument is named the name must partially match name.

is.call is used to determine whether x is a call (i.e., of mode "call").

Objects of mode "list" can be coerced to mode "call". The first element of the list becomes the function part of the call, so should be a function or the name of one (as a symbol; a quoted string will not do).

All three are [primitive](#) functions. call is 'special': it only evaluates its first argument.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[do.call](#) for calling a function by name and argument list; [Recall](#) for recursive calling of functions; further [is.language](#), [expression](#), [function](#).

## Examples

```
is.call(call) #-> FALSE: Functions are NOT calls

## set up a function call to round with argument 10.5
cl <- call("round", 10.5)
is.call(cl) # TRUE
cl
## such a call can also be evaluated.
eval(cl) # [1] 10

A <- 10.5
call("round", A)          # round(10.5)
call("round", quote(A)) # round(A)
f <- "round"
call(f, quote(A))       # round(A)
## if we want to supply a function we need to use as.call or similar
f <- round
## Not run: call(f, quote(A)) # error: first arg must be character
(g <- as.call(list(f, quote(A)))
eval(g)
## alternatively but less transparently
g <- list(f, quote(A))
mode(g) <- "call"
g
eval(g)
## see also the examples in the help for do.call
```

---

callCC

*Call With Current Continuation*

---

## Description

A downward-only version of Scheme's call with current continuation.

**Usage**

```
callCC(fun)
```

**Arguments**

`fun`                   function of one argument, the exit procedure.

**Details**

`callCC` provides a non-local exit mechanism that can be useful for early termination of a computation. `callCC` calls `fun` with one argument, an *exit function*. The exit function takes a single argument, the intended return value. If the body of `fun` calls the exit function then the call to `callCC` immediately returns, with the value supplied to the exit function as the value returned by `callCC`.

**Author(s)**

Luke Tierney

**Examples**

```
# The following all return the value 1
callCC(function(k) 1)
callCC(function(k) k(1))
callCC(function(k) {k(1); 2})
callCC(function(k) repeat k(1))
```

---

capabilities

*Report Capabilities of this Build of R*

---

**Description**

Report on the optional features which have been compiled into this build of R.

**Usage**

```
capabilities(what = NULL)
```

**Arguments**

`what`                   character vector or NULL, specifying required components. NULL implies that all are required.

**Value**

A named logical vector. Current components are

<code>jpeg</code>	Is the <code>jpeg</code> function operational?
<code>png</code>	Is the <code>png</code> function operational?
<code>tiff</code>	Is the <code>tiff</code> function operational?
<code>tcltk</code>	Is the <code>tcltk</code> package operational? Note that to make use of Tk you will almost always need to check that "X11" is also available.

X11	Are the <a href="#">X11</a> graphics device and the X11-based data editor available? This loads the X11 module if not already loaded, and checks that the default display can be contacted unless a X11 device has already been used.
aqua	Are the <code>R.app</code> GUI components and the <a href="#">quartz</a> function operational? Only on some Mac OS X builds. Note that this is distinct from <code>.Platform\$GUI == "AQUA"</code> , which is true when using the Mac <code>R.app</code> console.
http/ftp	Are <a href="#">url</a> and the internal method for <a href="#">download.file</a> available?
sockets	Are <a href="#">make.socket</a> and related functions available?
libxml	Is there support for integrating <code>libxml</code> with the <code>R</code> event loop?
fifo	are FIFO connections supported?
cledit	Is command-line editing available in the current <code>R</code> session? This is false in non-interactive sessions. It will be true for the command-line interface if <code>readline</code> support has been compiled in and <code>'--no-readline'</code> was <i>not</i> used when <code>R</code> was invoked.
iconv	is internationalization conversion via <a href="#">iconv</a> supported? Always true as from <code>R 2.10.0</code> .
NLS	is there Natural Language Support (for message translations)?
profmem	is there support for memory profiling?
cairo	is there support for <code>type="Cairo"</code> in <a href="#">X11</a> , <a href="#">png</a> , <a href="#">jpeg</a> , <a href="#">tiff</a> and <a href="#">bmp</a> , and for the <a href="#">svg</a> , <a href="#">cairo_pdf</a> and <a href="#">cairo_ps</a> devices?

### Note to Mac OS X users

Capabilities `"jpeg"`, `"png"` and `"tiff"` refer to the X11-based versions of these devices. If `capabilities("aqua")` is true, then these devices with `type="quartz"` will be available, and out-of-the-box will be the default type. Thus for example the `tiff` device will be available if `capabilities("aqua") || capabilities("tiff")` if the defaults are unchanged.

### See Also

[.Platform](#)

### Examples

```
capabilities()

if(!capabilities("http/ftp"))
  warning("internal download.file() is not available")

## See also the examples for 'connections'.
```

---

cat *Concatenate and Print*


---

**Description**

Outputs the objects, concatenating the representations. `cat` performs much less conversion than `print`.

**Usage**

```
cat(... , file = "", sep = " ", fill = FALSE, labels = NULL,
      append = FALSE)
```

**Arguments**

<code>...</code>	R objects (see ‘Details’ for the types of objects allowed).
<code>file</code>	A connection, or a character string naming the file to print to. If "" (the default), <code>cat</code> prints to the standard output connection, the console unless redirected by <code>sink</code> . If it is " <code> cmd</code> ", the output is piped to the command given by ‘ <code>cmd</code> ’, by opening a pipe connection.
<code>sep</code>	a character vector of strings to append after each element.
<code>fill</code>	a logical or (positive) numeric controlling how the output is broken into successive lines. If <code>FALSE</code> (default), only newlines created explicitly by “ <code>\n</code> ” are printed. Otherwise, the output is broken into lines with print width equal to the option <code>width</code> if <code>fill</code> is <code>TRUE</code> , or the value of <code>fill</code> if this is numeric. Non-positive <code>fill</code> values are ignored, with a warning.
<code>labels</code>	character vector of labels for the lines printed. Ignored if <code>fill</code> is <code>FALSE</code> .
<code>append</code>	logical. Only used if the argument <code>file</code> is the name of file (and not a connection or " <code> cmd</code> "). If <code>TRUE</code> output will be appended to <code>file</code> ; otherwise, it will overwrite the contents of <code>file</code> .

**Details**

`cat` is useful for producing output in user-defined functions. It converts its arguments to character vectors, concatenates them to a single character vector, appends the given `sep=` string(s) to each element and then outputs them.

No linefeeds are output unless explicitly requested by “`\n`” or if generated by filling (if argument `fill` is `TRUE` or numeric.)

If `file` is a connection and open for writing it is written from its current position. If it is not open, it is opened for the duration of the call in "`wt`" mode and then closed again.

Currently only `atomic` vectors and `names` are handled, together with `NULL` and other zero-length objects (which produce no output). Character strings are output ‘as is’ (unlike `print.default` which escapes non-printable characters and backslash — use `encodeString` if you want to output encoded strings using `cat`). Other types of R object should be converted (e.g. by `as.character` or `format`) before being passed to `cat`.

`cat` converts numeric/complex elements in the same way as `print` (and not in the same way as `as.character` which is used by the S equivalent), so `options` "`digits`" and "`scipen`" are relevant. However, it uses the minimum field width necessary for each element, rather than the same field width for all elements.

**Value**

None (invisible NULL).

**Note**

If any element of `sep` contains a newline character, it is treated as a vector of terminators rather than separators, an element being output after every vector element *and* a newline after the last. Entries are recycled as needed.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`print`, `format`, and `paste` which concatenates into a string.

**Examples**

```
iter <- stats::rpois(1, lambda=10)
## print an informative message
cat("iteration = ", iter <- iter + 1, "\n")

## 'fill' and label lines:
cat(paste(letters, 100* 1:26), fill = TRUE,
    labels = paste("{", 1:10, "}: ", sep=""))
```

---

cbind

---

*Combine R Objects by Rows or Columns*


---

**Description**

Take a sequence of vector, matrix or data frames arguments and combine by *columns* or *rows*, respectively. These are generic functions with methods for other R classes.

**Usage**

```
cbind(..., deparse.level = 1)
rbind(..., deparse.level = 1)
```

**Arguments**

... vectors or matrices. These can be given as named arguments. Other R objects will be coerced as appropriate: see sections ‘Details’ and ‘Value’. (For the "data.frame" method of `cbind` these can be further arguments to `data.frame` such as `stringsAsFactors`.)

`deparse.level`

integer controlling the construction of labels in the case of non-matrix-like arguments (for the default method):

`deparse.level = 0` constructs no labels; the default, `deparse.level = 1` or `2` constructs labels from the argument names, see the ‘Value’ section below.

## Details

The functions `cbind` and `rbind` are S3 generic, with methods for data frames. The data frame method will be used if at least one argument is a data frame and the rest are vectors or matrices. There can be other methods; in particular, there is one for time series objects. See the section on ‘Dispatch’ for how the method to be used is selected.

In the default method, all the vectors/matrices must be atomic (see `vector`) or lists. Expressions are not allowed. Language objects (such as formulae and calls) and pairlists will be coerced to lists: other objects (such as names and external pointers) will be included as elements in a list result. Any classes the inputs might have are discarded (in particular, factors are replaced by their internal codes).

If there are several matrix arguments, they must all have the same number of columns (or rows) and this will be the number of columns (or rows) of the result. If all the arguments are vectors, the number of columns (rows) in the result is equal to the length of the longest vector. Values in shorter arguments are recycled to achieve this length (with a `warning` if they are recycled only *fractionally*).

When the arguments consist of a mix of matrices and vectors the number of columns (rows) of the result is determined by the number of columns (rows) of the matrix arguments. Any vectors have their values recycled or subsetted to achieve this length.

For `cbind` (`rbind`), vectors of zero length (including `NULL`) are ignored unless the result would have zero rows (columns), for S compatibility. (Zero-extent matrices do not occur in S3 and are not ignored in R.)

## Value

For the default method, a matrix combining the . . . arguments column-wise or row-wise. (Exception: if there are no inputs or all the inputs are `NULL`, the value is `NULL`.)

The type of a matrix result determined from the highest type of any of the inputs in the hierarchy `raw < logical < integer < real < complex < character < list`.

For `cbind` (`rbind`) the column (row) names are taken from the `colnames` (`rownames`) of the arguments if these are matrix-like. Otherwise from the names of the arguments or where those are not supplied and `deparse.level > 0`, by deparsing the expressions given, for `deparse.level = 1` only if that gives a sensible name (a ‘symbol’, see `is.symbol`).

For `cbind` row names are taken from the first argument with appropriate names: `rownames` for a matrix, or names for a vector of length the number of rows of the result.

For `rbind` column names are taken from the first argument with appropriate names: `colnames` for a matrix, or names for a vector of length the number of columns of the result.

## Data frame methods

The `cbind` data frame method is just a wrapper for `data.frame(..., check.names = FALSE)`. This means that it will split matrix columns in data frame arguments, and convert character columns to factors unless `stringsAsFactors = FALSE` is specified.

The `rbind` data frame method first drops all zero-column and zero-row arguments. (If that leaves none, it returns the first argument with columns otherwise a zero-column zero-row data frame.) It then takes the classes of the columns from the first data frame, and matches columns by name (rather than by position). Factors have their levels expanded as necessary (in the order of the levels of the levelsets of the factors encountered) and the result is an ordered factor if and only if all the components were ordered factors. (The last point differs from S-PLUS.) Old-style categories (integer vectors with levels) are promoted to factors.

## Dispatch

The method dispatching is *not* done via `UseMethod()`, but by C-internal dispatching. Therefore there is no need for, e.g., `rbind.default`.

The dispatch algorithm is described in the source file (`'.../src/main/bind.c'`) as

1. For each argument we get the list of possible class memberships from the class attribute.
2. We inspect each class in turn to see if there is an applicable method.
3. If we find an applicable method we make sure that it is identical to any method determined for prior arguments. If it is identical, we proceed, otherwise we immediately drop through to the default code.

If you want to combine other objects with data frames, it may be necessary to coerce them to data frames first. (Note that this algorithm can result in calling the data frame method if all the arguments are either data frames or vectors, and this will result in the coercion of character vectors to factors.)

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

`c` to combine vectors (and lists) as vectors, `data.frame` to combine vectors and matrices as a data frame.

## Examples

```
m <- cbind(1, 1:7) # the '1' (= shorter vector) is recycled
m
m <- cbind(m, 8:14)[, c(1, 3, 2)] # insert a column
m
cbind(1:7, diag(3))# vector is subset -> warning

cbind(0, rbind(1, 1:3))
cbind(I=0, X=rbind(a=1, b=1:3)) # use some names
xx <- data.frame(I=rep(0,2))
cbind(xx, X=rbind(a=1, b=1:3)) # named differently

cbind(0, matrix(1, nrow=0, ncol=4))#> Warning (making sense)
dim(cbind(0, matrix(1, nrow=2, ncol=0)))#-> 2 x 1

## deparse.level
dd <- 10
rbind(1:4, c=2, "a++" = 10, dd, deparse.level=0)# middle 2 rownames
rbind(1:4, c=2, "a++" = 10, dd, deparse.level=1)# 3 rownames (default)
rbind(1:4, c=2, "a++" = 10, dd, deparse.level=2)# 4 rownames
```

---

char.expand	<i>Expand a String with Respect to a Target Table</i>
-------------	---

---

**Description**

Seeks a unique match of its first argument among the elements of its second. If successful, it returns this element; otherwise, it performs an action specified by the third argument.

**Usage**

```
char.expand(input, target, nomatch = stop("no match"))
```

**Arguments**

input	a character string to be expanded.
target	a character vector with the values to be matched against.
nomatch	an R expression to be evaluated in case expansion was not possible.

**Details**

This function is particularly useful when abbreviations are allowed in function arguments, and need to be uniquely expanded with respect to a target table of possible values.

**Value**

A length-one character vector, one of the elements of `target` (unless `nomatch` is changed to be a non-error, when it can be a zero-length character string).

**See Also**

[charmatch](#) and [pmatch](#) for performing partial string matching.

**Examples**

```
locPars <- c("mean", "median", "mode")
char.expand("me", locPars, warning("Could not expand!"))
char.expand("mo", locPars)
```

---

character	<i>Character Vectors</i>
-----------	--------------------------

---

**Description**

Create or test for objects of type "character".

**Usage**

```
character(length = 0)
as.character(x, ...)
is.character(x)
```



**Arguments**

length	desired length.
x	object to be coerced or tested.
...	further arguments passed to or from other methods.

**Details**

`as.character` and `is.character` are generic: you can write methods to handle specific classes of objects, see [InternalMethods](#). Further, for `as.character` the default method calls `as.vector`, so dispatch is first on methods for `as.character` and then for methods for `as.vector`.

`as.character` represents real and complex numbers to 15 significant digits (technically the compiler's setting of the ISO C constant `DBL_DIG`, which will be 15 on machines supporting IEC60559 arithmetic according to the C99 standard). This ensures that all the digits in the result will be reliable (and not the result of representation error), but does mean that conversion to character and back to numeric may change the number. If you want to convert numbers to character with the maximum possible precision, use [format](#).

**Value**

`character` creates a character vector of the specified length. The elements of the vector are all equal to "".

`as.character` attempts to coerce its argument to character type; like `as.vector` it strips attributes including names. For lists it deparses the elements individually, except that it extracts the first element of length-one character vectors.

`is.character` returns `TRUE` or `FALSE` depending on whether its argument is of character type or not.

**Note**

`as.character` truncates components of language objects to 500 characters (was about 70 before 1.3.1).

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[paste](#), [substr](#) and [strsplit](#) for character concatenation and splitting, [chartr](#) for character translation and casefolding (e.g., upper to lower case) and [sub](#), [grep](#) etc for string matching and substitutions. Note that `help.search(keyword = "character")` gives even more links.

[deparse](#), which is normally preferable to `as.character` for language objects.

**Examples**

```
form <- y ~ a + b + c
as.character(form) ## length 3
deparse(form)      ## like the input

a0 <- 11/999      # has a repeating decimal representation
```

```
(a1 <- as.character(a0))
format(a0, digits=16) # shows one more digit
a2 <- as.numeric(a1)
a2 - a0                # normally around -1e-17
as.character(a2)       # normally different from a1
print(c(a0, a2), digits = 16)
```

---

charmatch

*Partial String Matching*


---

## Description

charmatch seeks matches for the elements of its first argument among those of its second.

## Usage

```
charmatch(x, table, nomatch = NA_integer_)
```

## Arguments

x	the values to be matched: converted to a character vector by <a href="#">as.character</a> .
table	the values to be matched against: converted to a character vector.
nomatch	the (integer) value to be returned at non-matching positions.

## Details

Exact matches are preferred to partial matches (those where the value to be matched has an exact match to the initial part of the target, but the target is longer).

If there is a single exact match or no exact match and a unique partial match then the index of the matching value is returned; if multiple exact or multiple partial matches are found then 0 is returned and if no match is found then `nomatch` is returned.

NA values are treated as the string constant "NA".

## Value

An integer vector of the same length as `x`, giving the indices of the elements in `table` which matched, or `nomatch`.

## Author(s)

This function is based on a C function written by Terry Therneau.

## See Also

[pmatch](#), [match](#).

[grep](#) or [regexpr](#) for more general (regexp) matching of strings.

## Examples

```
charmatch("", "") # returns 1
charmatch("m", c("mean", "median", "mode")) # returns 0
charmatch("med", c("mean", "median", "mode")) # returns 2
```

**Description**

Translate characters in character vectors, in particular from upper to lower case or vice versa.

**Usage**

```
chartr(old, new, x)
tolower(x)
toupper(x)
casefold(x, upper = FALSE)
```

**Arguments**

<code>x</code>	a character vector, or an object that can be coerced to character by <a href="#">as.character</a> .
<code>old</code>	a character string specifying the characters to be translated. If a character vector of length 2 or more is supplied, the first element is used with a warning.
<code>new</code>	a character string specifying the translations. If a character vector of length 2 or more is supplied, the first element is used with a warning.
<code>upper</code>	logical: translate to upper or lower case?.

**Details**

`chartr` translates each character in `x` that is specified in `old` to the corresponding character specified in `new`. Ranges are supported in the specifications, but character classes and repeated characters are not. If `old` contains more characters than `new`, an error is signaled; if it contains fewer characters, the extra characters at the end of `new` are ignored.

`tolower` and `toupper` convert upper-case characters in a character vector to lower-case, or vice versa. Non-alphabetic characters are left unchanged.

`casefold` is a wrapper for `tolower` and `toupper` provided for compatibility with S-PLUS.

**Value**

A character vector of the same length and with the same attributes as `x` (after possible coercion).

Elements of the result will have the encoding declared as that of the current locale (see [Encoding](#) if the corresponding input had a declared encoding and the current locale is either Latin-1 or UTF-8. The result will be in the current locale's encoding unless the corresponding input was in UTF-8, when it will be in UTF-8 when the system has Unicode wide characters.

**See Also**

[sub](#) and [gsub](#) for other substitutions in strings.

**Examples**

```

x <- "MiXeD cAsE 123"
chartr("iXs", "why", x)
chartr("a-cX", "D-Fw", x)
tolower(x)
toupper(x)

## "Mixed Case" Capitalizing - toupper( every first letter of a word ) :

.simpleCap <- function(x) {
  s <- strsplit(x, " ")[[1]]
  paste(toupper(substring(s, 1,1)), substring(s, 2),
        sep=" ", collapse=" ")
}
.simpleCap("the quick red fox jumps over the lazy brown dog")
## -> [1] "The Quick Red Fox Jumps Over The Lazy Brown Dog"

## and the better, more sophisticated version:
capwords <- function(s, strict = FALSE) {
  cap <- function(s) paste(toupper(substring(s,1,1)),
                          {s <- substring(s,2); if(strict) tolower(s) else s},
                          sep = " ", collapse = " ")
  sapply(strsplit(s, split = " "), cap, USE.NAMES = !is.null(names(s)))
}
capwords(c("using AIC for model selection"))
## -> [1] "Using AIC For Model Selection"
capwords(c("using AIC", "for MODEL selection"), strict=TRUE)
## -> [1] "Using Aic" "For Model Selection"
##          ^^^      ^^^^^
##          'bad'   'good'

## -- Very simple insecure crypto --
rot <- function(ch, k = 13) {
  p0 <- function(...) paste(c(...), collapse="")
  A <- c(letters, LETTERS, " ")
  I <- seq_len(k); chartr(p0(A), p0(c(A[-I], A[I])), ch)
}

pw <- "my secret pass phrase"
(cryp <- rot(pw, 13)) #-> you can send this off

## now ``decrypt`` :
rot(cryp, 54 - 13) # -> the original:
stopifnot(identical(pw, rot(cryp, 54 - 13)))

```

**Description**

Compute the Choleski factorization of a real symmetric positive-definite square matrix.

**Usage**

```
chol(x, ...)  
  
## Default S3 method:  
chol(x, pivot = FALSE, LINPACK = pivot, ...)
```

**Arguments**

<code>x</code>	an object for which a method exists. The default method applies to real symmetric, positive-definite matrices.
<code>...</code>	arguments to be based to or from methods.
<code>pivot</code>	Should pivoting be used?
<code>LINPACK</code>	logical. Should LINPACK be used in the non-pivoting case (for compatibility with R < 1.7.0)?

**Details**

`chol` is generic: the description here applies to the default method.

This is an interface to the LAPACK routine DPOTRF and the LINPACK routines DPOFA and DCHDC.

Note that only the upper triangular part of `x` is used, so that  $R'R = x$  when `x` is symmetric.

If `pivot = FALSE` and `x` is not non-negative definite an error occurs. If `x` is positive semi-definite (i.e., some zero eigenvalues) an error will also occur, as a numerical tolerance is used.

If `pivot = TRUE`, then the Choleski decomposition of a positive semi-definite `x` can be computed. The rank of `x` is returned as `attr(Q, "rank")`, subject to numerical errors. The pivot is returned as `attr(Q, "pivot")`. It is no longer the case that `t(Q) %*% Q` equals `x`. However, setting `pivot <- attr(Q, "pivot")` and `oo <- order(pivot)`, it is true that `t(Q[, oo]) %*% Q[, oo]` equals `x`, or, alternatively, `t(Q) %*% Q` equals `x[pivot, pivot]`. See the examples.

**Value**

The upper triangular factor of the Choleski decomposition, i.e., the matrix  $R$  such that  $R'R = x$  (see example).

If pivoting is used, then two additional attributes `"pivot"` and `"rank"` are also returned.

**Warning**

The code does not check for symmetry.

If `pivot = TRUE` and `x` is not non-negative definite then there will be a warning message but a meaningless result will occur. So only use `pivot = TRUE` when `x` is non-negative definite by construction.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Dongarra, J. J., Bunch, J. R., Moler, C. B. and Stewart, G. W. (1978) *LINPACK Users Guide*. Philadelphia: SIAM Publications.

Anderson, E. and ten others (1999) *LAPACK Users' Guide*. Third Edition. SIAM.

Available on-line at [http://www.netlib.org/lapack/lug/lapack\\_lug.html](http://www.netlib.org/lapack/lug/lapack_lug.html).

**See Also**

[chol2inv](#) for its *inverse* (without pivoting), [backsolve](#) for solving linear systems with upper triangular left sides.

[qr](#), [svd](#) for related matrix factorizations.

**Examples**

```
( m <- matrix(c(5,1,1,3),2,2) )
( cm <- chol(m) )
t(cm) %*% cm #-- = 'm'
crossprod(cm) #-- = 'm'

# now for something positive semi-definite
x <- matrix(c(1:5, (1:5)^2), 5, 2)
x <- cbind(x, x[, 1] + 3*x[, 2])
m <- crossprod(x)
qr(m)$rank # is 2, as it should be

# chol() may fail, depending on numerical rounding:
# chol() unlike qr() does not use a tolerance.
try(chol(m))

(Q <- chol(m, pivot = TRUE)) # NB wrong rank here - see Warning section.
## we can use this by
pivot <- attr(Q, "pivot")
crossprod(Q[, order(pivot)]) # recover m

## now for a non-positive-definite matrix
( m <- matrix(c(5,-5,-5,3),2,2) )
try(chol(m)) # fails
try(chol(m, LINPACK=TRUE)) # fails
(Q <- chol(m, pivot = TRUE)) # warning
crossprod(Q) # not equal to m
```

---

chol2inv

*Inverse from Choleski (or QR) Decomposition*


---

**Description**

Invert a symmetric, positive definite square matrix from its Choleski decomposition. Equivalently, compute  $(X'X)^{-1}$  from the (*R* part) of the QR decomposition of *X*.

**Usage**

```
chol2inv(x, size = NCOL(x), LINPACK = FALSE)
```

**Arguments**

<code>x</code>	a matrix. The first <code>size</code> columns of the upper triangle contain the Choleski decomposition of the matrix to be inverted.
<code>size</code>	the number of columns of <code>x</code> containing the Choleski decomposition.
<code>LINPACK</code>	logical. Should LINPACK be used (for compatibility with R < 1.7.0)?

**Details**

This is an interface to the LAPACK routine DPOTRI and the LINPACK routine DPODI.

**Value**

The inverse of the matrix whose Choleski decomposition was given.

**References**

Dongarra, J. J., Bunch, J. R., Moler, C. B. and Stewart, G. W. (1978) *LINPACK Users Guide*. Philadelphia: SIAM Publications.

Anderson. E. and ten others (1999) *LAPACK Users' Guide*. Third Edition. SIAM. Available on-line at [http://www.netlib.org/lapack/lug/lapack\\_lug.html](http://www.netlib.org/lapack/lug/lapack_lug.html).

**See Also**

[chol](#), [solve](#).

**Examples**

```
cma <- chol(ma <- cbind(1, 1:3, c(1,3,7)))
ma %*% chol2inv(cma)
```

---

class

*Object Classes*

---

**Description**

R possesses a simple generic function mechanism which can be used for an object-oriented style of programming. Method dispatch takes place based on the class of the first argument to the generic function.

**Usage**

```
class(x)
class(x) <- value
unclass(x)
inherits(x, what, which = FALSE)

oldClass(x)
oldClass(x) <- value
```

**Arguments**

`x` a R object  
`what, value` a character vector naming classes. `value` can also be NULL.  
`which` logical affecting return value: see 'Details'.

## Details

Many R objects have a `class` attribute, a character vector giving the names of the classes from which the object *inherits*. If the object does not have a class attribute, it has an implicit class, "matrix", "array" or the result of `mode(x)` (except that integer vectors have implicit class "integer"). (Functions `oldClass` and `oldClass<-` get and set the attribute, which can also be done directly.)

When a generic function `fun` is applied to an object with class attribute `c("first", "second")`, the system searches for a function called `fun.first` and, if it finds it, applies it to the object. If no such function is found, a function called `fun.second` is tried. If no class name produces a suitable function, the function `fun.default` is used (if it exists). If there is no class attribute, the implicit class is tried, then the default method.

The function `class` prints the vector of names of classes an object inherits from. Correspondingly, `class<-` sets the classes an object inherits from. Assigning a zero-length vector or `NULL` removes the class attribute.

`unclass` returns (a copy of) its argument with its class attribute removed. (It is not allowed for objects which cannot be copied, namely environments and external pointers.)

`inherits` indicates whether its first argument inherits from any of the classes specified in the `what` argument. If `which` is `TRUE` then an integer vector of the same length as `what` is returned. Each element indicates the position in the `class(x)` matched by the element of `what`; zero indicates no match. If `which` is `FALSE` then `TRUE` is returned by `inherits` if any of the names in `what` match with any class.

All but `inherits` are [primitive](#) functions.

## Formal classes

An additional mechanism of *formal* classes is available in packages **methods** which is attached by default. For objects which have a formal class, its name is returned by `class` as a character vector of length one.

The replacement version of the function sets the class to the value provided. For classes that have a formal definition, directly replacing the class this way is strongly deprecated. The expression `as(object, value)` is the way to coerce an object to a particular class.

The analogue of `inherits` for formal classes is `is`.

## Note

Functions `oldClass` and `oldClass<-` behave in the same way as functions of those names in S-PLUS 5/6, *but* in R `UseMethod` dispatches on the class as returned by `class` (with some interpolated classes: see the link) rather than `oldClass`. *However*, [group generics](#) dispatch on the `oldClass` for efficiency, and [internal generics](#) only dispatch on objects for which `is.object` is true.

## See Also

[UseMethod](#), [NextMethod](#), [‘group generic’](#), [‘internal generic’](#)

## Examples

```
x <- 10
class(x) # "numeric"
oldClass(x) # NULL
inherits(x, "a") #FALSE
```



```
class(x) <- c("a", "b")
inherits(x, "a") #TRUE
inherits(x, "a", TRUE) # 1
inherits(x, c("a", "b", "c"), TRUE) # 1 2 0
```

---

col

*Column Indexes*

---

## Description

Returns a matrix of integers indicating their column number in a matrix-like object, or a factor of column labels.

## Usage

```
col(x, as.factor = FALSE)
```

## Arguments

<code>x</code>	a matrix-like object, that is one with a two-dimensional <code>dim</code> .
<code>as.factor</code>	a logical value indicating whether the value should be returned as a factor of column labels (created if necessary) rather than as numbers.

## Value

An integer (or factor) matrix with the same dimensions as `x` and whose  $i$   $j$ -th element is equal to  $j$  (or the  $j$ -th column label).

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[row](#) to get rows.

## Examples

```
# extract an off-diagonal of a matrix
ma <- matrix(1:12, 3, 4)
ma[row(ma) == col(ma) + 1]

# create an identity 5-by-5 matrix
x <- matrix(0, nrow = 5, ncol = 5)
x[row(x) == col(x)] <- 1
```

---

Colon

*Colon Operator*

---

### Description

Generate regular sequences.

### Usage

```
from:to  
a:b
```

### Arguments

from	starting value of sequence.
to	(maximal) end value of the sequence.
a, b	<code>factors</code> of same length.

### Details

The binary operator `:` has two meanings: for factors `a:b` is equivalent to `interaction(a, b)` (but the levels are ordered and labelled differently).

For numeric arguments `from:to` is equivalent to `seq(from, to)`, and generates a sequence from `from` to `to` in steps of 1 or 1-. Value `to` will be included if it differs from `from` by an integer up to a numeric fuzz of about  $1e-7$ .

### Value

For numeric arguments, a numeric vector. This will be of type `integer` if `from` is integer-valued and the result is representable in the integer type, otherwise of type `"double"` (aka `mode "numeric"`).

For factors, an unordered factor with levels labelled as `1a:1b` and ordered lexicographically (that is, `1b` varies fastest).

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.  
(for numeric arguments: S does not have `:` for factors.)

### See Also

`seq`.

As an alternative to using `:` for factors, `interaction`.

For `:` used in the formal representation of an interaction, see `formula`.

**Examples**

```

1:4
pi:6 # real
6:pi # integer

f1 <- gl(2,3); f1
f2 <- gl(3,2); f2
f1:f2 # a factor, the "cross"  f1 x f2

```

---

colSums

*Form Row and Column Sums and Means*


---

**Description**

Form row and column sums and means for numeric arrays.

**Usage**

```

colSums(x, na.rm = FALSE, dims = 1)
rowSums(x, na.rm = FALSE, dims = 1)
colMeans(x, na.rm = FALSE, dims = 1)
rowMeans(x, na.rm = FALSE, dims = 1)

```

**Arguments**

x	an array of two or more dimensions, containing numeric, complex, integer or logical values, or a numeric data frame.
na.rm	logical. Should missing values (including NaN) be omitted from the calculations?
dims	integer: Which dimensions are regarded as ‘rows’ or ‘columns’ to sum over. For <code>row*</code> , the sum or mean is over dimensions <code>dims+1, ...</code> ; for <code>col*</code> it is over dimensions <code>1:dims</code> .

**Details**

These functions are equivalent to use of `apply` with `FUN = mean` or `FUN = sum` with appropriate margins, but are a lot faster. As they are written for speed, they blur over some of the subtleties of NaN and NA. If `na.rm = FALSE` and either NaN or NA appears in a sum, the result will be one of NaN or NA, but which might be platform-dependent.

**Value**

A numeric or complex array of suitable size, or a vector if the result is one-dimensional. The `dimnames` (or `names` for a vector result) are taken from the original array.

If there are no values in a range to be summed over (after removing missing values with `na.rm = TRUE`), that component of the output is set to 0 (`*Sums`) or NA (`*Means`), consistent with `sum` and `mean`.

**See Also**

[apply](#), [rowsum](#)

**Examples**

```
## Compute row and column sums for a matrix:
x <- cbind(x1 = 3, x2 = c(4:1, 2:5))
rowSums(x); colSums(x)
dimnames(x)[[1]] <- letters[1:8]
rowSums(x); colSums(x); rowMeans(x); colMeans(x)
x[] <- as.integer(x)
rowSums(x); colSums(x)
x[] <- x < 3
rowSums(x); colSums(x)
x <- cbind(x1 = 3, x2 = c(4:1, 2:5))
x[3, ] <- NA; x[4, 2] <- NA
rowSums(x); colSums(x); rowMeans(x); colMeans(x)
rowSums(x, na.rm = TRUE); colSums(x, na.rm = TRUE)
rowMeans(x, na.rm = TRUE); colMeans(x, na.rm = TRUE)

## an array
dim(UCBAdmissions)
rowSums(UCBAdmissions); rowSums(UCBAdmissions, dims = 2)
colSums(UCBAdmissions); colSums(UCBAdmissions, dims = 2)

## complex case
x <- cbind(x1 = 3 + 2i, x2 = c(4:1, 2:5) - 5i)
x[3, ] <- NA; x[4, 2] <- NA
rowSums(x); colSums(x); rowMeans(x); colMeans(x)
rowSums(x, na.rm = TRUE); colSums(x, na.rm = TRUE)
rowMeans(x, na.rm = TRUE); colMeans(x, na.rm = TRUE)
```

---

commandArgs

*Extract Command Line Arguments*


---

**Description**

Provides access to a copy of the command line arguments supplied when this R session was invoked.

**Usage**

```
commandArgs(trailingOnly = FALSE)
```

**Arguments**

`trailingOnly` logical. Should only arguments after ‘--args’ be returned?

**Details**

These arguments are captured before the standard R command line processing takes place. This means that they are the unmodified values. This is especially useful with the ‘--args’ command-line flag to R, as all of the command line after that flag is skipped.

**Value**

A character vector containing the name of the executable and the user-supplied command line arguments. The first element is the name of the executable by which R was invoked. The exact form of this element is platform dependent: it may be the fully qualified name, or simply the last component (or basename) of the application, or for an embedded R it can be anything the programmer supplied.

If `trailingOnly = TRUE`, a character vector of those arguments (if any) supplied after `--args`.

**See Also**

[Startup BATCH](#)

**Examples**

```
commandArgs()
## Spawn a copy of this application as it was invoked,
## subject to shell quoting issues
## system(paste(commandArgs(), collapse=" "))
```

---

comment

*Query or Set a 'Comment' Attribute*

---

**Description**

These functions set and query a *comment* attribute for any R objects. This is typically useful for [data.frames](#) or model fits.

Contrary to other [attributes](#), the `comment` is not printed (by `print` or `print.default`).

Assigning `NULL` or a zero-length character vector removes the comment.

**Usage**

```
comment(x)
comment(x) <- value
```

**Arguments**

<code>x</code>	any R object
<code>value</code>	a character vector, or <code>NULL</code> .

**See Also**

[attributes](#) and [attr](#) for other attributes.

**Examples**

```
x <- matrix(1:12, 3, 4)
comment(x) <- c("This is my very important data from experiment #0234",
               "Jun 5, 1998")
x
comment(x)
```

## Description

Binary operators which allow the comparison of values in atomic vectors.

## Usage

```
x < y
x > y
x <= y
x >= y
x == y
x != y
```

## Arguments

`x`, `y` atomic vectors, symbols, calls, or other objects for which methods have been written.

## Details

The binary comparison operators are generic functions: methods can be written for them individually or via the [Ops](#) group generic function. (See [Ops](#) for how dispatch is computed.)

Comparison of strings in character vectors is lexicographic within the strings using the collating sequence of the locale in use: see [locales](#). The collating sequence of locales such as 'en\_US' is normally different from 'C' (which should use ASCII) and can be surprising. Beware of making *any* assumptions about the collation order: e.g. in Estonian Z comes between S and T, and collation is not necessarily character-by-character – in Danish aa sorts as a single letter, after z. In Welsh ng may or may not be a single sorting unit: if it is it follows g. Some platforms may not respect the locale and always sort in numerical order of the bytes in an 8-bit locale, or in Unicode point order for a UTF-8 locale (and may not sort in the same order for the same language in different character sets). Collation of non-letters (spaces, punctuation signs, hyphens, fractions and so on) is even more problematic.

Character strings can be compared with different marked encodings (see [Encoding](#)): they are translated to UTF-8 before comparison.

At least one of `x` and `y` must be an atomic vector, but if the other is a list `R` attempts to coerce it to the type of the atomic vector: this will succeed if the list is made up of elements of length one that can be coerced to the correct type.

If the two arguments are atomic vectors of different types, one is coerced to the type of the other, the (decreasing) order of precedence being character, complex, numeric, integer, logical and raw.

Missing values ([NA](#)) and [NaN](#) values are regarded as non-comparable even to themselves, so comparisons involving them will always result in [NA](#). Missing values can also result when character strings are compared and one is not valid in the current collation locale.

Language objects such as symbols and calls are deparsed to character strings before comparison.

**Value**

A logical vector indicating the result of the element by element comparison. The elements of shorter vectors are recycled as necessary.

Objects such as arrays or time-series can be compared this way provided they are conformable.

**S4 methods**

These operators are members of the S4 `Compare` group generic, and so methods can be written for them individually as well as for the group generic (or the `Ops` group generic), with arguments `c(e1, e2)`.

**Note**

Do not use `==` and `!=` for tests, such as in `if` expressions, where you must get a single `TRUE` or `FALSE`. Unless you are absolutely sure that nothing unusual can happen, you should use the `identical` function instead.

For numerical and complex values, remember `==` and `!=` do not allow for the finite representation of fractions, nor for rounding error. Using `all.equal` with `identical` is almost always preferable. See the examples.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Collation of character strings is a complex topic. For an introduction see [http://en.wikipedia.org/wiki/Collating\\_sequence](http://en.wikipedia.org/wiki/Collating_sequence). The *Unicode Collation Algorithm* (<http://unicode.org/reports/tr10/>) is likely to be increasingly influential. Where available R makes use of ICU (<http://site.icu-project.org/> for collation).

**See Also**

`factor` for the behaviour with factor arguments.

`Syntax` for operator precedence.

`icuSetCollate` to tune the string collation algorithm when ICU is in use.

**Examples**

```
x <- stats::rnorm(20)
x < 1
x[x > 0]

x1 <- 0.5 - 0.3
x2 <- 0.3 - 0.1
x1 == x2 # FALSE on most machines
identical(all.equal(x1, x2), TRUE) # TRUE everywhere

z <- c(32:126, 160:255) # range of most 8-bit charsets, Latin-1 in Unicode
x <- if (110n_info()$MBCS) {
  intToUtf8(z, multiple = TRUE)
} else rawToChar(as.raw(z), multiple= TRUE)
## by number
writeLines(strwrap(paste(x, collapse=" "), width = 60))
```

```
## by locale collation
writeLines(strwrap(paste(sort(x), collapse=" "), width = 60))
```

---

complex	<i>Complex Vectors</i>
---------	------------------------

---

## Description

Basic functions which support complex arithmetic in R.

## Usage

```
complex(length.out = 0, real = numeric(), imaginary = numeric(),
         modulus = 1, argument = 0)
as.complex(x, ...)
is.complex(x)
```

```
Re(z)
Im(z)
Mod(z)
Arg(z)
Conj(z)
```

## Arguments

length.out	numeric. Desired length of the output vector, inputs being recycled as needed.
real	numeric vector.
imaginary	numeric vector.
modulus	numeric vector.
argument	numeric vector.
x	an object, probably of mode <code>complex</code> .
z	an object of mode <code>complex</code> , or one of a class for which a methods has been defined.
...	further arguments passed to or from other methods.

## Details

Complex vectors can be created with `complex`. The vector can be specified either by giving its length, its real and imaginary parts, or modulus and argument. (Giving just the length generates a vector of complex zeroes.)

`as.complex` attempts to coerce its argument to be of complex type: like `as.vector` it strips attributes including names. All forms of NA and NaN are coerced to a complex NA, for which both the real and imaginary parts are NA.

Note that `is.complex` and `is.numeric` are never both TRUE.

The functions `Re`, `Im`, `Mod`, `Arg` and `Conj` have their usual interpretation as returning the real part, imaginary part, modulus, argument and complex conjugate for complex values. The modulus and argument are also called the *polar coordinates*. If  $z = x + iy$  with real  $x$  and  $y$ , for  $r = \text{Mod}(z) = \sqrt{x^2 + y^2}$ , and  $\phi = \text{Arg}(z)$ ,  $x = r * \cos(\phi)$  and  $y = r * \sin(\phi)$ . They are all [internal](#)



**generic primitive** functions: methods can be defined for them individually or *via* the `Complex` group generic.

In addition, the elementary trigonometric, logarithmic, exponential, square root and hyperbolic functions are implemented for complex values.

### S4 methods

`as.complex` is primitive and can have S4 methods set.

`Re`, `Im`, `Mod`, `Arg` and `Conj` constitute the S4 group generic `Complex` and so S4 methods can be set for them individually or via the group generic.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### Examples

```
require(graphics)

0i ^ (-3:3)

matrix(1i^ (-6:5), nrow=4) #- all columns are the same
0 ^ 1i # a complex NaN

## create a complex normal vector
z <- complex(real = stats::rnorm(100), imaginary = stats::rnorm(100))
## or also (less efficiently):
z2 <- 1:2 + 1i*(8:9)

## The Arg(.) is an angle:
zz <- (rep(1:4,len=9) + 1i*(9:1))/10
zz.shift <- complex(modulus = Mod(zz), argument= Arg(zz) + pi)
plot(zz, xlim=c(-1,1), ylim=c(-1,1), col="red", asp = 1,
     main = expression(paste("Rotation by ", " ", pi == 180^o)))
abline(h=0,v=0, col="blue", lty=3)
points(zz.shift, col="orange")
```

---

conditions

*Condition Handling and Recovery*

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### Description

These functions provide a mechanism for handling unusual conditions, including errors and warnings.

### Usage

```
tryCatch(expr, ..., finally)
withCallingHandlers(expr, ...)

signalCondition(cond)
```

```

simpleCondition(message, call = NULL)
simpleError      (message, call = NULL)
simpleWarning   (message, call = NULL)
simpleMessage   (message, call = NULL)

## S3 method for class 'condition':
as.character(x, ...)
## S3 method for class 'error':
as.character(x, ...)
## S3 method for class 'condition':
print(x, ...)
## S3 method for class 'restart':
print(x, ...)

conditionCall(c)
## S3 method for class 'condition':
conditionCall(c)
conditionMessage(c)
## S3 method for class 'condition':
conditionMessage(c)

withRestarts(expr, ...)

computeRestarts(cond = NULL)
findRestart(name, cond = NULL)
invokeRestart(r, ...)
invokeRestartInteractively(r)

isRestart(x)
restartDescription(r)
restartFormals(r)

.signalSimpleWarning(msg, call)
.handleSimpleError(h, msg, call)

```

### Arguments

<code>c</code>	a condition object.
<code>call</code>	call expression.
<code>cond</code>	a condition object.
<code>expr</code>	expression to be evaluated.
<code>finally</code>	expression to be evaluated before returning or exiting.
<code>h</code>	function.
<code>message</code>	character string.
<code>msg</code>	character string.
<code>name</code>	character string naming a restart.
<code>r</code>	restart object.
<code>x</code>	object.
<code>...</code>	additional arguments; see details below.

## Details

The condition system provides a mechanism for signaling and handling unusual conditions, including errors and warnings. Conditions are represented as objects that contain information about the condition that occurred, such as a message and the call in which the condition occurred. Currently conditions are S3-style objects, though this may eventually change.

Conditions are objects inheriting from the abstract class `condition`. Errors and warnings are objects inheriting from the abstract subclasses `error` and `warning`. The class `simpleError` is the class used by `stop` and all internal error signals. Similarly, `simpleWarning` is used by `warning`, and `simpleMessage` is used by `message`. The constructors by the same names take a string describing the condition as argument and an optional call. The functions `conditionMessage` and `conditionCall` are generic functions that return the message and call of a condition.

Conditions are signaled by `signalCondition`. In addition, the `stop` and `warning` functions have been modified to also accept condition arguments.

The function `tryCatch` evaluates its expression argument in a context where the handlers provided in the `...` argument are available. The `finally` expression is then evaluated in the context in which `tryCatch` was called; that is, the handlers supplied to the current `tryCatch` call are not active when the `finally` expression is evaluated.

Handlers provided in the `...` argument to `tryCatch` are established for the duration of the evaluation of `expr`. If no condition is signaled when evaluating `expr` then `tryCatch` returns the value of the expression.

If a condition is signaled while evaluating `expr` then established handlers are checked, starting with the most recently established ones, for one matching the class of the condition. When several handlers are supplied in a single `tryCatch` then the first one is considered more recent than the second. If a handler is found then control is transferred to the `tryCatch` call that established the handler, the handler found and all more recent handlers are disestablished, the handler is called with the condition as its argument, and the result returned by the handler is returned as the value of the `tryCatch` call.

Calling handlers are established by `withCallingHandlers`. If a condition is signaled and the applicable handler is a calling handler, then the handler is called by `signalCondition` in the context where the condition was signaled but with the available handlers restricted to those below the handler called in the handler stack. If the handler returns, then the next handler is tried; once the last handler has been tried, `signalCondition` returns `NULL`.

User interrupts signal a condition of class `interrupt` that inherits directly from class `condition` before executing the default interrupt action.

Restarts are used for establishing recovery protocols. They can be established using `withRestarts`. One pre-established restart is an `abort` restart that represents a jump to top level.

`findRestart` and `computeRestarts` find the available restarts. `findRestart` returns the most recently established restart of the specified name. `computeRestarts` returns a list of all restarts. Both can be given a condition argument and will then ignore restarts that do not apply to the condition.

`invokeRestart` transfers control to the point where the specified restart was established and calls the restart's handler with the arguments, if any, given as additional arguments to `invokeRestart`. The restart argument to `invokeRestart` can be a character string, in which case `findRestart` is used to find the restart.

New restarts for `withRestarts` can be specified in several ways. The simplest is in `name=function` form where the function is the handler to call when the restart is invoked. Another simple variant is as `name=string` where the string is stored in the `description` field of

the restart object returned by `findRestart`; in this case the handler ignores its arguments and returns `NULL`. The most flexible form of a restart specification is as a list that can include several fields, including `handler`, `description`, and `test`. The `test` field should contain a function of one argument, a condition, that returns `TRUE` if the restart applies to the condition and `FALSE` if it does not; the default function returns `TRUE` for all conditions.

One additional field that can be specified for a restart is `interactive`. This should be a function of no arguments that returns a list of arguments to pass to the restart handler. The list could be obtained by interacting with the user if necessary. The function `invokeRestartInteractively` calls this function to obtain the arguments to use when invoking the restart. The default `interactive` method queries the user for values for the formal arguments of the handler function.

`.signalSimpleWarning` and `.handleSimpleError` are used internally and should not be called directly.

## References

The `tryCatch` mechanism is similar to Java error handling. Calling handlers are based on Common Lisp and Dylan. Restarts are based on the Common Lisp restart mechanism.

## See Also

`stop` and `warning` signal conditions, and `try` is essentially a simplified version of `tryCatch`.

## Examples

```
tryCatch(1, finally=print("Hello"))
e <- simpleError("test error")
## Not run:
  stop(e)
  tryCatch(stop(e), finally=print("Hello"))
  tryCatch(stop("fred"), finally=print("Hello"))

## End(Not run)
tryCatch(stop(e), error = function(e) e, finally=print("Hello"))
tryCatch(stop("fred"), error = function(e) e, finally=print("Hello"))
withCallingHandlers({ warning("A"); 1+2 }, warning = function(w) {})
## Not run:
  { withRestarts(stop("A"), abort = function() {}); 1 }

## End(Not run)
withRestarts(invokeRestart("foo", 1, 2), foo = function(x, y) {x + y})
```

## Description

`conflicts` reports on objects that exist with the same name in two or more places on the `search` path, usually because an object in the user's workspace or a package is masking a system object of the same name. This helps discover unintentional masking.

**Usage**

```
conflicts(where = search(), detail = FALSE)
```

**Arguments**

where	A subset of the search path, by default the whole search path.
detail	If TRUE, give the masked or masking functions for all members of the search path.

**Value**

If `detail=FALSE`, a character vector of masked objects. If `detail=TRUE`, a list of character vectors giving the masked or masking objects in that member of the search path. Empty vectors are omitted.

**Examples**

```
lm <- 1:3
conflicts(, TRUE)
## gives something like
# $.GlobalEnv
# [1] "lm"
#
# $package:base
# [1] "lm"

## Remove things from your "workspace" that mask others:
remove(list = conflicts(detail=TRUE)$GlobalEnv)
```

---

connections

*Functions to Manipulate Connections*

---

**Description**

Functions to create, open and close connections.

**Usage**

```
file(description = "", open = "", blocking = TRUE,
      encoding = getOption("encoding"), raw = FALSE)

url(description, open = "", blocking = TRUE,
     encoding = getOption("encoding"))

gzfile(description, open = "", encoding = getOption("encoding"),
       compression = 6)

bzfile(description, open = "", encoding = getOption("encoding"),
       compression = 9)

xzfile(description, open = "", encoding = getOption("encoding"),
       compression = 6)
```

```

unz(description, filename, open = "",
      encoding = getOption("encoding"))

pipe(description, open = "", encoding = getOption("encoding"))

fifo(description, open = "", blocking = FALSE,
      encoding = getOption("encoding"))

socketConnection(host = "localhost", port, server = FALSE,
                 blocking = FALSE, open = "a+",
                 encoding = getOption("encoding"))

open(con, ...)
## S3 method for class 'connection':
open(con, open = "r", blocking = TRUE, ...)

close(con, ...)
## S3 method for class 'connection':
close(con, type = "rw", ...)

flush(con)

isOpen(con, rw = "")
isIncomplete(con)

```

### Arguments

<code>description</code>	character string. A description of the connection: see ‘Details’.
<code>open</code>	character. A description of how to open the connection (if it should be opened initially). See section ‘Modes’ for possible values.
<code>blocking</code>	logical. See the ‘Blocking’ section.
<code>encoding</code>	The name of the encoding to be used. See the ‘Encoding’ section.
<code>raw</code>	logical. If true, a ‘raw’ interface is used which will be more suitable for arguments which are not regular files, e.g. character devices. This suppresses the check for a compressed file when opening for text-mode reading, and asserts that the ‘file’ may not be seekable.
<code>compression</code>	integer in 0–9. The amount of compression to be applied when writing, from none to maximal available. For <code>xzfile</code> can also be negative: see the ‘Compression’ section.
<code>filename</code>	a filename within a zip file.
<code>host</code>	character. Host name for port.
<code>port</code>	integer. The TCP port number.
<code>server</code>	logical. Should the socket be a client or a server?
<code>con</code>	a connection.
<code>type</code>	character. Currently ignored.
<code>rw</code>	character. Empty or "read" or "write", partial matches allowed.
<code>...</code>	arguments passed to or from other methods.

## Details

The first nine functions create connections. By default the connection is not opened (except for `socketConnection`), but may be opened by setting a non-empty value of argument `open`.

For `file` the description is a path to the file to be opened or a complete URL (when it is the same as calling `url`), or "" (the default) or `"clipboard"` (see the ‘Clipboard’ section). Use `"stdin"` to refer to the C-level ‘standard input’ of the process (which need not be connected to anything in a console or embedded version of R), provided the C99 function `fdopen` is supported on the platform. (See also `stdin()` for the subtly different R-level concept of `stdin`.)

For `url` the description is a complete URL, including scheme (such as `'http://'`, `'ftp://'` or `'file://'`). Proxies can be specified for HTTP and FTP `url` connections: see [download.file](#).

For `gzfile` the description is the path to a file compressed by `gzip`: it can also open for reading uncompressed files and (as from R 2.10.0) those compressed by `bzip2`, `xz` or `lzma`.

For `bzfile` the description is the path to a file compressed by `bzip2`.

For `xzfile` the description is the path to a file compressed by `xz` (<http://en.wikipedia.org/wiki/Xz>) or (for reading only) `lzma` (<http://en.wikipedia.org/wiki/LZMA>).

`unz` reads (only) single files within zip files, in binary mode. The description is the full path to the zip file, with `‘.zip’` extension if required.

For `pipe` the description is the command line to be piped to or from.

For `fifo` the description is the path of the fifo. (Windows does not have fifos, so attempts to use this function there are an error.)

All platforms support `file`, `gzfile`, `bzfile`, `xzfile` `unz` and `url("file://")` connections. The other types may be partially implemented or not implemented at all. (They do work on most Unix platforms, and all but `fifo` on Windows.)

The intention is that `file` and `gzfile` can be used generally for text input (from files and URLs) and binary input respectively.

`open`, `close` and `seek` are generic functions: the following applies to the methods relevant to connections.

`open` opens a connection. In general functions using connections will open them if they are not open, but then close them again, so to leave a connection open call `open` explicitly.

`close` closes and destroys a connection. This will happen automatically in due course (with a warning) if there is no longer an R object referring to the connection.

A maximum of 128 connections can be allocated (not necessarily open) at any one time. Three of these are pre-allocated (see `stdout`). The OS will impose limits on the numbers of connections of various types, but these are usually larger than 125.

`flush` flushes the output stream of a connection `open` for write/append (where implemented).

If for a `file` or `fifo` connection the description is "", the file/fifo is immediately opened (in "w+" mode unless `open = "w+b"` is specified) and unlinked from the file system. This provides a temporary file/fifo to write to and then read from.

## Value

`file`, `pipe`, `fifo`, `url`, `gzfile`, `bzfile`, `xzfile`, `unz` and `socketConnection` return a connection object which inherits from class `"connection"` and has a first more specific class.

`isOpen` returns a logical value, whether the connection is currently open.

`isIncomplete` returns a logical value, whether last read attempt was blocked, or for an output text connection whether there is unflushed output.

## URLs

A note on 'file://' URLs. The most general form (from RFC1738) is 'file://host/path/to/file', but R only accepts the form with an empty host field referring to the local machine. This is then 'file:///path/to/file', where 'path/to/file' is relative to '/'. So although the third slash is strictly part of the specification not part of the path, this can be regarded as a way to specify the file '/path/to/file'. It is not possible to specify a relative path using a file URL.

No attempt is made to decode an encoded URL: call `URLdecode` if necessary.

Note that 'https://' connections are not supported.

## Modes

Possible values for the argument `open` are

- "r" or "rt" Open for reading in text mode.
- "w" or "wt" Open for writing in text mode.
- "a" or "at" Open for appending in text mode.
- "rb" Open for reading in binary mode.
- "wb" Open for writing in binary mode.
- "ab" Open for appending in binary mode.
- "r+", "r+b" Open for reading and writing.
- "w+", "w+b" Open for reading and writing, truncating file initially.
- "a+", "a+b" Open for reading and appending.

Not all modes are applicable to all connections: for example URLs can only be opened for reading. Only file and socket connections can be opened for both reading and writing.

If a file or fifo is created on a Unix-alike, its permissions will be the maximal allowed by the current setting of `umask` (see `Sys.umask`).

For many connections there is little or no difference between text and binary modes. For file-like connections on Windows, translation of line endings (between LF and CRLF) is done in text mode only (but text read operations on connections such as `readLines`, `scan` and `source` work for any form of line ending). Various R operations are possible in only one of the modes: for example `pushBack` is text-oriented and is only allowed on connections open for reading in text mode, and binary operations such as `readBin`, `load` and `save` operations can only be done on binary-mode connections.

The mode of a connection is determined when actually opened, which is deferred if `open = ""` is given (the default for all but socket connections). An explicit call to `open` can specify the mode, but otherwise the mode will be "r". (`gzipfile`, `bzfile` and `xzfile` connections are exceptions, as the compressed file always has to be opened in binary mode and no conversion of line-endings is done even on Windows, so the default mode is interpreted as "rb".) Most operations that need write access or text-only or binary-only mode will override the default mode of a non-yet-open connection.

## Compression

R has for a long time supported `gzip` and `bzip2` compression, and support for `xz` compression (and read-only support for its precursor `lzma` compression) was added in R 2.10.0.

For reading, the type of compression (if any) can be determined from the first few bytes of the file, and this is exploited as from R 2.10.0. Thus for `file(raw = FALSE)` connections, if



`open` is "", "r" or "rt" the connection can read any of the compressed file types as well as uncompressed files. (Using "rb" will allow compressed files to be read byte-by-byte.) Similarly, `gzfile` connections can read any of the forms of compression and uncompressed files in any read mode.

(The type of compression is determined when the connection is created if `open` is unspecified and a file of that name exists. If the intention is to open the connection to write a file with a *different* form of compression under that name, specify `open = "w"` when the connection is created or `unlink` the file before creating the connection.)

For write-mode connections, `compress` specifies how hard the compressor works to minimize the file size, and higher values need more CPU time and more working memory (up to ca 800Mb for `xzfile(compress = 9)`). For `xzfile` negative values of `compress` correspond to adding the `xz` argument '-e': this takes more time (double?) to compress but may achieve (slightly) better compression. The default (6) has good compression and modest (100Mb memory usage): but if you are using `xz` compression you are probably looking for high compression.

Choosing the type of compression involves tradeoffs: `gzip`, `bzip2` and `xz` are successively less widely supported, need more resources for both compression and decompression, and achieve more compression (although individual files may buck the general trend). Typical experience is that `bzip2` compression is 15% better on text files than `gzip` compression, and `xz` with maximal compression 30% better. The experience with R `save` files is similar, but on some large '.rda' files `xz` compression is much better than the other two. With current computers decompression times even with `compress = 9` are typically modest and reading compressed files is usually faster than uncompressed ones because of the reduction in disc activity.

## Encoding

The encoding of the input/output stream of a connection can be specified by name in the same way as it would be given to `iconv`: see that help page for how to find out what encoding names are recognized on your platform. Additionally, "" and "native.enc" both mean the 'native' encoding, that is the internal encoding of the current locale and hence no translation is done.

Re-encoding only works for connections in text mode.

The encoding "UCS-2LE" is treated specially, as it is the appropriate value for Windows 'Unicode' text files. If the first two bytes are the Byte Order Mark 0xFFFE then these are removed as most implementations of `iconv` do not accept BOMs. Note that some implementations will handle BOMs using encoding "UCS-2" but many will not.

Requesting a conversion that is not supported is an error, reported when the connection is opened. Exactly what happens when the requested translation cannot be done is in general undocumented. On output the result is likely to be that up to the error, with a warning. On input, it will most likely be all or some of the input up to the error.

## Blocking

Whether or not the connection blocks can be specified for file, url (default yes) fifo and socket connections (default not).

In blocking mode, functions using the connection do not return to the R evaluator until the read/write is complete. In non-blocking mode, operations return as soon as possible, so on input they will return with whatever input is available (possibly none) and for output they will return whether or not the write succeeded.

The function `readLines` behaves differently in respect of incomplete last lines in the two modes: see its help page.

Even when a connection is in blocking mode, attempts are made to ensure that it does not block the event loop and hence the operation of GUI parts of R. These do not always succeed, and the whole R process will be blocked during a DNS lookup on Unix, for example.

Most blocking operations on HTTP/FTP URLs and on sockets are subject to the timeout set by `options("timeout")`. Note that this is a timeout for no response, not for the whole operation. The timeout is set at the time the connection is opened (more precisely, when the last connection of that type – ‘http:’, ‘ftp:’ or socket – was opened).

### Fifos

Fifos default to non-blocking. That follows S version 4 and is probably most natural, but it does have some implications. In particular, opening a non-blocking fifo connection for writing (only) will fail unless some other process is reading on the fifo.

Opening a fifo for both reading and writing (in any mode: one can only append to fifos) connects both sides of the fifo to the R process, and provides an similar facility to `file()`.

### Clipboard

`file` can be used with `description = "clipboard"` in mode "r" only. This reads the X11 primary selection (see <http://standards.freedesktop.org/clipboards-spec/clipboards-latest.txt>), which can also be specified as "X11\_primary" and the secondary selection as "X11\_secondary". On most systems the clipboard selection (that used by ‘Copy’ from an ‘Edit’ menu) can be specified as "X11\_clipboard".

When a clipboard is opened for reading, the contents are immediately copied to internal storage in the connection.

Unix users wishing to *write* to one of the selections may be able to do so via `xclip` (<http://sourceforge.net/projects/xclip/>), for example by `pipe("xclip -i", "w")` for the primary selection.

Mac OS X users can use `pipe("pbpaste")` and `pipe("pbcopy", "w")` to read from and write to that system’s clipboard.

### Note

R’s connections are modelled on those in S version 4 (see Chambers, 1998). However R goes well beyond the S model, for example in output text connections and URL, compressed and socket connections.

The default open mode in R is "r" except for socket connections. This differs from S, where it is the equivalent of "r+", known as "\*".

On (rare) platforms where `vsprintf` does not return the needed length of output there is a 100,000 character output limit on the length of line for `fifo`, `gzfile`, `bzfile` and `xzfile` connections: longer lines will be truncated with a warning.

### References

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

### See Also

[textConnection](#), [seek](#), [showConnections](#), [pushBack](#).

Functions making direct use of connections are `readLines`, `readBin`, `readChar`, `writeLines`, `writeBin`, `writeChar`, `cat`, `sink`, `scan`, `parse`, `read.dcf`, `load`, `save`, `dput` and `dump`.

`capabilities` to see if HTTP/FTP url, fifo and `socketConnection` are supported by this build of R.

`gzcon` to wrap gzip (de)compression around a connection.

`memCompress` for more ways to (de)compress and references on data compression.

## Examples

```
zz <- file("ex.data", "w") # open an output file connection
cat("TITLE extra line", "2 3 5 7", "", "11 13 17", file = zz, sep = "\n")
cat("One more line\n", file = zz)
close(zz)
readLines("ex.data")
unlink("ex.data")
```

```
zz <- gzfile("ex.gz", "w") # compressed file
cat("TITLE extra line", "2 3 5 7", "", "11 13 17", file = zz, sep = "\n")
close(zz)
readLines(zz <- gzfile("ex.gz"))
close(zz)
unlink("ex.gz")
```

```
zz <- bzfile("ex.bz2", "w") # bzip2-ed file
cat("TITLE extra line", "2 3 5 7", "", "11 13 17", file = zz, sep = "\n")
close(zz)
print(readLines(zz <- bzfile("ex.bz2")))
close(zz)
unlink("ex.bz2")
```

```
## An example of a file open for reading and writing
Tfile <- file("test1", "w+")
c(isOpen(Tfile, "r"), isOpen(Tfile, "w")) # both TRUE
cat("abc\ndef\n", file=Tfile)
readLines(Tfile)
seek(Tfile, 0, rw="r") # reset to beginning
readLines(Tfile)
cat("ghi\n", file=Tfile)
readLines(Tfile)
close(Tfile)
unlink("test1")
```

```
## We can do the same thing with an anonymous file.
Tfile <- file()
cat("abc\ndef\n", file=Tfile)
readLines(Tfile)
close(Tfile)
```

```
## fifo example -- may fail, e.g. on Cygwin, even with OS support for fifos
if(capabilities("fifo")) {
  zz <- fifo("foo-fifo", "w+")
  writeLines("abc", zz)
  print(readLines(zz))
  close(zz)
  unlink("foo-fifo")
}
```

```

}

## Unix examples of use of pipes

# read listing of current directory
readLines(pipe("ls -l"))

# remove trailing commas. Suppose

## Not run: % cat data2
450, 390, 467, 654, 30, 542, 334, 432, 421,
357, 497, 493, 550, 549, 467, 575, 578, 342,
446, 547, 534, 495, 979, 479
## End(Not run)
# Then read this by
scan(pipe("sed -e s/,,$// data2_"), sep=",")

# convert decimal point to comma in output: see also write.table
# both R strings and (probably) the shell need \ doubled
zz <- pipe(paste("sed s/\\\\. / >", "outfile"), "w")
cat(format(round(stats::rnorm(48), 4)), fill=70, file = zz)
close(zz)
file.show("outfile", delete.file=TRUE)

## example for a machine running a finger daemon

con <- socketConnection(port = 79, blocking = TRUE)
writeLines(paste(system("whoami", intern=TRUE), "\r", sep=""), con)
gsub(" *$", "", readLines(con))
close(con)

## Not run:
## two R processes communicating via non-blocking sockets
# R process 1
con1 <- socketConnection(port = 6011, server=TRUE)
writeLines(LETTERS, con1)
close(con1)

# R process 2
con2 <- socketConnection(Sys.info()["nodename"], port = 6011)
# as non-blocking, may need to loop for input
readLines(con2)
while(isIncomplete(con2)) {Sys.sleep(1); readLines(con2)}
close(con2)

## examples of use of encodings
# write a file in UTF-8
cat(x, file = (con <- file("foo", "w", encoding="UTF-8"))); close(con)
# read a 'Windows Unicode' file
A <- read.table(con <- file("students", encoding="UCS-2LE")); close(con)

## End(Not run)

```

---

Constants

*Built-in Constants*

---

## Description

Constants built into R.

## Usage

```
LETTERS
letters
month.abb
month.name
pi
```

## Details

R has a small number of built-in constants (there is also a rather larger library of data sets which can be loaded with the function [data](#)).

The following constants are available:

- `LETTERS`: the 26 upper-case letters of the Roman alphabet;
- `letters`: the 26 lower-case letters of the Roman alphabet;
- `month.abb`: the three-letter abbreviations for the English month names;
- `month.name`: the English names for the months of the year;
- `pi`: the ratio of the circumference of a circle to its diameter.

These are implemented as variables in the base name space taking appropriate values.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[data](#), [DateTimeClasses](#).

[Quotes](#) for the parsing of character constants, [NumericConstants](#) for numeric constants.

## Examples

```
## John Machin (ca 1706) computed pi to over 100 decimal places
## using the Taylor series expansion of the second term of
pi - 4*(4*atan(1/5) - atan(1/239))

## months in English
month.name
## months in your current locale
format(ISOdate(2000, 1:12, 1), "%B")
format(ISOdate(2000, 1:12, 1), "%b")
```

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contributors	<i>R Project Contributors</i>
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**Description**

The R Who-is-who, describing who made significant contributions to the development of R.

**Usage**

```
contributors()
```

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Control	<i>Control Flow</i>
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---

**Description**

These are the basic control-flow constructs of the R language. They function in much the same way as control statements in any Algol-like language. They are all [reserved](#) words.

**Usage**

```
if(cond) expr
if(cond) cons.expr else alt.expr

for(var in seq) expr
while(cond) expr
repeat expr
break
next
```

**Arguments**

cond	A length-one logical vector that is not NA. Conditions of length greater than one are accepted with a warning, but only the first element is used. Other types are coerced to logical if possible, ignoring any class.
var	A syntactical name for a variable.
seq	An expression evaluating to a vector (including a list and an <a href="#">expression</a> ) or to a <a href="#">pairlist</a> or NULL. A factor value will be coerced to a character vector.
expr, cons.expr, alt.expr	An <i>expression</i> in a formal sense. This is either a simple expression or a so called <i>compound expression</i> , usually of the form { expr1 ; expr2 }.

## Details

`break` breaks out of a `for`, `while` or `repeat` loop; control is transferred to the first statement outside the inner-most loop. `next` halts the processing of the current iteration and advances the looping index. Both `break` and `next` apply only to the innermost of nested loops.

Note that it is a common mistake to forget to put braces (`{ ... }`) around your statements, e.g., after `if(..)` or `for(...)`. In particular, you should not have a newline between `}` and `else` to avoid a syntax error in entering a `if ... else` construct at the keyboard or via `source`. For that reason, one (somewhat extreme) attitude of defensive programming is to always use braces, e.g., for `if` clauses.

The `seq` in a `for` loop is evaluated at the start of the loop; changing it subsequently does not affect the loop. If `seq` has length zero the body of the loop is skipped. Otherwise the variable `var` is assigned in turn the value of each element of `seq`. You can assign to `var` within the body of the loop, but this will not affect the next iteration. When the loop terminates, `var` remains as a variable containing its latest value.

## Value

`if` returns the value of the expression evaluated, or `NULL` invisibly if none was (which may happen if there is no `else`).

`for`, `while` and `repeat` return `NULL` invisibly. `for` sets `var` to the last used element of `seq`, or to `NULL` if it was of length zero.

`break` and `next` do not return a value as they transfer control within the loop.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[Syntax](#) for the basic R syntax and operators, [Paren](#) for parentheses and braces.

[ifelse](#), [switch](#) for other ways to control flow.

## Examples

```
for(i in 1:5) print(1:i)
for(n in c(2,5,10,20,50)) {
  x <- stats::rnorm(n)
  cat(n,":", sum(x^2),"\n")
}
f = factor(sample(letters[1:5], 10, replace=TRUE))
for( i in unique(f) ) print(i)
```

**Description**

These functions provide facilities to manage the extensible list of converters used to translate R objects to C pointers for use in `.C` calls. The number and a description of each element in the list can be retrieved. One can also query and set the activity status of individual elements, temporarily ignoring them. And one can remove individual elements.

**Usage**

```
getNumCConverters()
getCConverterDescriptions()
getCConverterStatus()
setCConverterStatus(id, status)
removeCConverter(id)
```

**Arguments**

<code>id</code>	either a number or a string identifying the element of interest in the converter list. A string is matched against the description strings for each element to identify the element. Integers are specified starting at 1 (rather than 0).
<code>status</code>	a logical value specifying whether the element is to be considered active (TRUE) or not (FALSE).

**Details**

The internal list of converters is potentially used when converting individual arguments in a `.C` call. If an argument has a non-trivial class attribute, we iterate over the list of converters looking for the first that matches. If we find a matching converter, we have it create the C-level pointer corresponding to the R object. When the call to the C routine is complete, we use the same converter for that argument to reverse the conversion and create an R object from the current value in the C pointer. This is done separately for all the arguments.

The functions documented here provide R user-level capabilities for investigating and managing the list of converters. There is currently no mechanism for adding an element to the converter list within the R language. This must be done in C code using the routine `R_addToCConverter()`.

**Value**

`getNumCConverters` returns an integer giving the number of elements in the list, both active and inactive.

`getCConverterDescriptions` returns a character vector containing the description string of each element of the converter list.

`getCConverterStatus` returns a logical vector with a value for each element in the converter list. Each value indicates whether that converter is active (TRUE) or inactive (FALSE). The names of the elements are the description strings returned by `getCConverterDescriptions`.

`setCConverterStatus` returns the logical value indicating the activity status of the specified element before the call to change it took effect. This is TRUE for active and FALSE for inactive.

`removeCConverter` returns TRUE if an element in the converter list was identified and removed. In the case that no such element was found, an error occurs.



**Author(s)**

Duncan Temple Lang

**References**

<http://developer.R-project.org/CObjectConversion.pdf>

**See Also**

[.C](#)

**Examples**

```
getNumCConverters()
getCConverterDescriptions()
getCConverterStatus()
## Not run:
old <- setCConverterStatus(1, FALSE)

setCConverterStatus(1, old)

## End(Not run)
## Not run:
removeCConverter(1)
removeCConverter(getCConverterDescriptions()[1])

## End(Not run)
```

---

copyright

*Copyrights of Files Used to Build R*

---

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---

crossprod                      *Matrix Crossproduct*

---

### Description

Given matrices `x` and `y` as arguments, return a matrix cross-product. This is formally equivalent to (but usually slightly faster than) the call `t(x) %*% y` (`crossprod`) or `x %*% t(y)` (`tcrossprod`).

### Usage

```
crossprod(x, y = NULL)
```

```
tcrossprod(x, y = NULL)
```

### Arguments

`x`, `y`                      numeric or complex matrices: `y = NULL` is taken to be the same matrix as `x`. Vectors are promoted to single-column or single-row matrices, depending on the context.

### Value

A double or complex matrix, with appropriate `dimnames` taken from `x` and `y`.

### Note

When `x` or `y` are not matrices, they are treated as column or row matrices, but their `names` are usually **not** promoted to `dimnames`. Hence, currently, the last example has empty `dimnames`.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

`%*%` and outer product `%O%`.

### Examples

```
(z <- crossprod(1:4))        # = sum(1 + 2^2 + 3^2 + 4^2)
drop(z)                    # scalar
x <- 1:4; names(x) <- letters[1:4]; x
tcrossprod(as.matrix(x)) # is
identical(tcrossprod(as.matrix(x)),
          crossprod(t(x)))
tcrossprod(x)             # no dimnames

m <- matrix(1:6, 2,3) ; v <- 1:3; v2 <- 2:1
stopifnot(identical(tcrossprod(v, m), v %*% t(m)),
          identical(tcrossprod(v, m), crossprod(v, t(m))),
          identical(crossprod(m, v2), t(m) %*% v2))
```

---

`Cstack_info`                      *Report Information on C Stack Size and Usage*

---

### Description

Report information on the C stack size and usage (if available).

### Usage

```
Cstack_info()
```

### Details

On most platforms, C stack information is recorded when R is initialized and used for stack-checking. If this information is unavailable, the `size` will be returned as `NA`, and stack-checking is not performed.

The information on the stack base address is thought to be accurate on Windows, Linux and FreeBSD (including Mac OS X), but a heuristic is used on other platforms. Because this might be slightly inaccurate, the current usage could be estimated as negative. (The heuristic is not used on embedded uses of R on platforms where the stack base is not thought to be accurate.)

### Value

An integer vector. This has named elements

<code>size</code>	The size of the stack (in bytes), or <code>NA</code> if unknown.
<code>current</code>	The estimated current usage (in bytes), possibly <code>NA</code> .
<code>direction</code>	1 (stack grows down, the usual case) or <code>-1</code> (stack grows up).
<code>eval_depth</code>	The current evaluation depth (including two calls for the call to <code>Cstack_info</code> ).

### Examples

```
Cstack_info()
```

---

`cumsum`                              *Cumulative Sums, Products, and Extremes*

---

### Description

Returns a vector whose elements are the cumulative sums, products, minima or maxima of the elements of the argument.

### Usage

```
cumsum(x)
cumprod(x)
cummax(x)
cummin(x)
```

**Arguments**

`x` a numeric or complex (not `cummin` or `cummax`) object, or an object that can be coerced to one of these.

**Details**

These are generic functions: methods can be defined for them individually or via the `Math` group generic.

**Value**

A vector of the same length and type as `x` (after coercion), except that `cumprod` returns a numeric vector for integer input (for consistency with `*`). Names are preserved.

An NA value in `x` causes the corresponding and following elements of the return value to be NA, as does integer overflow in `cumsum` (with a warning).

**S4 methods**

`cumsum` and `cumprod` are S4 generic functions: methods can be defined for them individually or via the `Math` group generic. `cummax` and `cummin` are individually S4 generic functions.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (`cumsum` only.)

**Examples**

```
cumsum(1:10)
cumprod(1:10)
cummin(c(3:1, 2:0, 4:2))
cummax(c(3:1, 2:0, 4:2))
```

---

cut

---

*Convert Numeric to Factor*


---

**Description**

`cut` divides the range of `x` into intervals and codes the values in `x` according to which interval they fall. The leftmost interval corresponds to level one, the next leftmost to level two and so on.

**Usage**

```
cut(x, ...)

## Default S3 method:
cut(x, breaks, labels = NULL,
     include.lowest = FALSE, right = TRUE, dig.lab = 3,
     ordered_result = FALSE, ...)
```

**Arguments**

<code>x</code>	a numeric vector which is to be converted to a factor by cutting.
<code>breaks</code>	either a numeric vector of two or more cut points or a single number (greater than or equal to 2) giving the number of intervals into which <code>x</code> is to be cut.
<code>labels</code>	labels for the levels of the resulting category. By default, labels are constructed using " <code>(a,b]</code> " interval notation. If <code>labels = FALSE</code> , simple integer codes are returned instead of a factor.
<code>include.lowest</code>	logical, indicating if an ' <code>x[i]</code> ' equal to the lowest (or highest, for <code>right = FALSE</code> ) ' <code>breaks</code> ' value should be included.
<code>right</code>	logical, indicating if the intervals should be closed on the right (and open on the left) or vice versa.
<code>dig.lab</code>	integer which is used when labels are not given. It determines the number of digits used in formatting the break numbers.
<code>ordered_result</code>	logical: should the result be an ordered factor?
<code>...</code>	further arguments passed to or from other methods.

**Details**

When `breaks` is specified as a single number, the range of the data is divided into `breaks` pieces of equal length, and then the outer limits are moved away by 0.1% of the range to ensure that the extreme values both fall within the break intervals. (If `x` is a constant vector, equal-length intervals are created that cover the single value.)

If a `labels` parameter is specified, its values are used to name the factor levels. If none is specified, the factor level labels are constructed as "`(b1, b2]`", "`(b2, b3]`" etc. for `right = TRUE` and as "`[b1, b2)`", ...if `right = FALSE`. In this case, `dig.lab` indicates the minimum number of digits should be used in formatting the numbers `b1, b2, ...`. A larger value (up to 12) will be used if needed to distinguish between any pair of endpoints: if this fails labels such as "Range3" will be used.

**Value**

A `factor` is returned, unless `labels = FALSE` which results in the mere integer level codes.

**Note**

Instead of `table(cut(x, br))`, `hist(x, br, plot = FALSE)` is more efficient and less memory hungry. Instead of `cut(*, labels = FALSE)`, `findInterval()` is more efficient.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`split` for splitting a variable according to a group factor; `factor`, `tabulate`, `table`, `findInterval()`.

`quantile` for ways of choosing breaks of roughly equal content (rather than length), `cut2` in package **Hmisc** for a canned way to form quantile groups.

**Examples**

```

Z <- stats::rnorm(10000)
table(cut(Z, breaks = -6:6))
sum(table(cut(Z, breaks = -6:6, labels=FALSE)))
sum(graphics::hist(Z, breaks = -6:6, plot=FALSE)$counts)

cut(rep(1,5),4)##-- dummy
tx0 <- c(9, 4, 6, 5, 3, 10, 5, 3, 5)
x <- rep(0:8, tx0)
stopifnot(table(x) == tx0)

table( cut(x, b = 8))
table( cut(x, breaks = 3*(-2:5)))
table( cut(x, breaks = 3*(-2:5), right = FALSE))

##--- some values OUTSIDE the breaks :
table(cx <- cut(x, breaks = 2*(0:4)))
table(cx1 <- cut(x, breaks = 2*(0:4), right = FALSE))
which(is.na(cx)); x[is.na(cx)] ##-- the first 9 values 0
which(is.na(cx1)); x[is.na(cx1)] ##-- the last 5 values 8

## Label construction:
y <- stats::rnorm(100)
table(cut(y, breaks = pi/3*(-3:3)))
table(cut(y, breaks = pi/3*(-3:3), dig.lab=4))

table(cut(y, breaks = 1*(-3:3), dig.lab=4))
# extra digits don't "harm" here
table(cut(y, breaks = 1*(-3:3), right = FALSE))
#- the same, since no exact INT!

## sometimes the default dig.lab is not enough to be avoid confusion:
aaa <- c(1,2,3,4,5,2,3,4,5,6,7)
cut(aaa, 3)
cut(aaa, 3, dig.lab=4, ordered = TRUE)

## one way to extract the breakpoints
labs <- levels(cut(aaa, 3))
cbind(lower = as.numeric( sub("\\((.+),.*", "\\1", labs) ),
      upper = as.numeric( sub("[^,]*,([^\"]*)\\]", "\\1", labs) ))

```

cut.POSIXt

*Convert a Date or Date-Time Object to a Factor***Description**

Method for `cut` applied to date-time objects.

**Usage**

```

## S3 method for class 'POSIXt':
cut(x, breaks, labels = NULL, start.on.monday = TRUE,
    right = FALSE, ...)

```

```
## S3 method for class 'Date':
cut(x, breaks, labels = NULL, start.on.monday = TRUE,
    right = FALSE, ...)
```

### Arguments

<code>x</code>	an object inheriting from class "POSIXt" or "Date".
<code>breaks</code>	a vector of cut points <i>or</i> number giving the number of intervals which <code>x</code> is to be cut into <i>or</i> an interval specification, one of "sec", "min", "hour", "day", "DSTday", "week", "month", "quarter" or "year", optionally preceded by an integer and a space, or followed by "s". For "Date" objects only "day", "week", "month", "quarter" and "year" are allowed.
<code>labels</code>	labels for the levels of the resulting category. By default, labels are constructed from the left-hand end of the intervals (which are include for the default value of <code>right</code> ). If <code>labels = FALSE</code> , simple integer codes are returned instead of a factor.
<code>start.on.monday</code>	logical. If <code>breaks = "weeks"</code> , should the week start on Mondays or Sundays?
<code>right, ...</code>	arguments to be passed to or from other methods.

### Details

Using both `right = TRUE` and `include.lowest = TRUE` will include both ends of the range of dates.

Using `breaks = "quarter"` will create intervals of 3 calendar months, with the intervals beginning on January 1, April 1, July 1 or October 1, based upon `min(x)` as appropriate.

### Value

A factor is returned, unless `labels = FALSE` which returns the integer level codes.

### See Also

[seq.POSIXt](#), [seq.Date](#), [cut](#)

### Examples

```
## random dates in a 10-week period
cut(ISOdate(2001, 1, 1) + 70*86400*stats::runif(100), "weeks")
cut(as.Date("2001/1/1") + 70*stats::runif(100), "weeks")
```

---

data.class	<i>Object Classes</i>
------------	-----------------------

---

### Description

Determine the class of an arbitrary R object.

### Usage

```
data.class(x)
```

### Arguments

`x` an R object.

### Value

character string giving the *class* of `x`.

The class is the (first element) of the `class` attribute if this is non-NULL, or inferred from the object's `dim` attribute if this is non-NULL, or `mode(x)`.

Simply speaking, `data.class(x)` returns what is typically useful for method dispatching. (Or, what the basic creator functions already and maybe eventually all will attach as a class attribute.)

### Note

For compatibility reasons, there is one exception to the rule above: When `x` is *integer*, the result of `data.class(x)` is "numeric" even when `x` is classed.

### See Also

[class](#)

### Examples

```
x <- LETTERS
data.class(factor(x))           # has a class attribute
data.class(matrix(x, ncol = 13)) # has a dim attribute
data.class(list(x))            # the same as mode(x)
data.class(x)                  # the same as mode(x)

stopifnot(data.class(1:2) == "numeric") # compatibility "rule"
```



---

 data.frame

*Data Frames*


---

### Description

This function creates data frames, tightly coupled collections of variables which share many of the properties of matrices and of lists, used as the fundamental data structure by most of R's modeling software.

### Usage

```
data.frame(..., row.names = NULL, check.rows = FALSE,
           check.names = TRUE,
           stringsAsFactors = default.stringsAsFactors())

default.stringsAsFactors()
```

### Arguments

...	these arguments are of either the form <code>value</code> or <code>tag = value</code> . Component names are created based on the tag (if present) or the deparsed argument itself.
<code>row.names</code>	NULL or a single integer or character string specifying a column to be used as row names, or a character or integer vector giving the row names for the data frame.
<code>check.rows</code>	if TRUE then the rows are checked for consistency of length and names.
<code>check.names</code>	logical. If TRUE then the names of the variables in the data frame are checked to ensure that they are syntactically valid variable names and are not duplicated. If necessary they are adjusted (by <code>make.names</code> ) so that they are.
<code>stringsAsFactors</code>	logical: should character vectors be converted to factors? The 'factory-fresh' default is TRUE, but this can be changed by setting <code>options(stringsAsFactors = FALSE)</code> .

### Details

A data frame is a list of variables of the same number of rows with unique row names, given class "data.frame". If no variables are included, the row names determine the number of rows.

The column names should be non-empty, and attempts to use empty names will have unsupported results. Duplicate column names are allowed, but you need to use `check.names = FALSE` for `data.frame` to generate such a data frame. However, not all operations on data frames will preserve duplicated column names: for example matrix-like subsetting will force column names in the result to be unique.

`data.frame` converts each of its arguments to a data frame by calling `as.data.frame(optional=TRUE)`. As that is a generic function, methods can be written to change the behaviour of arguments according to their classes: R comes with many such methods. Character variables passed to `data.frame` are converted to factor columns unless protected by `I` or argument `stringsAsFactors` is false. If a list or data frame or matrix is passed to `data.frame` it is as if each component or column had been passed as a separate argument (except for matrices of class "model.matrix" and those protected by `I`).

Objects passed to `data.frame` should have the same number of rows, but atomic vectors, factors and character vectors protected by `I` will be recycled a whole number of times if necessary (including as from R 2.9.0, elements of list arguments).

If row names are not supplied in the call to `data.frame`, the row names are taken from the first component that has suitable names, for example a named vector or a matrix with rownames or a data frame. (If that component is subsequently recycled, the names are discarded with a warning.) If `row.names` was supplied as `NULL` or no suitable component was found the row names are the integer sequence starting at one (and such row names are considered to be ‘automatic’, and not preserved by `as.matrix`).

If row names are supplied of length one and the data frame has a single row, the `row.names` is taken to specify the row names and not a column (by name or number).

Names are removed from vector inputs not protected by `I`.

`default.stringsAsFactors` is a utility that takes `getOption("stringsAsFactors")` and ensures the result is `TRUE` or `FALSE` (or throws an error if the value is not `NULL`).

## Value

A data frame, a matrix-like structure whose columns may be of differing types (numeric, logical, factor and character and so on).

How the names of the data frame are created is complex, and the rest of this paragraph is only the basic story. If the arguments are all named and simple objects (not lists, matrices of data frames) then the argument names give the column names. For an unnamed simple argument, a deparsed version of the argument is used as the name (with an enclosing `I(...)` removed). For a named matrix/list/data frame argument with more than one named column, the names of the columns are the name of the argument followed by a dot and the column name inside the argument: if the argument is unnamed, the argument’s column names are used. For a named or unnamed matrix/list/data frame argument that contains a single column, the column name in the result is the column name in the argument. Finally, the names are adjusted to be unique and syntactically valid unless `check.names = FALSE`.

## Note

In versions of R prior to 2.4.0 `row.names` had to be character: to ensure compatibility with such versions of R, supply a character vector as the `row.names` argument.

## References

Chambers, J. M. (1992) *Data for models*. Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

## See Also

`I`, `plot.data.frame`, `print.data.frame`, `row.names`, `names` (for the column names), `[.data.frame` for subsetting methods, `Math.data.frame` etc, about *Group* methods for `data.frames`; `read.table`, `make.names`.

## Examples

```
L3 <- LETTERS[1:3]
(d <- data.frame(cbind(x=1, y=1:10), fac=sample(L3, 10, replace=TRUE)))

## The same with automatic column names:
```

```

data.frame(cbind( 1, 1:10), sample(L3, 10, replace=TRUE))

is.data.frame(d)

## do not convert to factor, using I() :
(dd <- cbind(d, char = I(letters[1:10])))
rbind(class=sapply(dd, class), mode=sapply(dd, mode))

stopifnot(1:10 == row.names(d))# {coercion}

(d0 <- d[, FALSE]) # NULL data frame with 10 rows
(d.0 <- d[FALSE, ]) # <0 rows> data frame (3 cols)
(d00 <- d0[FALSE,]) # NULL data frame with 0 rows

```

---

data.matrix

*Convert a Data Frame to a Numeric Matrix*


---

### Description

Return the matrix obtained by converting all the variables in a data frame to numeric mode and then binding them together as the columns of a matrix. Factors and ordered factors are replaced by their internal codes.

### Usage

```
data.matrix(frame, rownames.force = NA)
```

### Arguments

`frame` a data frame whose components are logical vectors, factors or numeric vectors.  
`rownames.force` logical indicating if the resulting matrix should have character (rather than NULL) `rownames`. The default, NA, uses NULL rownames if the data frame has ‘automatic’ row.names or for a zero-row data frame.

### Details

Logical and factor columns are converted to integers. Any other column which is not numeric (according to `is.numeric`) is converted by `as.numeric` or, for S4 objects, `as(, "numeric")`. If all columns are integer (after conversion) the result is an integer matrix, otherwise a numeric (double) matrix.

### Value

If `frame` inherits from class "data.frame", an integer or numeric matrix of the same dimensions as `frame`, with `dimnames` taken from the `row.names` (or NULL, depending on `rownames.force`) and `names`.

Otherwise, the result of `as.matrix`.

### Note

The default behaviour for data frames differs from R < 2.5.0 which always gave the result character rownames.

## References

Chambers, J. M. (1992) *Data for models*. Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

## See Also

[as.matrix](#), [data.frame](#), [matrix](#).

## Examples

```
DF <- data.frame(a=1:3, b=letters[10:12],
                 c=seq(as.Date("2004-01-01"), by = "week", len = 3),
                 stringsAsFactors = TRUE)
data.matrix(DF[1:2])
data.matrix(DF)
```

---

date

*System Date and Time*

---

## Description

Returns a character string of the current system date and time.

## Usage

```
date()
```

## Value

The string has the form "Fri Aug 20 11:11:00 1999", i.e., length 24, since it relies on POSIX's `ctime` ensuring the above fixed format. Timezone and Daylight Saving Time are taken account of, but *not* indicated in the result.

The day and month abbreviations are always in English, irrespective of locale.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[Sys.Date](#) and [Sys.time](#); [Date](#) and [DateTimeClasses](#) for objects representing date and time.

## Examples

```
(d <- date())
nchar(d) == 24

## something similar in the current locale
format(Sys.time(), "%a %b %d %H:%M:%S %Y")
```

**Description**

Description of the class "Date" representing calendar dates.

**Usage**

```
## S3 method for class 'Date':  
summary(object, digits = 12, ...)
```

**Arguments**

<code>object</code>	An object summarized.
<code>digits</code>	Number of significant digits for the computations.
<code>...</code>	Further arguments to be passed from or to other methods.

**Details**

Dates are represented as the number of days since 1970-01-01, with negative values for earlier dates. They are always printed following the rules of the current Gregorian calendar, even though that calendar was not in use long ago (it was adopted in 1752 in Great Britain and its colonies).

It is intended that the date should be an integer, but this is not enforced in the internal representation. Fractional days will be ignored when printing. It is possible to produce fractional days via the `mean` method or by adding or subtracting (see [Ops.Date](#)).

**See Also**

[Sys.Date](#) for the current date.  
[Ops.Date](#) for operators on "Date" objects.  
[format.Date](#) for conversion to and from character strings.  
[plot.Date](#) and [hist.Date](#) for plotting.  
[weekdays](#) for convenience extraction functions.  
[seq.Date](#), [cut.Date](#), [round.Date](#) for utility operations.  
[DateTimeClasses](#) for date-time classes.

**Examples**

```
(today <- Sys.Date())  
format(today, "%d %b %Y") # with month as a word  
(tenweeks <- seq(today, length.out=10, by="1 week")) # next ten weeks  
weekdays(today)  
months(tenweeks)  
as.Date(.leap.seconds)
```

**Description**

Description of the classes "`POSIX1t`" and "`POSIXct`" representing calendar dates and times (to the nearest second).

**Usage**

```
## S3 method for class 'POSIXct':
print(x, ...)

## S3 method for class 'POSIXct':
summary(object, digits = 15, ...)

time + z
z + time
time - z
time1 lop time2
```

**Arguments**

<code>x</code> , <code>object</code>	An object to be printed or summarized from one of the date-time classes.
<code>digits</code>	Number of significant digits for the computations: should be high enough to represent the least important time unit exactly.
<code>...</code>	Further arguments to be passed from or to other methods.
<code>time</code>	date-time objects
<code>time1</code> , <code>time2</code>	date-time objects or character vectors. (Character vectors are converted by <a href="#">as.POSIXct</a> .)
<code>z</code>	a numeric vector (in seconds)
<code>lop</code>	One of <code>==</code> , <code>!=</code> , <code>&lt;</code> , <code>&lt;=</code> , <code>&gt;</code> or <code>&gt;=</code> .

**Details**

There are two basic classes of date/times. Class "`POSIXct`" represents the (signed) number of seconds since the beginning of 1970 (in the UTC timezone) as a numeric vector. Class "`POSIX1t`" is a named list of vectors representing

```
sec 0-61: seconds
min 0-59: minutes
hour 0-23: hours
mday 1-31: day of the month
mon 0-11: months after the first of the year.
year years since 1900.
yday 0-6 day of the week, starting on Sunday.
yday 0-365: day of the year.
```

`isdst` Daylight Savings Time flag. Positive if in force, zero if not, negative if unknown.

The classes correspond to the POSIX/C99 constructs of ‘calendar time’ (the `time_t` data type) and ‘local time’ (or broken-down time, the `struct tm` data type), from which they also inherit their names. The components of `"POSIXlt"` are integer vectors, except `sec`.

`"POSIXct"` is more convenient for including in data frames, and `"POSIXlt"` is closer to human-readable forms. A virtual class `"POSIXt"` inherits from both of the classes: it is used to allow operations such as subtraction to mix the two classes. Note that `length(x)` is the length of the corresponding (abstract) date/time vector, also in the `"POSIXlt"` case.

Components `wday` and `yday` of `"POSIXlt"` are for information, and are not used in the conversion to calendar time. However, `isdst` is needed to distinguish times at the end of DST: typically 1am to 2am occurs twice, first in DST and then in standard time. At all other times `isdst` can be deduced from the first six values, but the behaviour if it is set incorrectly is platform-dependent.

Logical comparisons and limited arithmetic are available for both classes. One can add or subtract a number of seconds from a date-time object, but not add two date-time objects. Subtraction of two date-time objects is equivalent to using `difftime`. Be aware that `"POSIXlt"` objects will be interpreted as being in the current timezone for these operations, unless a timezone has been specified.

`"POSIXlt"` objects will often have an attribute `"tzone"`, a character vector of length 3 giving the timezone name from the `TZ` environment variable and the names of the base timezone and the alternate (daylight-saving) timezone. Sometimes this may just be of length one, giving the timezone name.

`"POSIXct"` objects may also have an attribute `"tzone"`, a character vector of length one. If set to a non-empty value, it will determine how the object is converted to class `"POSIXlt"` and in particular how it is printed. This is usually desirable, but if you want to specify an object in a particular timezone but to be printed in the current timezone you may want to remove the `"tzone"` attribute (e.g. by `c(x)`).

Unfortunately, the conversion is complicated by the operation of time zones and leap seconds (24 days have been 86401 seconds long so far: the times of the extra seconds are in the object `.leap.seconds`). The details of this are entrusted to the OS services where possible. This always covers the period 1970–2037, and on most machines back to 1902 (when time zones were in their infancy). Outside the platform limits we use our own C code. This uses the offset from GMT in use either for 1902 (when there was no DST) or that predicted for one of 2030 to 2037 (chosen so that the likely DST transition days are Sundays), and uses the alternate (daylight-saving) timezone only if `isdst` is positive or (if `-1`) if DST was predicted to be in operation in the 2030s on that day. (There is no reason to suppose that the DST rules will remain the same in the future, and indeed the US legislated in 2005 to change its rules as from 2007, with a possible future reversion.)

It seems that some rare systems use leap seconds, but most ignore them (as required by POSIX). This is detected and corrected for at build time, so all `"POSIXct"` times used by R do not include leap seconds. (Conceivably this could be wrong if the system has changed since build time, just possibly by changing locales or the ‘zoneinfo’ database.)

Using `c` on `"POSIXlt"` objects converts them to the current time zone, and on `"POSIXct"` objects drops any `"tzone"` attributes (even if they are all marked with the same time zone).

A few times have specific issues. First, the leapseconds are ignored, and real times such as `"2005-12-31 23:59:60"` are (probably) treated as the next second. However, they will never be generated by R, and are unlikely to arise as input. Second, on some OSes there is a problem in the POSIX/C99 standard with `"1969-12-31 23:59:59"`, which is `-1` in calendar time and that value is on those OSes also used as an error code. Thus `as.POSIXct("1969-12-31 23:59:59", format="%Y-%m-%d %H:%M:%S", tz="UTC")` may give NA, and hence `as.POSIXct("1969-12-31 23:59:59", tz="UTC")` will give `"1969-12-31`

23:59:50". Other OSes (including the code used by R on Windows) report errors separately and so are able to handle that time as valid.

### Sub-second Accuracy

Classes "POSIXct" and "POSIXlt" are able to express fractions of a second. (Conversion of fractions between the two forms may not be exact, but will have better than microsecond accuracy.)

Fractional seconds are printed only if `options("digits.secs")` is set: see `strftime`.

### Warning

Some Unix-like systems (especially Linux ones) do not have "TZ" set, yet have internal code that expects it (as does POSIX). We have tried to work around this, but if you get unexpected results try setting "TZ". See `Sys.timezone` for valid settings.

### See Also

`Dates` for dates without times.

`as.POSIXct` and `as.POSIXlt` for conversion between the classes.

`strftime` for conversion to and from character representations.

`Sys.time` for clock time as a "POSIXct" object.

`difftime` for time intervals.

`cut.POSIXt`, `seq.POSIXt`, `round.POSIXt` and `trunc.POSIXt` for methods for these classes.

`weekdays` for convenience extraction functions.

### Examples

```
(z <- Sys.time())           # the current date, as class "POSIXct"

Sys.time() - 3600          # an hour ago

as.POSIXlt(Sys.time(), "GMT") # the current time in GMT
format(.leap.seconds)       # all 24 leapseconds in your timezone
print(.leap.seconds, tz="PST8PDT") # and in Seattle's
```

### Description

Reads or writes an R object from/to a file in Debian Control File format.

### Usage

```
read.dcf(file, fields = NULL, all = FALSE)

write.dcf(x, file = "", append = FALSE,
          indent = 0.1 * getOption("width"),
          width = 0.9 * getOption("width"))
```



**Arguments**

<code>file</code>	either a character string naming a file or a connection. "" indicates output to the console. For <code>read.dcf</code> this can name a compressed file (see <a href="#">gzfile</a> ).
<code>fields</code>	Fields to read from the DCF file. Default is to read all fields.
<code>all</code>	a logical indicating whether in case of multiple occurrences of a field in a record, all these should be gathered. If <code>all</code> is false (default), only the last such occurrence is used.
<code>x</code>	the object to be written, typically a data frame. If not, it is attempted to coerce <code>x</code> to a data frame.
<code>append</code>	logical. If <code>TRUE</code> , the output is appended to the file. If <code>FALSE</code> , any existing file of the name is destroyed.
<code>indent</code>	a positive integer specifying the indentation for continuation lines in output entries.
<code>width</code>	a positive integer giving the target column for wrapping lines in the output.

**Details**

DCF is a simple format for storing databases in plain text files that can easily be directly read and written by humans. DCF is used in various places to store R system information, like descriptions and contents of packages.

The DCF rules as implemented in R are:

1. A database consists of one or more records, each with one or more named fields. Not every record must contain each field. Fields may appear more than once in a record.
2. Regular lines start with a non-whitespace character.
3. Regular lines are of form `tag:value`, i.e., have a name `tag` and a value for the field, separated by `:` (only the first `:` counts). The value can be empty (=whitespace only).
4. Lines starting with whitespace are continuation lines (to the preceding field) if at least one character in the line is non-whitespace. Continuation lines where the only non-whitespace character is a `'.'` are taken as blank lines (allowing for multi-paragraph field values).
5. Records are separated by one or more empty (=whitespace only) lines.

By default, `read.dcf` returns a character matrix with one row per record and one column per field. Leading and trailing whitespace of field values is ignored. If a tag name is specified, but the corresponding value is empty, then an empty string is returned. If the tag name of a field is never used in a record, then `NA` is returned. If fields are repeated within a record, the last one encountered is returned. Malformed lines lead to an error. If `all` is true, a data frame is returned, again with one row per record and one column per field, and columns lists of character vectors for fields with multiple occurrences, and character vectors otherwise.

Note that `read.dcf(all = FALSE)` reads the file byte-by-byte. This allows a 'DESCRIPTION' file to be read and only its ASCII fields used, or its 'Encoding' field used to re-encode the remaining fields.

`write.dcf` does not write `NA` fields.

**See Also**

[write.table](#).

**Examples**

```
## Not run:
## Create a reduced version of the 'CONTENTS' file in package 'splines'
x <- read.dcf(file = system.file("CONTENTS", package = "splines"),
              fields = c("Entry", "Description"))
write.dcf(x)

## End(Not run)
```

debug

*Debug a Function***Description**

Set, unset or query the debugging flag on a function. The `text` and `condition` arguments are the same as those that can be supplied via a call to `browser`. They can be retrieved by the user once the browser has been entered, and provide a mechanism to allow users to identify which breakpoint has been activated.

**Usage**

```
debug(fun, text="", condition=NULL)
debugonce(fun, text="", condition=NULL)
undebug(fun)
isdebugged(fun)
```

**Arguments**

<code>fun</code>	any interpreted R function.
<code>text</code>	a text string that can be retrieved when the browser is entered.
<code>condition</code>	a condition that can be retrieved when the browser is entered.

**Details**

When a function flagged for debugging is entered, normal execution is suspended and the body of function is executed one statement at a time. A new browser context is initiated for each step (and the previous one destroyed).

At the debug prompt the user can enter commands or R expressions. The commands are

- `n` (or just return). Advance to the next step.
- `c` continue to the end of the current context: e.g. to the end of the loop if within a loop or to the end of the function.
- `cont` synonym for `c`.
- `where` print a stack trace of all active function calls.
- `Q` exit the browser and the current evaluation and return to the top-level prompt.

(Leading and trailing whitespace is ignored, except for return).

Anything else entered at the debug prompt is interpreted as an R expression to be evaluated in the calling environment: in particular typing an object name will cause the object to be printed, and `ls()` lists the objects in the calling frame. (If you want to look at an object with a name such as `n`, print it explicitly.)

To debug a function is defined inside a function, single-step though to the end of its definition, and then call `debug` on its name.

Using `debug` is persistent, and unless debugging is turned off the debugger will be entered on every invocation (note that if the function is removed and replaced the debug state is not preserved). Use `debugonce` to enter the debugger only the next time the function is invoked.

In order to debug S4 methods (see [Methods](#)), you need to use `trace`, typically calling `browser`, e.g., as

```
trace("plot", browser, exit=browser, signature = c("track",
"missing"))
```

The number of lines printed for the deparsed call when a function is entered for debugging can be limited by setting `options(deparse.max.lines)`.

### See Also

[browser](#), [trace](#); [traceback](#) to see the stack after an `Error`: `... message`; [recover](#) for another debugging approach.

Defunct

*Marking Objects as Defunct*

### Description

When a function is removed from R it should be replaced by a function which calls `.Defunct`.

### Usage

```
.Defunct(new, package = NULL, msg)
```

### Arguments

<code>new</code>	character string: A suggestion for a replacement function.
<code>package</code>	character string: The package to be used when suggesting where the defunct function might be listed.
<code>msg</code>	character string: A message to be printed, if missing a default message is used.

### Details

`.Defunct` is called from defunct functions. Functions should be listed in `help("pkg-defunct")` for an appropriate `pkg`, including `base`.

### See Also

[Deprecated](#).

`base-defunct` and so on which list the defunct functions in the packages.

---

delayedAssign      *Delay Evaluation*

---

### Description

`delayedAssign` creates a *promise* to evaluate the given expression if its value is requested. This provides direct access to the *lazy evaluation* mechanism used by R for the evaluation of (interpreted) functions.

### Usage

```
delayedAssign(x, value, eval.env = parent.frame(1),
              assign.env = parent.frame(1))
```

### Arguments

<code>x</code>	a variable name (given as a quoted string in the function call)
<code>value</code>	an expression to be assigned to <code>x</code>
<code>eval.env</code>	an environment in which to evaluate <code>value</code>
<code>assign.env</code>	an environment in which to assign <code>x</code>

### Details

Both `eval.env` and `assign.env` default to the currently active environment.

The expression assigned to a promise by `delayedAssign` will not be evaluated until it is eventually ‘forced’. This happens when the variable is first accessed.

When the promise is eventually forced, it is evaluated within the environment specified by `eval.env` (whose contents may have changed in the meantime). After that, the value is fixed and the expression will not be evaluated again.

### Value

This function is invoked for its side effect, which is assigning a promise to evaluate `value` to the variable `x`.

### See Also

[substitute](#), to see the expression associated with a promise.

### Examples

```
msg <- "old"
delayedAssign("x", msg)
msg <- "new!"
x #- new!
substitute(x) #- x (was 'msg' ?)
```

```
delayedAssign("x", {
  for(i in 1:3)
    cat("yippee!\n")
})
10
```

```

})

x^2 #- yippee
x^2 #- simple number

e <- (function(x, y = 1, z) environment())(1+2, "y", {cat(" HO! "); pi+2})
(1e <- as.list(e)) # evaluates the promises

```

---

deparse

*Expression Deparsing*


---

## Description

Turn unevaluated expressions into character strings.

## Usage

```

deparse(expr, width.cutoff = 60L,
        backtick = mode(expr) %in% c("call", "expression", "(", "function"),
        control = c("keepInteger", "showAttributes", "keepNA"),
        nlines = -1L)

```

## Arguments

<code>expr</code>	any R expression.
<code>width.cutoff</code>	integer in [20, 500] determining the cutoff at which line-breaking is tried.
<code>backtick</code>	logical indicating whether symbolic names should be enclosed in backticks if they do not follow the standard syntax.
<code>control</code>	character vector of deparsing options. See <code>.deparseOpts</code> .
<code>nlines</code>	integer: the maximum number of lines to produce. Negative values indicate no limit.

## Details

This function turns unevaluated expressions (where ‘expression’ is taken in a wider sense than the strict concept of a vector of mode "expression" used in [expression](#)) into character strings (a kind of inverse to [parse](#)).

A typical use of this is to create informative labels for data sets and plots. The example shows a simple use of this facility. It uses the functions `deparse` and `substitute` to create labels for a plot which are character string versions of the actual arguments to the function `myplot`.

The default for the `backtick` option is not to quote single symbols but only composite expressions. This is a compromise to avoid breaking existing code.

Using `control = "all"` comes closest to making `deparse()` an inverse of `parse()`. However, not all objects are deparse-able even with this option and a warning will be issued if the function recognizes that it is being asked to do the impossible.

Numeric and complex vectors are converted using 15 significant digits: see [as.character](#) for more details.

`width.cutoff` is a lower bound for the line lengths: deparsing a line proceeds until at least `width.cutoff bytes` have been output and e.g. `arg = value` expressions will not be split across lines.

**Note**

To avoid the risk of a source attribute out of sync with the actual function definition, the source attribute of a function will never be deparsed as an attribute.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[substitute](#), [parse](#), [expression](#).

Quotes for quoting conventions, including backticks.

**Examples**

```
require(stats); require(graphics)

deparse(args(lm))
deparse(args(lm), width = 500)
myplot <-
function(x, y) {
  plot(x, y, xlab=deparse(substitute(x)),
       ylab=deparse(substitute(y)))
}
e <- quote(`foo bar`)
deparse(e)
deparse(e, backtick=TRUE)
e <- quote(`foo bar`+1)
deparse(e)
deparse(e, control = "all")
```

---

deparseOpts

*Options for Expression Deparsing*

---

**Description**

Process the deparsing options for `deparse`, `dput` and `dump`.

**Usage**

```
.deparseOpts(control)
```

**Arguments**

`control` character vector of deparsing options.

## Details

This is called by `deparse`, `dput` and `dump` to process their `control` argument.

The `control` argument is a vector containing zero or more of the following strings. Partial string matching is used.

`keepInteger` Either surround integer vectors by `as.integer()` or use suffix `L`, so they are not converted to type `double` when parsed. This includes making sure that integer NAs are preserved (via `NA_integer_` if there are no non-NA values in the vector, unless `"S_compatible"` is set).

`quoteExpressions` Surround expressions with `quote()`, so they are not evaluated when re-parsed.

`showAttributes` If the object has attributes (other than a `source` attribute), use `structure()` to display them as well as the object value. This is the default for `deparse` and `dput`.

`useSource` If the object has a `source` attribute, display that instead of deparsing the object. Currently only applies to function definitions.

`warnIncomplete` Some exotic objects such as [environments](#), external pointers, etc. can not be deparsed properly. This option causes a warning to be issued if the deparser recognizes one of these situations.

Also, the parser in R < 2.7.0 would only accept strings of up to 8192 bytes, and this option gives a warning for longer strings.

`keepNA` Integer, real and character NAs are surrounded by coercion where necessary to ensure that they are parsed to the same type.

`all` An abbreviated way to specify all of the options listed above. This is the default for `dump`, and the options used by `edit` (which are fixed).

`delayPromises` Deparse promises in the form `<promise: expression>` rather than evaluating them. The value and the environment of the promise will not be shown and the deparsed code cannot be sourced.

`S_compatible` Make deparsing as far as possible compatible with S and R < 2.5.0. For compatibility with S, integer values of double vectors are deparsed with a trailing decimal point. Backticks are not used.

For the most readable (but perhaps incomplete) display, use `control = NULL`. This displays the object's value, but not its attributes. The default in `deparse` is to display the attributes as well, but not to use any of the other options to make the result parseable. (`dput` and `dump` do use more default options, and printing of functions without sources uses `c("keepInteger", "keepNA")`.)

Using `control = "all"` comes closest to making `deparse()` an inverse of `parse()`. However, not all objects are deparse-able even with this option. A warning will be issued if the function recognizes that it is being asked to do the impossible.

## Value

A numerical value corresponding to the options selected.

---

Deprecated

*Marking Objects as Deprecated*

---

### Description

When an object is about removed from R it is first deprecated and should include a call to `.Deprecated`.

### Usage

```
.Deprecated(new, package=NULL, msg)
```

### Arguments

<code>new</code>	character string: A suggestion for a replacement function.
<code>package</code>	character string: The package to be used when suggesting where the deprecated function might be listed.
<code>msg</code>	character string: A message to be printed, if missing a default message is used.

### Details

`.Deprecated("<new name>")` is called from deprecated functions. The original help page for these functions is often available at `help("oldName-deprecated")` (note the quotes). Functions should be listed in `help("pkg-deprecated")` for an appropriate `pkg`, including `base`.

### See Also

[Defunct](#)

`base-deprecated` and so on which list the deprecated functions in the packages.

---

det

*Calculate the Determinant of a Matrix*

---

### Description

`det` calculates the determinant of a matrix. `determinant` is a generic function that returns separately the modulus of the determinant, optionally on the logarithm scale, and the sign of the determinant.

### Usage

```
det(x, ...)  
determinant(x, logarithm = TRUE, ...)
```



**Arguments**

<code>x</code>	numeric matrix.
<code>logarithm</code>	logical; if TRUE (default) return the logarithm of the modulus of the determinant.
<code>...</code>	Optional arguments. At present none are used. Previous versions of <code>det</code> allowed an optional <code>method</code> argument. This argument will be ignored but will not produce an error.

**Details**

The determinant function uses an LU decomposition and the `det` function is simply a wrapper around a call to `determinant`.

Often, computing the determinant is *not* what you should be doing to solve a given problem.

**Value**

For `det`, the determinant of `x`. For `determinant`, a list with components

<code>modulus</code>	a numeric value. The modulus (absolute value) of the determinant if <code>logarithm</code> is FALSE; otherwise the logarithm of the modulus.
<code>sign</code>	integer; either +1 or -1 according to whether the determinant is positive or negative.

**Examples**

```
(x <- matrix(1:4, ncol=2))
unlist(determinant(x))
det(x)

det(print(cbind(1,1:3,c(2,0,1))))
```

---

detach

*Detach Objects from the Search Path*

---

**Description**

Detach a database, i.e., remove it from the `search()` path of available R objects. Usually this is either a `data.frame` which has been `attached` or a package which was attached by `library`.

**Usage**

```
detach(name, pos = 2, unload = FALSE, character.only = FALSE, force = FALSE)
```

**Arguments**

<code>name</code>	The object to detach. Defaults to <code>search()[pos]</code> . This can be an unquoted name or a character string but <i>not</i> a character vector. If a number is supplied this is taken as <code>pos</code> .
<code>pos</code>	Index position in <code>search()</code> of the database to detach. When <code>name</code> is a number, <code>pos = name</code> is used.

<code>unload</code>	A logical value indicating whether or not to attempt to unload the namespace when a package is being detached. If the package has a namespace and <code>unload</code> is <code>TRUE</code> , then <code>detach</code> will attempt to unload the namespace <i>via</i> <code>unloadNamespace</code> : if the namespace is imported by another namespace or <code>unload</code> is <code>FALSE</code> , no unloading will occur.
<code>character.only</code>	a logical indicating whether <code>name</code> can be assumed to be character strings.
<code>force</code>	logical: should a package be detached even though other loaded packages depend on it?

### Details

This is most commonly used with a single number argument referring to a position on the search list, and can also be used with a unquoted or quoted name of an item on the search list such as `package:tools`.

If a package has a namespace, detaching it does not by default unload the namespace (and may not even with `unload=TRUE`), and detaching will not in general unload any dynamically loaded compiled code (DLLs). Further, registered S3 methods from the namespace will not be removed. If you use `library` on a package whose name space is loaded, it attaches the exports of the already loaded name space. So detaching and re-attaching a package may not refresh some or all components of the package, and is inadvisable.

### Value

The return value is `invisible`. It is `NULL` when a package is detached, otherwise the environment which was returned by `attach` when the object was attached (incorporating any changes since it was attached).

### Note

You cannot detach either the workspace (position 1) nor the **base** package (the last item in the search list), and attempting to do so will throw an error.

Unloading some name spaces has undesirable side effects: e.g. unloading **grid** closes all graphics devices, and on most systems **tcltk** cannot be reloaded once it has been unloaded and may crash **R** if this is attempted.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

`attach`, `library`, `search`, `objects`, `unloadNamespace`, `library.dynam.unload`.

### Examples

```
require(splines) # package
detach(package:splines)
## or also
library(splines)
pkg <- "package:splines"
```

```
detach(pkg, character.only = TRUE)

## careful: do not do this unless 'splines' is not already loaded.
library(splines)
detach(2) # 'pos' used for 'name'

## an example of the name argument to attach
## and of detaching a database named by a character vector
attach_and_detach <- function(db, pos=2)
{
  name <- deparse(substitute(db))
  attach(db, pos=pos, name=name)
  print(search()[pos])
  detach(name, character.only = TRUE)
}
attach_and_detach(women, pos=3)
```

diag

*Matrix Diagonals***Description**

Extract or replace the diagonal of a matrix, or construct a diagonal matrix.

**Usage**

```
diag(x = 1, nrow, ncol)
diag(x) <- value
```

**Arguments**

<code>x</code>	a matrix, vector or 1D array, or missing.
<code>nrow</code> , <code>ncol</code>	Optional dimensions for the result when <code>x</code> is not a matrix.
<code>value</code>	either a single value or a vector of length equal to that of the current diagonal. Should be of a mode which can be coerced to that of <code>x</code> .

**Details**

`diag` has four distinct usages:

1. `x` is a matrix, when it extracts the diagonal.
2. `x` is missing and `nrow` is specified, it returns an identity matrix.
3. `x` is a scalar (length-one vector) and the only argument, it returns a square identity matrix of size given by the scalar.
4. `x` is a vector, either of length at least 2 or there were further arguments. This returns a matrix with the given diagonal and zero off-diagonal entries.

It is an error to specify `nrow` or `ncol` in the first case.

**Value**

If `x` is a matrix then `diag(x)` returns the diagonal of `x`. The resulting vector will have `names` if the matrix `x` has matching column and rownames.

The replacement form sets the diagonal of the matrix `x` to the given value(s).

In all other cases the value is a diagonal matrix with `nrow` rows and `ncol` columns (if `ncol` is not given the matrix is square). Here `nrow` is taken from the argument if specified, otherwise inferred from `x`: if that is a vector (or 1D array) of length two or more, then its length is the number of rows, but if it is of length one and neither `nrow` nor `ncol` is specified, `nrow = as.integer(x)`.

When a diagonal matrix is returned, the diagonal elements are one except in the fourth case, when `x` gives the diagonal elements: it will be recycled or truncated as needed, but fractional recycling and truncation will give a warning.

**Note**

Using `diag(x)` can have unexpected effects if `x` is a vector that could be of length one. Use `diag(x, nrow = length(x))` for consistent behaviour.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`upper.tri`, `lower.tri`, `matrix`.

**Examples**

```
require(stats)
dim(diag(3))
diag(10,3,4) # guess what?
all(diag(1:3) == {m <- matrix(0,3,3); diag(m) <- 1:3; m})

diag(var(M <- cbind(X = 1:5, Y = stats::rnorm(5))))
#-> vector with names "X" and "Y"

rownames(M) <- c(colnames(M), rep("", 3));
M; diag(M) # named as well
```

**Description**

Returns suitably lagged and iterated differences.

**Usage**

```
diff(x, ...)

## Default S3 method:
diff(x, lag = 1, differences = 1, ...)

## S3 method for class 'POSIXt':
diff(x, lag = 1, differences = 1, ...)

## S3 method for class 'Date':
diff(x, lag = 1, differences = 1, ...)
```

**Arguments**

`x` a numeric vector or matrix containing the values to be differenced.  
`lag` an integer indicating which lag to use.  
`differences` an integer indicating the order of the difference.  
`...` further arguments to be passed to or from methods.

**Details**

`diff` is a generic function with a default method and ones for classes `"ts"`, `"POSIXt"` and `"Date"`.

[NA](#)'s propagate.

**Value**

If `x` is a vector of length `n` and `differences=1`, then the computed result is equal to the successive differences `x[(1+lag):n] - x[1:(n-lag)]`.

If `differences` is larger than one this algorithm is applied recursively to `x`. Note that the returned value is a vector which is shorter than `x`.

If `x` is a matrix then the difference operations are carried out on each column separately.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[diff.ts](#), [diffinv](#).

**Examples**

```
diff(1:10, 2)
diff(1:10, 2, 2)
x <- cumsum(cumsum(1:10))
diff(x, lag = 2)
diff(x, differences = 2)

diff(.leap.seconds)
```

---

difftime                      *Time Intervals*

---

### Description

Time intervals creation, printing, and some arithmetic.

### Usage

```
time1 - time2

difftime(time1, time2, tz = "",
         units = c("auto", "secs", "mins", "hours",
                  "days", "weeks"))

as.difftime(tim, format = "%X", units = "auto")

## S3 method for class 'difftime':
format(x, ...)
## S3 method for class 'difftime':
units(x)
## S3 replacement method for class 'difftime':
units(x) <- value
## S3 method for class 'difftime':
as.double(x, units = "auto", ...)

## Group methods, notably for round(), signif(), floor(), ceiling(),
## trunc(), abs(); called directly, *not* as Math():
## S3 method for class 'difftime':
Math(x, ...)
```

### Arguments

`time1`, `time2` [date-time](#) or [date](#) objects.

`tz` a timezone specification to be used for the conversion. System-specific, but " " is the current time zone, and "GMT" is UTC.

`units` character. Units in which the results are desired. Can be abbreviated.

`value` character. Like `units` above, except that abbreviations are not allowed.

`tim` character string or numeric value specifying a time interval.

`format` character specifying the format of `tim`: see [strptime](#). The default is a locale-specific time format.

`x` an object inheriting from class "difftime".

... arguments to be passed to or from other methods.

### Details

Function `difftime` calculates a difference of two date/time objects and returns an object of class "difftime" with an attribute indicating the units. The `Math` group method provides [round](#),

[signif](#), [floor](#), [ceiling](#), [trunc](#), [abs](#), and [sign](#) methods for objects of this class, and there are methods for the group-generic (see [Ops](#)) logical and arithmetic operations.

If `units = "auto"`, a suitable set of units is chosen, the largest possible (excluding "weeks") in which all the absolute differences are greater than one.

Subtraction of date-time objects gives an object of this class, by calling `difftime` with `units = "auto"`. Alternatively, `as.difftime()` works on character-coded or numeric time intervals; in the latter case, `units` must be specified, and `format` has no effect.

Limited arithmetic is available on "difftime" objects: they can be added or subtracted, and multiplied or divided by a numeric vector. In addition, adding or subtracting a numeric vector by a "difftime" object implicitly converts the numeric vector to a "difftime" object with the same units as the "difftime" object. There are methods for [mean](#) and [sum](#) (via the [Summary](#) group generic).

The units of a "difftime" object can be extracted by the `units` function, which also has an replacement form. If the units are changed, the numerical value is scaled accordingly.

The `as.double` method returns the numeric value expressed in the specified units. Using `units = "auto"` means the units of the object.

The `format` method simply formats the numeric value and appends the units as a text string.

### See Also

[DateTimeClasses](#).

### Examples

```
(z <- Sys.time() - 3600)
Sys.time() - z           # just over 3600 seconds.

## time interval between releases of R 1.2.2 and 1.2.3.
ISOdate(2001, 4, 26) - ISOdate(2001, 2, 26)

as.difftime(c("0:3:20", "11:23:15"))
as.difftime(c("3:20", "23:15", "2:"), format= "%H:%M")# 3rd gives NA
(z <- as.difftime(c(0,30,60), units="mins"))
as.numeric(z, units="secs")
as.numeric(z, units="hours")
format(z)
```

---

dim

*Dimensions of an Object*

---

### Description

Retrieve or set the dimension of an object.

### Usage

```
dim(x)
dim(x) <- value
```

**Arguments**

`x` an R object, for example a matrix, array or data frame.

`value` For the default method, either `NULL` or a numeric vector, which is coerced to integer (by truncation).

**Details**

The functions `dim` and `dim<-` are [internal generic primitive](#) functions.

`dim` has a method for `data.frames`, which returns the lengths of the `row.names` attribute of `x` and of `x` (as the numbers of rows and columns respectively).

**Value**

For an array (and hence in particular, for a matrix) `dim` retrieves the `dim` attribute of the object. It is `NULL` or a vector of mode `integer`.

The replacement method changes the `"dim"` attribute (provided the new value is compatible) and removes any `"dimnames"` *and* `"names"` attributes.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`ncol`, `nrow` and `dimnames`.

**Examples**

```
x <- 1:12 ; dim(x) <- c(3,4)
x

# simple versions of nrow and ncol could be defined as follows
nrow0 <- function(x) dim(x)[1]
ncol0 <- function(x) dim(x)[2]
```

---

dimnames

*Dimnames of an Object*

---

**Description**

Retrieve or set the `dimnames` of an object.

**Usage**

```
dimnames(x)
dimnames(x) <- value
```

**Arguments**

`x` an R object, for example a matrix, array or data frame.

`value` a possible value for `dimnames(x)`: see the ‘Value’ section.



## Details

The functions `dimnames` and `dimnames<-` are generic.

For an `array` (and hence in particular, for a `matrix`), they retrieve or set the `dimnames` attribute (see `attributes`) of the object. A list value can have names, and these will be used to label the dimensions of the array where appropriate.

The replacement method for arrays/matrices coerces vector and factor elements of `value` to character, but does not dispatch methods for `as.character`. It coerces zero-length elements to `NULL`, and a zero-length list to `NULL`. If `value` is a list shorter than the number of dimensions, as from R 2.8.0 it is extended with `NULL`s to the needed length.

Both have methods for data frames. The `dimnames` of a data frame are its `row.names` and its `names`. For the replacement method each component of `value` will be coerced by `as.character`.

For a 1D matrix the `names` are the same thing as the (only) component of the `dimnames`.

Both are `primitive` functions.

## Value

The `dimnames` of a matrix or array can be `NULL` or a list of the same length as `dim(x)`. If a list, its components are either `NULL` or a character vector with positive length of the appropriate dimension of `x`. The list can be named.

For the `"data.frame"` method both `dimnames` are character vectors, and the `rownames` must contain no duplicates nor missing values.

## Note

Setting components of the `dimnames`, e.g. `dimnames(A)[[1]] <- value` is a common paradigm, but note that it will not work if the value assigned is `NULL`. Use `rownames` instead, or (as it does) manipulate the whole `dimnames` list.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

`rownames`, `colnames`; `array`, `matrix`, `data.frame`.

## Examples

```
## simple versions of rownames and colnames
## could be defined as follows
rownames0 <- function(x) dimnames(x)[[1]]
colnames0 <- function(x) dimnames(x)[[2]]
```

---

`do.call`*Execute a Function Call*

---

### Description

`do.call` constructs and executes a function call from a name or a function and a list of arguments to be passed to it.

### Usage

```
do.call(what, args, quote = FALSE, envir = parent.frame())
```

### Arguments

<code>what</code>	either a function or a non-empty character string naming the function to be called.
<code>args</code>	a <i>list</i> of arguments to the function call. The <code>names</code> attribute of <code>args</code> gives the argument names.
<code>quote</code>	a logical value indicating whether to quote the arguments.
<code>envir</code>	an environment within which to evaluate the call. This will be most useful if <code>what</code> is a character string and the arguments are symbols or quoted expressions.

### Details

If `quote` is `FALSE`, the default, then the arguments are evaluated (in the calling environment, not `envir`). If `quote` is `TRUE` then each argument is quoted (see [quote](#)) so that the effect of argument evaluation is to remove the quotes – leaving the original arguments unevaluated when the call is constructed.

The behavior of some functions, such as [substitute](#), will not be the same for functions evaluated using `do.call` as if they were evaluated from the interpreter. The precise semantics are currently undefined and subject to change.

### Value

The result of the (evaluated) function call.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[call](#) which creates an unevaluated call.

**Examples**

```
do.call("complex", list(imag = 1:3))

## if we already have a list (e.g. a data frame)
## we need c() to add further arguments
tmp <- expand.grid(letters[1:2], 1:3, c("+", "-"))
do.call("paste", c(tmp, sep=""))

do.call(paste, list(as.name("A"), as.name("B")), quote=TRUE)

## examples of where objects will be found.
A <- 2
f <- function(x) print(x^2)
env <- new.env()
assign("A", 10, envir = env)
assign("f", f, envir = env)
f <- function(x) print(x)
f(A) # 2
do.call("f", list(A)) # 2
do.call("f", list(A), envir=env) # 4
do.call(f, list(A), envir=env) # 2
do.call("f", list(quote(A)), envir=env) # 100
do.call(f, list(quote(A)), envir=env) # 10
do.call("f", list(as.name("A")), envir=env) # 100

eval(call("f", A)) # 2
eval(call("f", quote(A))) # 2
eval(call("f", A), envir=env) # 4
eval(call("f", quote(A)), envir=env) # 100
```

---

double

---

*Double-Precision Vectors*


---

**Description**

Create, coerce to or test for a double-precision vector.

**Usage**

```
double(length = 0)
as.double(x, ...)
is.double(x)
```

```
single(length = 0)
as.single(x, ...)
```

**Arguments**

length	desired length.
x	object to be coerced or tested.
...	further arguments passed to or from other methods.

## Details

`double` creates a double-precision vector of the specified length. The elements of the vector are all equal to 0. It is identical to `numeric` (and `real`).

`as.double` is a generic function. It is identical to `as.numeric` (and `as.real`). Methods should return an object of base type "double".

`is.double` is a test of double [type](#).

**R has no single precision data type. All real numbers are stored in double precision format.** The functions `as.single` and `single` are identical to `as.double` and `double` except they set the attribute `Csingle` that is used in the `.C` and `.Fortran` interface, and they are intended only to be used in that context.

## Value

`double` creates a double-precision vector of the specified length. The elements of the vector are all equal to 0.

`as.double` attempts to coerce its argument to be of double type: like `as.vector` it strips attributes including names. (To ensure that an object is of double type without stripping attributes, use `storage.mode`.) Character strings containing optional whitespace followed by either a decimal representation or a hexadecimal representation (starting with `0x` or `0X`) can be converted. `as.double` for factors yields the codes underlying the factor levels, not the numeric representation of the labels, see also [factor](#).

`is.double` returns `TRUE` or `FALSE` depending on whether its argument is of double [type](#) or not.

## Note on names

It is a historical anomaly that **R** has three names for its floating-point vectors, `double`, `numeric` and `real`.

`double` is the name of the [type](#). `numeric` is the name of the [mode](#) and also of the implicit [class](#). As an S4 formal class, use "numeric".

`real` is deprecated and should not be used in new code.

The potential confusion is that **R** has used *mode* "numeric" to mean 'double or integer', which conflicts with the S4 usage. Thus `is.numeric` tests the mode, not the class, but `as.numeric` (which is identical to `as.double`) coerces to the class.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[integer](#), [numeric](#), [storage.mode](#).

## Examples

```
is.double(1)
all(double(3) == 0)
```

---

dput

*Write an Object to a File or Recreate it*

---

### Description

Writes an ASCII text representation of an R object to a file or connection, or uses one to recreate the object.

### Usage

```
dput(x, file = "",
      control = c("keepNA", "keepInteger", "showAttributes"))

dget(file)
```

### Arguments

<code>x</code>	an object.
<code>file</code>	either a character string naming a file or a connection. "" indicates output to the console.
<code>control</code>	character vector indicating deparsing options. See <code>.deparseOpts</code> for their description.

### Details

`dput` opens `file` and deparses the object `x` into that file. The object name is not written (unlike `dump`). If `x` is a function the associated environment is stripped. Hence scoping information can be lost.

Deparsing an object is difficult, and not always possible. With the default `control`, `dput()` attempts to deparse in a way that is readable, but for more complex or unusual objects (see `dump`, not likely to be parsed as identical to the original. Use `control = "all"` for the most complete deparsing; use `control = NULL` for the simplest deparsing, not even including attributes.

`dput` will warn if fewer characters were written to a file than expected, which may indicate a full or corrupt file system.

To display saved source rather than deparsing the internal representation include `"useSource"` in `control`. R currently saves source only for function definitions.

### Value

For `dput`, the first argument invisibly.

For `dget`, the object created.

### Note

To avoid the risk of a source attribute out of sync with the actual function definition, the source attribute of a function will never be written as an attribute.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[deparse](#), [dump](#), [write](#).

**Examples**

```
## Write an ASCII version of mean to the file "foo"
dput(mean, "foo")
## And read it back into 'bar'
bar <- dget("foo")
unlink("foo")
## Create a function with comments
baz <- function(x) {
  # Subtract from one
  1-x
}
## and display it
dput(baz)
## and now display the saved source
dput(baz, control = "useSource")
```

---

drop

*Drop Redundant Extent Information*

---

**Description**

Delete the dimensions of an array which have only one level.

**Usage**

```
drop(x)
```

**Arguments**

`x` an array (including a matrix).

**Value**

If `x` is an object with a `dim` attribute (e.g., a matrix or [array](#)), then `drop` returns an object like `x`, but with any extents of length one removed. Any accompanying `dimnames` attribute is adjusted and returned with `x`: if the result is a vector the names are taken from the `dimnames` (if any). If the result is a length-one vector, the names are taken from the first dimension with a `dimname`.

Array subsetting (`[]`) performs this reduction unless used with `drop = FALSE`, but sometimes it is useful to invoke `drop` directly.

**See Also**

[drop1](#) which is used for dropping terms in models.

**Examples**

```
dim(drop(array(1:12, dim=c(1,3,1,1,2,1,2))))# = 3 2 2
drop(1:3 %**% 2:4)# scalar product
```

---

 dump

*Text Representations of R Objects*


---

### Description

This function takes a vector of names of R objects and produces text representations of the objects on a file or connection. A dump file can usually be [sourced](#) into another R (or S) session.

### Usage

```
dump(list, file = "dumpdata.R", append = FALSE,
      control = "all", envir = parent.frame(), evaluate = TRUE)
```

### Arguments

<code>list</code>	character. The names of one or more R objects to be dumped.
<code>file</code>	either a character string naming a file or a connection. "" indicates output to the console.
<code>append</code>	if TRUE and <code>file</code> is a character string, output will be appended to <code>file</code> ; otherwise, it will overwrite the contents of <code>file</code> .
<code>control</code>	character vector indicating deparsing options. See <a href="#">.deparseOpts</a> for their description.
<code>envir</code>	the environment to search for objects.
<code>evaluate</code>	logical. Should promises be evaluated?

### Details

If some of the objects named do not exist (in scope), they are omitted, with a warning. If `file` is a file and no objects exist then no file is created.

`sourcing` may not produce an identical copy of dumped objects. A warning is issued if it is likely that problems will arise, for example when dumping exotic or complex objects (see the Note).

`dump` will also warn if fewer characters were written to a file than expected, which may indicate a full or corrupt file system.

A dump file can be [sourced](#) into another R (or perhaps S) session, but the function [save](#) is designed to be used for transporting R data, and will work with R objects that `dump` does not handle.

To produce a more readable representation of an object, use `control = NULL`. This will skip attributes, and will make other simplifications that make `source` less likely to produce an identical copy. See [deparse](#) for details.

To deparse the internal representation of a function rather than displaying the saved source, use `control = c("keepInteger", "warnIncomplete", "keepNA")`. This will lose all formatting and comments, but may be useful in those cases where the saved source is no longer correct.

Promises will normally only be encountered by users as a result of lazy-loading (when the default `evaluate = TRUE` is essential) and after the use of [delayedAssign](#), when `evaluate = FALSE` might be intended.

**Value**

An invisible character vector containing the names of the objects which were dumped.

**Note**

As `dump` is defined in the base name space, the **base** package will be searched *before* the global environment unless `dump` is called from the top level prompt or the `envir` argument is given explicitly.

To avoid the risk of a source attribute becoming out of sync with the actual function definition, the source attribute of a function will never be dumped as an attribute.

Currently environments, external pointers, weak references and objects of type `S4` are not deparsed in a way that can be sourced. In addition, language objects are deparsed in a simple way whatever the value of `control`, and this includes not dumping their attributes (which will result in a warning).

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[dput](#), [dget](#), [write](#).  
[save](#) for a more reliable way to save R objects.

**Examples**

```
x <- 1; y <- 1:10
dump(ls(pattern = '^[xyz]'), "xyz.Rdumped")
print(.Last.value)
unlink("xyz.Rdumped")
```

---

duplicated

*Determine Duplicate Elements*


---

**Description**

Determines which elements of a vector or data frame are duplicates of elements with smaller subscripts, and returns a logical vector indicating which elements (rows) are duplicates.

**Usage**

```
duplicated(x, incomparables = FALSE, ...)

## Default S3 method:
duplicated(x, incomparables = FALSE,
           fromLast = FALSE, ...)

## S3 method for class 'array':
duplicated(x, incomparables = FALSE, MARGIN = 1,
           fromLast = FALSE, ...)
```



```

anyDuplicated(x, incomparables = FALSE, ...)
## Default S3 method:
anyDuplicated(x, incomparables = FALSE,
              fromLast = FALSE, ...)
## S3 method for class 'array':
anyDuplicated(x, incomparables = FALSE,
              MARGIN = 1, fromLast = FALSE, ...)

```

### Arguments

<code>x</code>	a vector or a data frame or an array or NULL.
<code>incomparables</code>	a vector of values that cannot be compared. <code>FALSE</code> is a special value, meaning that all values can be compared, and may be the only value accepted for methods other than the default. It will be coerced internally to the same type as <code>x</code> .
<code>fromLast</code>	logical indicating if duplication should be considered from the reverse side, i.e., the last (or rightmost) of identical elements would correspond to <code>duplicated=FALSE</code> .
<code>...</code>	arguments for particular methods.
<code>MARGIN</code>	the array margin to be held fixed: see <a href="#">apply</a> .

### Details

These are generic functions with methods for vectors (including lists), data frames and arrays (including matrices).

For the default methods, and whenever there are equivalent method definitions for `duplicated` and `anyDuplicated`, `anyDuplicated(x, ...)` is a “generalized” shortcut for `any(duplicated(x, ...))`, in the sense that it returns the *index* `i` of the first duplicated entry `x[i]` if there is one, and 0 otherwise. Their behaviours may be different when at least one of `duplicated` and `anyDuplicated` has a relevant method.

`duplicated(x, fromLast=TRUE)` is equivalent to but faster than `rev(duplicated(rev(x)))`.

The data frame method works by pasting together a character representation of the rows separated by `\r`, so may be imperfect if the data frame has characters with embedded carriage returns or columns which do not reliably map to characters.

The array method calculates for each element of the sub-array specified by `MARGIN` if the remaining dimensions are identical to those for an earlier (or later, when `fromLast=TRUE`) element (in row-major order). This would most commonly be used to find duplicated rows (the default) or columns (with `MARGIN = 2`).

Missing values are regarded as equal, but `NaN` is not equal to `NA_real_`.

Values in `incomparables` will never be marked as duplicated. This is intended to be used for a fairly small set of values and will not be efficient for a very large set.

### Value

`duplicated()`: For a vector input, a logical vector of the same length as `x`. For a data frame, a logical vector with one element for each row. For a matrix or array, a logical array with the same dimensions and dimnames.

`anyDuplicated()`: a non-negative integer (of length one).

**Warning**

Using this for lists is potentially slow, especially if the elements are not atomic vectors (see [vector](#)) or differ only in their attributes. In the worst case it is  $O(n^2)$ .

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[unique](#).

**Examples**

```
x <- c(9:20, 1:5, 3:7, 0:8)
## extract unique elements
(xu <- x[!duplicated(x)])
## similar, but not the same:
(xu2 <- x[!duplicated(x, fromLast = TRUE)])

## xu == unique(x) but unique(x) is more efficient
stopifnot(identical(xu, unique(x)),
          identical(xu2, unique(x, fromLast = TRUE)))

duplicated(iris)[140:143]

duplicated(iris3, MARGIN = c(1, 3))
anyDuplicated(iris) ## 143

anyDuplicated(x)
anyDuplicated(x, fromLast = TRUE)
```

---

 dyn.load

*Foreign Function Interface*


---

**Description**

Load or unload DLLs (also known as shared objects), and test whether a C function or Fortran subroutine is available.

**Usage**

```
dyn.load(x, local = TRUE, now = TRUE, ...)
dyn.unload(x)
```

```
is.loaded(symbol, PACKAGE = "", type = "")
```

**Arguments**

<code>x</code>	a character string giving the pathname to a DLL, also known as a dynamic shared object. (See ‘Details’ for what these terms mean.)
<code>local</code>	a logical value controlling whether the symbols in the DLL are stored in their own local table and not shared across DLLs, or added to the global symbol table. Whether this has any effect is system-dependent.
<code>now</code>	a logical controlling whether all symbols are resolved (and relocated) immediately the library is loaded or deferred until they are used. This control is useful for developers testing whether a library is complete and has all the necessary symbols, and for users to ignore missing symbols. Whether this has any effect is system-dependent.
<code>...</code>	other arguments for future expansion.
<code>symbol</code>	a character string giving a symbol name.
<code>PACKAGE</code>	if supplied, confine the search for the <code>name</code> to the DLL given by this argument (plus the conventional extension, ‘.so’, ‘.sl’, ‘.dll’, ...). This is intended to add safety for packages, which can ensure by using this argument that no other package can override their external symbols. Use <code>PACKAGE="base"</code> for symbols linked in to R. This is used in the same way as in <code>.C</code> , <code>.Call</code> , <code>.Fortran</code> and <code>.External</code> functions
<code>type</code>	The type of symbol to look for: can be any (“”, the default), "Fortran", "Call" or "External".

**Details**

The objects `dyn.load` loads are called ‘dynamically loadable libraries’ (abbreviated to ‘DLL’ on all platforms except Mac OS X, which unfortunately uses the term for a different sort of object. On Unix-alikes they are also called ‘dynamic shared objects’ (‘DSO’), or ‘shared objects’ for short. (The POSIX standards use ‘executable object file’, but no one else does.)

See ‘See Also’ and the ‘Writing R Extensions’ and ‘R Installation and Administration’ manuals for how to create and install a suitable DLL.

Unfortunately a very few platforms (e.g. Compaq Tru64) do not handle the `PACKAGE` argument correctly, and may incorrectly find symbols linked into R.

The additional arguments to `dyn.load` mirror the different aspects of the mode argument to the `dlopen()` routine on POSIX systems. They are available so that users can exercise greater control over the loading process for an individual library. In general, the default values are appropriate and you should override them only if there is good reason and you understand the implications.

The `local` argument allows one to control whether the symbols in the DLL being attached are visible to other DLLs. While maintaining the symbols in their own name space is good practice, the ability to share symbols across related ‘chapters’ is useful in many cases. Additionally, on certain platforms and versions of an operating system, certain libraries must have their symbols loaded globally to successfully resolve all symbols.

One should be careful of the potential side-effect of using lazy loading via the `now` argument as `FALSE`. If a routine is called that has a missing symbol, the process will terminate immediately. The intended use is for library developers to call with value `TRUE` to check that all symbols are actually resolved and for regular users to call with `FALSE` so that missing symbols can be ignored and the available ones can be called.

The initial motivation for adding these was to avoid such termination in the `_init()` routines of the Java virtual machine library. However, symbols loaded locally may not be (read probably)

available to other DLLs. Those added to the global table are available to all other elements of the application and so can be shared across two different DLLs.

Some (very old) systems do not provide (explicit) support for local/global and lazy/eager symbol resolution. This can be the source of subtle bugs. One can arrange to have warning messages emitted when unsupported options are used. This is done by setting either of the options `verbose` or `warn` to be non-zero via the `options` function.

There is a short discussion of these additional arguments with some example code available at <http://cm.bell-labs.com/stat/duncan/R/dynload>.

## Value

The function `dyn.load` is used for its side effect which links the specified DLL to the executing R image. Calls to `.C`, `.Call`, `.Fortran` and `.External` can then be used to execute compiled C functions or Fortran subroutines contained in the library. The return value of `dyn.load` is an object of class `DLLInfo`. See `getLoadedDLLs` for information about this class.

The function `dyn.unload` unlinks the DLL. Note that unloading a DLL and then re-loading a DLL of the same name may or may not work: on Solaris it uses the first version loaded.

`is.loaded` checks if the symbol name is loaded and hence available for use in `.C` or `.Fortran` or `.Call` or `.External`. It will succeed if any one of the four calling functions would succeed in using the entry point unless `type` is specified. (See `.Fortran` for how Fortran symbols are mapped.)

## Warning

Do not use `dyn.unload` on a DLL loaded by `library.dynam`: use `library.dynam.unload`. This is needed for system housekeeping.

## Note

`is.loaded` requires the name you would give to `.C` etc and **not** (as in S) that remapped by defunct functions `symbol.C` or `symbol.For`.

The creation of DLLs and the runtime linking of them into executing programs is very platform dependent. In recent years there has been some simplification in the process because the C subroutine call `dlopen` has become the POSIX standard for doing this. Under Unix-alikes `dyn.load` uses the `dlopen` mechanism and should work on all platforms which support it. On Windows it uses the standard mechanism (`LoadLibrary`) for loading DLLs.

The original code for loading DLLs in Unix-alikes was provided by Heiner Schwarte.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

`library.dynam` to be used inside a package's `.First.lib` initialization.

`SHLIB` for how to create suitable DLLs.

`.C`, `.Fortran`, `.External`, `.Call`.

**Examples**

```
is.loaded("hclass2") #-> probably TRUE, as stats is loaded
is.loaded("supsmu") # Fortran entry point in stats
is.loaded("supsmu", "stats", "Fortran")
is.loaded("PDF", type = "External")
```

---

eapply

*Apply a Function Over Values in an Environment*


---

**Description**

`eapply` applies `FUN` to the named values from an [environment](#) and returns the results as a list. The user can request that all named objects are used (normally names that begin with a dot are not). The output is not sorted and no parent environments are searched.

This is a [primitive](#) function.

**Usage**

```
eapply(env, FUN, ..., all.names = FALSE, USE.NAMES = TRUE)
```

**Arguments**

<code>env</code>	environment to be used.
<code>FUN</code>	the function to be applied, found <i>via</i> <a href="#">match.fun</a> . In the case of functions like <code>+</code> , <code>%*%</code> , etc., the function name must be backquoted or quoted.
<code>...</code>	optional arguments to <code>FUN</code> .
<code>all.names</code>	a logical indicating whether to apply the function to all values.
<code>USE.NAMES</code>	logical indicating whether the resulting list should have <a href="#">names</a> . Setting this to <code>FALSE</code> is faster, useful however typically only when <code>ls(env)</code> is already given.

**See Also**

[environment](#), [lapply](#).

**Examples**

```
require(utils); require(stats)

env <- new.env()
env$a <- 1:10
env$beta <- exp(-3:3)
env$logic <- c(TRUE, FALSE, FALSE, TRUE)
# what have we there?
eapply(env, str)
## note however, that 'ls.str(env)' is slightly nicer ..

# compute the mean for each list element
eapply(env, mean)
unlist(eapply(env, mean, USE.NAMES = FALSE))
```

```
# median and quartiles for each element (making use of "..." passing):
eapply(env, quantile, probs = 1:3/4)
eapply(env, quantile)
```

---

eigen *Spectral Decomposition of a Matrix*

---

### Description

Computes eigenvalues and eigenvectors of real (double, integer, logical) or complex matrices.

### Usage

```
eigen(x, symmetric, only.values = FALSE, EISPACK = FALSE)
```

### Arguments

<code>x</code>	a matrix whose spectral decomposition is to be computed.
<code>symmetric</code>	if TRUE, the matrix is assumed to be symmetric (or Hermitian if complex) and only its lower triangle (diagonal included) is used. If <code>symmetric</code> is not specified, the matrix is inspected for symmetry.
<code>only.values</code>	if TRUE, only the eigenvalues are computed and returned, otherwise both eigenvalues and eigenvectors are returned.
<code>EISPACK</code>	logical. Should EISPACK be used (for compatibility with R < 1.7.0)?

### Details

By default `eigen` uses the LAPACK routines DSYEVR, DGEEV, ZHEEV and ZGEEV whereas `eigen(EISPACK = TRUE)` provides an interface to the EISPACK routines RS, RG, CH and CG.

If `symmetric` is unspecified, the code attempts to determine if the matrix is symmetric up to plausible numerical inaccuracies. It is faster and surer to set the value yourself.

`eigen` is preferred to `eigen(EISPACK = TRUE)` for new projects, but its eigenvectors may differ in sign and (in the asymmetric case) in normalization. (They may also differ between methods and between platforms.)

Computing the eigenvectors is the slow part for large matrices.

Computing the eigendecomposition of a matrix is subject to errors on a real-world computer: the definitive analysis is Wilkinson (1965). All you can hope for is a solution to a problem suitably close to `x`. So even though a real asymmetric `x` may have an algebraic solution with repeated real eigenvalues, the computed solution may be of a similar matrix with complex conjugate pairs of eigenvalues.

### Value

The spectral decomposition of `x` is returned as components of a list with components

<code>values</code>	a vector containing the $p$ eigenvalues of <code>x</code> , sorted in <i>decreasing</i> order, according to <code>Mod(values)</code> in the asymmetric case when they might be complex (even for real matrices). For real asymmetric matrices the vector will be complex only if complex conjugate pairs of eigenvalues are detected.
---------------------	---

vectors either a  $p \times p$  matrix whose columns contain the eigenvectors of  $x$ , or NULL if `only.values` is TRUE.  
 For `eigen(, symmetric = FALSE, EISPACK = TRUE)` the choice of length of the eigenvectors is not defined by EISPACK. In all other cases the vectors are normalized to unit length.  
 Recall that the eigenvectors are only defined up to a constant: even when the length is specified they are still only defined up to a scalar of modulus one (the sign for real matrices).

## References

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- Smith, B. T, Boyle, J. M., Dongarra, J. J., Garbow, B. S., Ikebe, Y., Klema, V., and Moler, C. B. (1976). *Matrix Eigensystems Routines – EISPACK Guide*. Springer-Verlag Lecture Notes in Computer Science **6**.
- Anderson. E. and ten others (1999) *LAPACK Users' Guide*. Third Edition. SIAM.  
 Available on-line at [http://www.netlib.org/lapack/lug/lapack\\_lug.html](http://www.netlib.org/lapack/lug/lapack_lug.html).
- Wilkinson, J. H. (1965) *The Algebraic Eigenvalue Problem*. Clarendon Press, Oxford.

## See Also

`svd`, a generalization of `eigen`; `qr`, and `chol` for related decompositions.  
 To compute the determinant of a matrix, the `qr` decomposition is much more efficient: `det`.

## Examples

```
eigen(cbind(c(1,-1),c(-1,1)))
eigen(cbind(c(1,-1),c(-1,1)), symmetric = FALSE)
# same (different algorithm).

eigen(cbind(1,c(1,-1)), only.values = TRUE)
eigen(cbind(-1,2:1)) # complex values
eigen(print(cbind(c(0,1i), c(-1i,0)))) # Hermite ==> real Eigen values
## 3 x 3:
eigen(cbind( 1,3:1,1:3))
eigen(cbind(-1,c(1:2,0),0:2)) # complex values
```

---

encodeString

*Encode Character Vector as for Printing*

---

## Description

`encodeString` escapes the strings in a character vector in the same way `print.default` does, and optionally fits the encoded strings within a field width.

## Usage

```
encodeString(x, width = 0, quote = "\"", na.encode = TRUE,
             justify = c("left", "right", "centre", "none"))
```

**Arguments**

<code>x</code>	A character vector, or an object that can be coerced to one by <code>as.character</code> .
<code>width</code>	integer: the minimum field width. If <code>NULL</code> or <code>NA</code> , this is taken to be the largest field width needed for any element of <code>x</code> .
<code>quote</code>	character: quoting character, if any.
<code>na.encode</code>	logical: should <code>NA</code> strings be encoded?
<code>justify</code>	character: partial matches are allowed. If padding to the minimum field width is needed, how should spaces be inserted? <code>justify == "none"</code> is equivalent to <code>width = 0</code> , for consistency with <code>format.default</code> .

**Details**

This escapes backslash and the control characters `'\a'` (bell), `'\b'` (backspace), `'\f'` (formfeed), `'\n'` (line feed), `'\r'` (carriage return), `'\t'` (tab) and `'\v'` (vertical tab) as well as any non-printable characters in a single-byte locale, which are printed in octal notation (`'\xyz'` with leading zeroes).

Which characters are non-printable depends on the current locale. Windows' reporting of printable characters is unreliable, so there all other control characters are regarded as non-printable, and all characters with codes 32–255 as printable in a single-byte locale. See `print.default` for how non-printable characters are handled in multi-byte locales.

If `quote` is a single or double quote any embedded quote of the same type is escaped. Note that justification is of the quoted string, hence spaces are added outside the quotes.

**Value**

A character vector of the same length as `x`, with the same attributes (including names and dimensions) but with no class set.

**Note**

The default for `width` is different from `format.default`, which does similar things for character vectors but without encoding using escapes.

**See Also**

`print.default`

**Examples**

```
x <- "ab\bc\ndef"
print(x)
cat(x) # interprets escapes
cat(encodeString(x), "\n", sep="") # similar to print()

factor(x) # makes use of this to print the levels

x <- c("a", "ab", "abcde")
encodeString(x, width = NA) # left justification
encodeString(x, width = NA, justify = "c")
encodeString(x, width = NA, justify = "r")
encodeString(x, width = NA, quote = "'", justify = "r")
```



Encoding

*Read or Set the Declared Encodings for a Character Vector***Description**

Read or set the declared encodings for a character vector.

**Usage**

```
Encoding(x)
```

```
Encoding(x) <- value
```

```
enc2native(x)
```

```
enc2utf8(x)
```

**Arguments**

<code>x</code>	A character vector.
<code>value</code>	A character vector of positive length.

**Details**

Character strings in **R** can be declared to be in "latin1" or "UTF-8". These declarations can be read by `Encoding`, which will return a character vector of values "latin1", "UTF-8" or "unknown", or `set`, when `value` is recycled as needed and other values are silently treated as "unknown". ASCII strings will never be marked with a declared encoding, since their representation is the same in all encodings.

`enc2native` and `enc2utf8` convert elements of character vectors to the native encoding or UTF-8 respectively, taking any marked encoding into account. They are [primitive](#) functions, designed to do minimal copying.

There are other ways for character strings to acquire a declared encoding apart from explicitly setting it (and these have changed as **R** has evolved). Functions `scan`, `read.table`, `readLines`, and `parse` have an `encoding` argument that is used to declare encodings, `iconv` declares encodings from its `from` argument, and console input in suitable locales is also declared. `intToUtf8` declares its output as "UTF-8", and output text connections are marked if running in a suitable locale. Under some circumstances (see its help page) `source(encoding=)` will mark encodings of character strings it outputs.

Most character manipulation functions will set the encoding on output strings if it was declared on the corresponding input. These include `chartr`, `strsplit` (`useBytes = FALSE`), `tolower` and `toupper` as well as `sub` (`useBytes = FALSE`) and `gsub` (`useBytes = FALSE`). Note that such functions do not *preserve* the encoding, but if they know the input encoding and that the string has been successfully re-encoded (to the current encoding or UTF-8), they mark the output.

`substr` does preserve the encoding, and `chartr`, `tolower` and `toupper` preserve UTF-8 encoding on systems with Unicode wide characters. With their `fixed` and `perl` options, `strsplit`, `sub` and `gsub` will give a marked UTF-8 result if any of the inputs are UTF-8.

`paste` and `sprintf` return a UTF-8 marked element if any of the inputs to that element is marked as UTF-8.

`match`, `pmatch`, `charmatch`, `duplicated` and `unique` all match in UTF-8 if any of the elements are marked as UTF-8.

## Value

A character vector.

## Examples

```
## x is intended to be in latin1
x <- "fa\xE7ile"
Encoding(x)
Encoding(x) <- "latin1"
x
xx <- iconv(x, "latin1", "UTF-8")
Encoding(c(x, xx))
c(x, xx)
```

---

environment

*Environment Access*

---

## Description

Get, set, test for and create environments.

## Usage

```
environment(fun = NULL)
environment(fun) <- value
```

```
is.environment(x)
```

```
.GlobalEnv
globalenv()
.BaseNamespaceEnv
```

```
emptyenv()
baseenv()
```

```
new.env(hash = FALSE, parent = parent.frame(), size = 29L)
```

```
parent.env(env)
parent.env(env) <- value
```

```
environmentName(env)
```

```
env.profile(env)
```

**Arguments**

<code>fun</code>	a <a href="#">function</a> , a <a href="#">formula</a> , or <code>NULL</code> , which is the default.
<code>value</code>	an environment to associate with the function
<code>x</code>	an arbitrary R object.
<code>hash</code>	a logical, if <code>TRUE</code> the environment will be hashed
<code>parent</code>	an environment to be used as the enclosure of the environment created.
<code>env</code>	an environment
<code>size</code>	an integer specifying the initial size for a hashed environment. An internal default value will be used if <code>size</code> is <code>NA</code> or zero. This argument is ignored if <code>hash</code> is <code>FALSE</code> .

**Details**

Environments consist of a *frame*, or collection of named objects, and a pointer to an *enclosing environment*. The most common example is the frame of variables local to a function call; its enclosure is the environment where the function was defined. The enclosing environment is distinguished from the *parent frame*: the latter (returned by `parent.frame`) refers to the environment of the caller of a function.

When `get` or `exists` search an environment with the default `inherits = TRUE`, they look for the variable in the frame, then in the enclosing frame, and so on.

The global environment `.GlobalEnv`, more often known as the user's workspace, is the first item on the search path. It can also be accessed by `globalenv()`. On the search path, each item's enclosure is the next item.

The object `.BaseNamespaceEnv` is the name space environment for the base package. The environment of the base package itself is available as `baseenv()`. The ultimate enclosure of any environment is the empty environment `emptyenv()`, to which nothing may be assigned. If one follows the `parent.env()` chain of enclosures back far enough from any environment, eventually one reaches the empty environment.

The replacement function `parent.env<-` is extremely dangerous as it can be used to destructively change environments in ways that violate assumptions made by the internal C code. It may be removed in the near future.

The replacement form of `environment`, `is.environment`, `baseenv`, `emptyenv` and `globalenv` are [primitive](#) functions.

**Value**

If `fun` is a function or a formula then `environment(fun)` returns the environment associated with that function or formula. If `fun` is `NULL` then the current evaluation environment is returned.

The replacement form sets the environment of the function or formula `fun` to the `value` given.

`is.environment(obj)` returns `TRUE` if and only if `obj` is an environment.

`new.env` returns a new (empty) environment enclosed in the parent's environment, by default.

`parent.env` returns the parent environment of its argument.

`parent.env<-` sets the enclosing environment of its first argument.

`environmentName` returns a character string, that given when the environment is printed or "" if it is not a named environment.

`env.profile` returns a list with the following components: `size` the number of chains that can be stored in the hash table, `nchains` the number of non-empty chains in the table (as reported

by HASHPRI), and `counts` an integer vector giving the length of each chain (zero for empty chains). This function is intended to assess the performance of hashed environments. When `env` is a non-hashed environment, `NULL` is returned.

### See Also

The `envir` argument of `eval`, `get`, and `exists`.

`ls` may be used to view the objects in an environment, and hence `ls.str` may be useful for an overview.

`sys.source` can be used to populate an environment.

### Examples

```
f <- function() "top level function"

##-- all three give the same:
environment()
environment(f)
.GlobalEnv

ls(envir=environment(stats::approxfun(1:2,1:2, method="const")))

is.environment(.GlobalEnv) # TRUE

e1 <- new.env(parent = baseenv()) # this one has enclosure package:base.
e2 <- new.env(parent = e1)
assign("a", 3, envir=e1)
ls(e1)
ls(e2)
exists("a", envir=e2) # this succeeds by inheritance
exists("a", envir=e2, inherits = FALSE)
exists("+", envir=e2) # this succeeds by inheritance

eh <- new.env(hash = TRUE, size = NA)
with(env.profile(eh), stopifnot(size == length(counts)))
```

---

EnvVar

*Environment Variables*

---

### Description

Details of some of the environment variables which affect an R session.

### Details

It is impossible to list all the environment variables which can affect an R session: some affect the OS system functions which R uses, and others will affect add-on packages. But here are notes on some of the more important ones. Those that set the defaults for options are consulted only at startup (as are some of the others).

**HOME:** The user's 'home' directory.

**LANGUAGE:** Optional. The language(s) to be used for message translations. This is consulted when needed.

- LC\_ALL:** (etc) Optional. Use to set various aspects of the locale – see [Sys.getlocale](#). Consulted at startup.
- R\_BATCH:** Optional – set in a batch session.
- R\_BROWSER:** The path to the default browser. Used to set the default value of `options("browser")`.
- R\_COMPLETION:** Optional. If set to `FALSE`, command-line completion is not used. (Not used by Mac OS GUI.)
- R\_DEFAULT\_PACKAGES:** A comma-separated list of packages which are to be loaded in every session. See [options](#).
- R\_DOC\_DIR:** The location of the R ‘doc’ directory. Set by R.
- R\_DVIPSCMD:** The path to `dvips`. Defaults to the value of `DVIPS`, and if that is unset to a value determined when R was built. Used at startup to set the default for `options("dvipscmd")`, used by `help(help_type="ps")`.
- R\_ENVIRON:** Optional. The path to the site environment file: see [Startup](#). Consulted at startup.
- R\_GSCMD:** Optional. The path to GhostScript, used by `dev2bitmap`, `bitmap` and `embedFonts`. Consulted when those functions are invoked.
- R\_HISTFILE:** Optional. The path of the history file: see [Startup](#). Consulted at startup and when the history is saved.
- R\_HISTSIZE:** Optional. The maximum size of the history file, in lines. Exactly how this is used depends on the interface. For the `readline` command-line interface it takes effect when the history is saved (by `savehistory` or at the end of a session).
- R\_HOME:** The top-level directory of the R installation: see [R.home](#). Set by R.
- R\_INCLUDE\_DIR:** The location of the R ‘include’ directory. Set by R.
- R\_LATEXCMD:** The path to `latex`. Defaults to the value of `LATEX`, and if that is unset to a value determined when R was built. Used by R CMD `Rd2dvi`.
- R\_LIBS:** Optional. Used for initial setting of `.libPaths`.
- R\_LIBS\_SITE:** Optional. Used for initial setting of `.libPaths`.
- R\_LIBS\_USER:** Optional. Used for initial setting of `.libPaths`.
- R\_MAKEINDEXCMD:** The path to `makeindex`. Defaults at startup to the value of `MAKEINDEX`, and if that is unset to a value determined when R was built. Used by R CMD `Rd2dvi`.
- R\_PAPERSIZE:** Optional. Used to set the default for `options("papersize")`, e.g. used by `pdf` and `postscript`.
- R\_PDFLATEXCMD:** The path to `pdflatex`. Defaults at startup to the value of `PDFLATEX`, and if that is unset to a value determined when R was built. Used by R CMD `Rd2dvi`.
- R\_PDFVIEWER:** The path to the default PDF viewer. Used by R CMD `Rd2dvi --pdf`.
- R\_PLATFORM:** The platform – a string of the form `cpu-vendor-os`, see [R.Version](#).
- R\_PROFILE:** Optional. The path to the site profile file: see [Startup](#). Consulted at startup.
- R\_RD4DVI:** Options for `latex` processing of Rd files. Used by R CMD `Rd2dvi`.
- R\_RD4PDF:** Options for `pdflatex` processing of Rd files. Used by R CMD `Rd2dvi`.
- R\_SHARE\_DIR:** The location of the R ‘share’ directory. Set by R.
- R\_TEXI2DVICMD:** The path to `texi2dvi`. Defaults to the value of `TEXI2DVI`, and if that is unset to a value determined when R was built. Consulted at startup to set the default for `options("texi2dvi")`, used by `texi2dvi` in package `tools`.
- R\_UNZIPCMD:** The path to `unzip`. Sets the initial value for `options("unzip")` on a Unix-like when package `utils` is loaded.

**R\_ZIPCMD:** The path to `zip`. Only used in R itself by `R CMD INSTALL --build` on Windows.

**TMPDIR, TMP, TEMP:** Consulted (in that order) when setting the temporary directory for the session: see [tempdir](#). `TMPDIR` is also used by some of the utilities see the help for [build](#).

**TZ:** Optional. The current timezone. See [Sys.timezone](#) for the system-specific formats. Consulted as needed.

**no\_proxy, http\_proxy, ftp\_proxy:** (and more). Optional. Settings for [download.file](#): see its help for further details.

### Unix-specific

Some variables set on Unix-alikes, and not (in general) on Windows.

**DISPLAY:** Optional: used by [X11](#), [Tk](#) (in package `tktk`), the data editor and various packages.

**EDITOR:** The path to the default editor: sets the default for `options("editor")` when package `utils` is loaded.

**PAGER:** The path to the pager with the default setting of `options("pager")`. The default value is chosen at configuration, usually as the path to `less`.

**R\_PRINTCMD:** Sets the default for `options("printcmd")`, which sets the default print command to be used by `postscript`.

### See Also

[Sys.getenv](#) and [Sys.setenv](#) to read and set environmental variables in an R session.

---

 eval

*Evaluate an (Unevaluated) Expression*


---

### Description

Evaluate an R expression in a specified environment.

### Usage

```
eval(expr, envir = parent.frame(),
      enclos = if(is.list(envir) || is.pairlist(envir))
                parent.frame() else baseenv())
evalq(expr, envir, enclos)
eval.parent(expr, n = 1)
local(expr, envir = new.env())
```

### Arguments

<code>expr</code>	an object to be evaluated. See ‘Details’.
<code>envir</code>	the <a href="#">environment</a> in which <code>expr</code> is to be evaluated. May also be <code>NULL</code> , a list, a data frame, a pairlist or an integer as specified to <a href="#">sys.call</a> .
<code>enclos</code>	Relevant when <code>envir</code> is a (pair)list or a data frame. Specifies the enclosure, i.e., where R looks for objects not found in <code>envir</code> . This can be <code>NULL</code> (interpreted as the base package environment) or an environment.
<code>n</code>	number of parent generations to go back

## Details

`eval` evaluates the `expr` argument in the environment specified by `envir` and returns the computed value. If `envir` is not specified, then the default is `parent.frame()` (the environment where the call to `eval` was made).

Objects to be evaluated can be of types `call` or `expression` or `name` (when the name is looked up in the current scope and its binding is evaluated), a `promise` or any of the basic types such as vectors, functions and environments (which are returned unchanged).

The `evalq` form is equivalent to `eval(quote(expr), ...)`. `eval` evaluates its first argument in the current scope before passing it to the evaluator: `evalq` avoids this.

`eval.parent(expr, n)` is a shorthand for `eval(expr, parent.frame(n))`.

If `envir` is a list (such as a data frame) or pairlist, it is copied into a temporary environment (with enclosure `enclos`), and the temporary environment is used for evaluation. So if `expr` changes any of the components named in the (pair)list, the changes are lost.

If `envir` is `NULL` it is interpreted as an empty list so no values could be found in `envir` and look-up goes directly to `enclos`.

`local` evaluates an expression in a local environment. It is equivalent to `evalq` except that its default argument creates a new, empty environment. This is useful to create anonymous recursive functions and as a kind of limited name space feature since variables defined in the environment are not visible from the outside.

## Value

The result of evaluating the object: for an expression vector this is the result of evaluating the last elements.

## Note

Due to the difference in scoping rules, there are some differences between R and S in this area. In particular, the default enclosure in S is the global environment.

When evaluating expressions in a data frame that has been passed as an argument to a function, the relevant enclosure is often the caller's environment, i.e., one needs `eval(x, data, parent.frame())`.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (eval only.)

## See Also

`expression`, `quote`, `sys.frame`, `parent.frame`, `environment`.

Further, `force` to *force* evaluation, typically of function arguments.

## Examples

```
eval(2 ^ 2 ^ 3)
mEx <- expression(2^2^3); mEx; 1 + eval(mEx)
eval({ xx <- pi; xx^2}) ; xx

a <- 3 ; aa <- 4 ; evalq(evalq(a+b+aa, list(a=1)), list(b=5)) # == 10
a <- 3 ; aa <- 4 ; evalq(evalq(a+b+aa, -1), list(b=5))      # == 12
```

```

ev <- function() {
  e1 <- parent.frame()
  ## Evaluate a in e1
  aa <- eval(expression(a),e1)
  ## evaluate the expression bound to a in e1
  a <- expression(x+y)
  list(aa = aa, eval = eval(a, e1))
}
tst.ev <- function(a = 7) { x <- pi; y <- 1; ev() }
tst.ev()#-> aa : 7,  eval : 4.14

a <- list(a=3, b=4)
with(a, a <- 5) # alters the copy of a from the list, discarded.

##
## Example of evalq()
##

N <- 3
env <- new.env()
assign("N", 27, envir=env)
## this version changes the visible copy of N only, since the argument
## passed to eval is '4'.
eval(N <- 4, env)
N
get("N", envir=env)
## this version does the assignment in env, and changes N only there.
evalq(N <- 5, env)
N
get("N", envir=env)

##
## Uses of local()
##

# Mutually recursive.
# gg gets value of last assignment, an anonymous version of f.

gg <- local({
  k <- function(y)f(y)
  f <- function(x) if(x) x*k(x-1) else 1
})
gg(10)
sapply(1:5, gg)

# Nesting locals. a is private storage accessible to k
gg <- local({
  k <- local({
    a <- 1
    function(y){print(a <<- a+1);f(y)}
  })
  f <- function(x) if(x) x*k(x-1) else 1
})
sapply(1:5, gg)

```



```
ls(envir=environment(gg))
ls(envir=environment(get("k", envir=environment(gg)))
```

exists

*Is an Object Defined?***Description**

Look for an R object of the given name.

**Usage**

```
exists(x, where = -1, envir = , frame, mode = "any",
       inherits = TRUE)
```

**Arguments**

<code>x</code>	a variable name (given as a character string).
<code>where</code>	where to look for the object (see the details section); if omitted, the function will search as if the name of the object appeared unquoted in an expression.
<code>envir</code>	an alternative way to specify an environment to look in, but it is usually simpler to just use the <code>where</code> argument.
<code>frame</code>	a frame in the calling list. Equivalent to giving <code>where</code> as <code>sys.frame(frame)</code> .
<code>mode</code>	the mode or type of object sought: see the ‘Details’ section.
<code>inherits</code>	should the enclosing frames of the environment be searched?

**Details**

The `where` argument can specify the environment in which to look for the object in any of several ways: as an integer (the position in the [search](#) list); as the character string name of an element in the search list; or as an [environment](#) (including using `sys.frame` to access the currently active function calls). The `envir` argument is an alternative way to specify an environment, but is primarily there for back compatibility.

This function looks to see if the name `x` has a value bound to it in the specified environment. If `inherits` is `TRUE` and a value is not found for `x` in the specified environment, the enclosing frames of the environment are searched until the name `x` is encountered. See [environment](#) and the ‘R Language Definition’ manual for details about the structure of environments and their enclosures.

**Warning:** `inherits = TRUE` is the default behaviour for R but not for S.

If `mode` is specified then only objects of that type are sought. The `mode` may specify one of the collections "numeric" and "function" (see [mode](#)): any member of the collection will suffice. (This is true even if a member of a collection is specified, so for example `mode="special"` will seek any type of function.)

**Value**

Logical, true if and only if an object of the correct name and mode is found.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[get](#).

## Examples

```
## Define a substitute function if necessary:
if(!exists("some.fun", mode="function"))
  some.fun <- function(x) { cat("some.fun(x)\n"); x }
search()
exists("ls", 2) # true even though ls is in pos=3
exists("ls", 2, inherits = FALSE) # false
```

---

expand.grid

*Create a Data Frame from All Combinations of Factors*

---

## Description

Create a data frame from all combinations of the supplied vectors or factors. See the description of the return value for precise details of the way this is done.

## Usage

```
expand.grid(..., KEEP.OUT.ATTRS = TRUE, stringsAsFactors = TRUE)
```

## Arguments

`...` vectors, factors or a list containing these.

`KEEP.OUT.ATTRS` a logical indicating the "out.attrs" attribute (see below) should be computed and returned.

`stringsAsFactors` logical specifying if character vectors are converted to factors.

## Value

A data frame containing one row for each combination of the supplied factors. The first factors vary fastest. The columns are labelled by the factors if these are supplied as named arguments or named components of a list. The row names are 'automatic'.

Attribute "out.attrs" is a list which gives the dimension and dimnames for use by [predict](#) methods.

## Note

Character vectors have always been converted to factors: this became optional in R 2.9.1. Conversion is done with levels in the order they occur in the character vectors (and not alphabetically, as is most common when converting to factors).

## References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

## See Also

`combn` (package `utils`) for the generation of all combinations of `n` elements, taken `m` at a time.

## Examples

```
require(utils)

expand.grid(height = seq(60, 80, 5), weight = seq(100, 300, 50),
            sex = c("Male", "Female"))

x <- seq(0,10, length.out=100)
y <- seq(-1,1, length.out=20)
d1 <- expand.grid(x=x, y=y)
d2 <- expand.grid(x=x, y=y, KEEP.OUT.ATTRS = FALSE)
object.size(d1) - object.size(d2)
##-> 5992 or 8832 (on 32- / 64-bit platform)
```

---

expression

*Unevaluated Expressions*

---

## Description

Creates or tests for objects of mode "expression".

## Usage

```
expression(...)

is.expression(x)
as.expression(x, ...)
```

## Arguments

...            expression: R objects, typically calls, symbols or constants.  
               as.expression: arguments to be passed to methods.

x              an arbitrary R object.

## Details

‘Expression’ here is not being used in its colloquial sense, that of mathematical expressions. Those are calls (see [call](#)) in R, and an R expression vector is a list of calls, symbols etc, typically as returned by [parse](#).

As an object of mode "expression" is a list, it can be subsetted by both `[` and by `[[`, the latter extracting individual calls etc.

`expression` and `is.expression` are [primitive](#) functions. `expression` is ‘special’: it does not evaluate its arguments.

**Value**

`expression` returns a vector of type "expression" containing its arguments (unevaluated).

`is.expression` returns TRUE if `expr` is an expression object and FALSE otherwise.

`as.expression` attempts to coerce its argument into an expression object. It is generic, and only the default method is described here. NULL, calls, symbols (see [as.symbol](#)) and pairlists are returned as the element of a length-one expression vector. Vectors (including lists) are placed element-by-element into an expression vector. Other types are not currently supported.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[call](#), [eval](#), [function](#). Further, [text](#) and [legend](#) for plotting mathematical expressions.

**Examples**

```
length(ex1 <- expression(1+ 0:9))# 1
ex1
eval(ex1)# 1:10

length(ex3 <- expression(u,v, 1+ 0:9))# 3
mode(ex3 [3]) # expression
mode(ex3[[3]])# call
rm(ex3)
```

---

 Extract

---

*Extract or Replace Parts of an Object*


---

**Description**

Operators acting on vectors, matrices, arrays and lists to extract or replace parts.

**Usage**

```
x[i]
x[i, j, ... , drop = TRUE]
x[[i, exact = TRUE]]
x[[i, j, ..., exact = TRUE]]
x$name

x[i] <- value
x[i, j, ...] <- value
x$i <- value
```

**Arguments**

<code>x</code>	object from which to extract element(s) or in which to replace element(s).
<code>i, j, ...</code>	indices specifying elements to extract or replace. Indices are <code>numeric</code> or <code>character</code> vectors or empty (missing) or <code>NULL</code> . Numeric values are coerced to integer as by <code>as.integer</code> (and hence truncated towards zero). Character vectors will be matched to the <code>names</code> of the object (or for matrices/arrays, the <code>dimnames</code> ): see ‘Character indices’ below for further details. For [-indexing only: <code>i, j, ...</code> can be logical vectors, indicating elements/slices to select. Such vectors are recycled if necessary to match the corresponding extent. <code>i, j, ...</code> can also be negative integers, indicating elements/slices to leave out of the selection. When indexing arrays by <code>[</code> a single argument <code>i</code> can be a matrix with as many columns as there are dimensions of <code>x</code> ; the result is then a vector with elements corresponding to the sets of indices in each row of <code>i</code> . An index value of <code>NULL</code> is treated as if it were <code>integer(0)</code> .
<code>name</code>	A literal character string or a <code>name</code> (possibly <code>backtick</code> quoted). For extraction, this is normally (see under ‘Environments’) partially matched to the <code>names</code> of the object.
<code>drop</code>	For matrices and arrays. If <code>TRUE</code> the result is coerced to the lowest possible dimension (see the examples). This only works for extracting elements, not for the replacement. See <code>drop</code> for further details.
<code>exact</code>	Controls possible partial matching of <code>[</code> when extracting by a character vector (for most objects, but see under ‘Environments’). The default is no partial matching. Value <code>NA</code> allows partial matching but issues a warning when it occurs. Value <code>FALSE</code> allows partial matching without any warning.
<code>value</code>	typically an array-like R object of a similar class as <code>x</code> .

**Details**

These operators are generic. You can write methods to handle indexing of specific classes of objects, see [InternalMethods](#) as well as `[.data.frame` and `[.factor`. The descriptions here apply only to the default methods. Note that separate methods are required for the replacement functions `[<-`, `[<=<-` and `$<-` for use when indexing occurs on the assignment side of an expression.

The most important distinction between `[`, `[` and `$` is that the `[` can select more than one element whereas the other two select a single element.

The default methods work somewhat differently for atomic vectors, matrices/arrays and for recursive (list-like, see [is.recursive](#)) objects. `$` is only valid for recursive objects, and is only discussed in the section below on recursive objects. Its use on non-recursive objects was deprecated in R 2.5.0 and removed in R 2.7.0.

Subsetting (except by an empty index) will drop all attributes except `names`, `dim` and `dimnames`.

Indexing can occur on the right-hand-side of an expression for extraction, or on the left-hand-side for replacement. When an index expression appears on the left side of an assignment (known as *subassignment*) then that part of `x` is set to the value of the right hand side of the assignment. In this case no partial matching of character indices is done, and the left-hand-side is coerced as needed to accept the values. Attributes are preserved (although `names`, `dim` and `dimnames` will be adjusted suitably). Subassignment is done sequentially, so if an index is specified more than once the latest assigned value for an index will result.

It is an error to apply any of these operators to an object which is not subsettable (e.g. a function).

### Atomic vectors

The usual form of indexing is `"["`. `"[[["` can be used to select a single element *dropping names*, whereas `"["` keeps them, e.g., in `c(abc = 123)[1]`.

The index object `i` can be numeric, logical, character or empty. Indexing by factors is allowed and is equivalent to indexing by the numeric codes (see `factor`) and not by the character values which are printed (for which use `[as.character(i)]`).

An empty index selects all values: this is most often used to replace all the entries but keep the `attributes`.

### Matrices and arrays

Matrices and arrays are vectors with a dimension attribute and so all the vector forms of indexing can be used with a single index. The result will be an unnamed vector unless `x` is one-dimensional when it will be a one-dimensional array.

The most common form of indexing a  $k$ -dimensional array is to specify  $k$  indices to `[`. As for vector indexing, the indices can be numeric, logical, character, empty or even factor. An empty index (a comma separated blank) indicates that all entries in that dimension are selected. The argument `drop` applies to this form of indexing.

A third form of indexing is via a numeric matrix with the one column for each dimension: each row of the index matrix then selects a single element of the array, and the result is a vector. Negative indices are not allowed in the index matrix. `NA` and zero values are allowed: rows of an index matrix containing a zero are ignored, whereas rows containing an `NA` produce an `NA` in the result.

Indexing via a character matrix with one column per dimensions is also supported if the array has dimension names. As with numeric matrix indexing, each row of the index matrix selects a single element of the array. Indices are matched against the appropriate dimension names. `NA` is allowed and will produce an `NA` in the result. Unmatched indices as well as the empty string `" "` are not allowed and will result in an error.

A vector obtained by matrix indexing will be unnamed unless `x` is one-dimensional when the row names (if any) will be indexed to provide names for the result.

### Recursive (list-like) objects

Indexing by `[` is similar to atomic vectors and selects a list of the specified element(s).

Both `[[` and `$` select a single element of the list. The main difference is that `$` does not allow computed indices, whereas `[[` does. `x$name` is equivalent to `x[["name", exact = FALSE]]`. Also, the partial matching behavior of `[[` can be controlled using the `exact` argument.

`[` and `[[` are sometimes applied to other recursive objects such as `calls` and `expressions`. Pairlists are coerced to lists for extraction by `[`, but all three operators can be used for replacement.

`[[` can be applied recursively to lists, so that if the single index `i` is a vector of length `p`, `alist[[i]]` is equivalent to `alist[[i1]]...[[ip]]` providing all but the final indexing results in a list.

When either `[[` or `$` is used for replacement, a value of `NULL` deletes the corresponding item of the list.

When `$<-` is applied to a `NULL` `x`, it first coerces `x` to `list()`. This is what also happens with `[[<-` if the replacement value `value` is of length greater than one: if `value` has length 1 or 0, `x` is first coerced to a zero-length vector of the type of `value`.

## Environments

Both `$` and `[[` can be applied to environments. Only character indices are allowed and no partial matching is done. The semantics of these operations are those of `get(i, env=x, inherits=FALSE)`. If no match is found then `NULL` is returned. The replacement versions, `$<-` and `[[<-`, can also be used. Again, only character arguments are allowed. The semantics in this case are those of `assign(i, value, env=x, inherits=FALSE)`. Such an assignment will either create a new binding or change the existing binding in `x`.

## NAs in indexing

When extracting, a numerical, logical or character NA index picks an unknown element and so returns NA in the corresponding element of a logical, integer, numeric, complex or character result, and `NULL` for a list. (It returns `00` for a raw result.)

When replacing (that is using indexing on the lhs of an assignment) NA does not select any element to be replaced. As there is ambiguity as to whether an element of the rhs should be used or not, this is only allowed if the rhs value is of length one (so the two interpretations would have the same outcome).

## Argument matching

Note that these operations do not match their index arguments in the standard way: argument names are ignored and positional matching only is used. So `m[j=2, i=1]` is equivalent to `m[2, 1]` and **not** to `m[1, 2]`.

This may not be true for methods defined for them; for example it is not true for the `data.frame` methods described in `[.data.frame]` which warn if `i` or `j` is named and have undocumented behaviour in that case.

To avoid confusion, do not name index arguments (but `drop` and `exact` must be named).

## S4 methods

These operators are also implicit S4 generics, but as primitives, S4 methods will be dispatched only on S4 objects `x`.

The implicit generics for the `$` and `$<-` operators do not have `name` in their signature because the grammar only allows symbols or string constants for the `name` argument.

## Character indices

Character indices can in some circumstances be partially matched (see `pmatch`) to the names or `dimnames` of the object being subsetted (but never for subassignment). Unlike S (Becker *et al* p. 358), R has never used partial matching when extracting by `[`, and as from R 2.7.0 partial matching is not by default used by `[[` (see argument `exact`).

Thus the default behaviour is to use partial matching only when extracting from recursive objects (except environments) by `$`. Even in that case, warnings can be switched on by `options(warnPartialMatchAttr = TRUE)`.

Neither empty (`" "`) nor NA indices match any names, not even empty nor missing names. If any object has no names or appropriate `dimnames`, they are taken as all `" "` and so match nothing.

## Note

The documented behaviour of S is that an NA replacement index ‘goes nowhere’ but uses up an element of `value` (Becker *et al* p. 359). However, that has not been true of other implementations.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[names](#) for details of matching to names, and [pmatch](#) for partial matching.

[list](#), [array](#), [matrix](#).

[\[.data.frame\]](#) and [\[.factor\]](#) for the behaviour when applied to data.frame and factors.

[Syntax](#) for operator precedence, and the *R Language* reference manual about indexing details.

## Examples

```
x <- 1:12
m <- matrix(1:6, nrow=2, dimnames=list(c("a", "b"), LETTERS[1:3]))
li <- list(pi=pi, e = exp(1))
x[10]           # the tenth element of x
x <- x[-1]      # delete the 1st element of x
m[1,]          # the first row of matrix m
m[1, , drop = FALSE] # is a 1-row matrix
m[,c(TRUE,FALSE,TRUE)] # logical indexing
m[cbind(c(1,2,1),3:1)] # matrix numeric index
ci <- cbind(c("a", "b", "a"), c("A", "C", "B"))
m[ci]          # matrix character index
m <- m[, -1]   # delete the first column of m
li[[1]]        # the first element of list li
y <- list(1,2,a=4,5)
y[c(3,4)]      # a list containing elements 3 and 4 of y
y$a           # the element of y named a

## non-integer indices are truncated:
(i <- 3.999999999) # "4" is printed
(1:5)[i] # 3

## named atomic vectors, compare "[" and "[[" :
nx <- c(abc = 123, pi = pi)
nx[1] ; nx["pi"] # keeps names, whereas "[" does not:
nx[[1]] ; nx[["pi"]]
```

```
## recursive indexing into lists
z <- list( a=list( b=9, c='hello'), d=1:5)
unlist(z)
z[[c(1, 2)]]
z[[c(1, 2, 1)]] # both "hello"
z[[c("a", "b")]] <- "new"
unlist(z)
```

```
## check $ and [[ for environments
e1 <- new.env()
e1$a <- 10
e1[["a"]]
e1[["b"]] <- 20
e1$b
ls(e1)
```



---

Extract.data.frame *Extract or Replace Parts of a Data Frame*

---

## Description

Extract or replace subsets of data frames.

## Usage

```
## S3 method for class 'data.frame':
x[i, j, drop = ]
## S3 replacement method for class 'data.frame':
x[i, j] <- value
## S3 method for class 'data.frame':
x[ [..., exact = TRUE]]
## S3 replacement method for class 'data.frame':
x[[i, j]] <- value
## S3 replacement method for class 'data.frame':
x$name <- value
```

## Arguments

<code>x</code>	data frame.
<code>i, j, ...</code>	elements to extract or replace. For <code>[</code> and <code>[[</code> , these are numeric or character or, for <code>[</code> only, empty. Numeric values are coerced to integer as if by <code>as.integer</code> . For replacement by <code>[</code> , a logical matrix is allowed.
<code>name</code>	A literal character string or a <a href="#">name</a> (possibly <a href="#">backtick</a> quoted).
<code>drop</code>	logical. If <code>TRUE</code> the result is coerced to the lowest possible dimension. The default is to drop if only one column is left, but <b>not</b> to drop if only one row is left.
<code>value</code>	A suitable replacement value: it will be repeated a whole number of times if necessary and it may be coerced: see the <a href="#">Coercion</a> section. If <code>NULL</code> , deletes the column if a single column is selected.
<code>exact</code>	logical: see <code>[</code> , and applies to column names.

## Details

Data frames can be indexed in several modes. When `[` and `[[` are used with a single index (`x[i]` or `x[[i]]`), they index the data frame as if it were a list. In this usage a `drop` argument is ignored, with a warning.

Note that there is no `data.frame` method for `$`, so `x$name` uses the default method which treats `x` as a list. There is a replacement method which checks `value` for the correct number of rows, and replicates it if necessary.

When `[` and `[[` are used with two indices (`x[i, j]` and `x[[i, j]]`) they act like indexing a matrix: `[[` can only be used to select one element.

If `[` returns a data frame it will have unique (and non-missing) row names, if necessary transforming the row names using `make.unique`. Similarly, if columns are selected column names will be transformed to be unique if necessary (e.g. if columns are selected more than once, or if more than one column of a given name is selected if the data frame has duplicate column names).

When `drop = TRUE`, this is applied to the subsetting of any matrices contained in the data frame as well as to the data frame itself.

The replacement methods can be used to add whole column(s) by specifying non-existent column(s), in which case the column(s) are added at the right-hand edge of the data frame and numerical indices must be contiguous to existing indices. On the other hand, rows can be added at any row after the current last row, and the columns will be in-filled with missing values. Missing values in the indices are not allowed for replacement.

For `[` the replacement value can be a list: each element of the list is used to replace (part of) one column, recycling the list as necessary. If columns specified by number are created, the names (if any) of the corresponding list elements are used to name the columns. If the replacement is not selecting rows, list values can contain `NULL` elements which will cause the corresponding columns to be deleted. (See the Examples.)

Matrix indexing using `[` is not recommended, and barely supported. For extraction, `x` is first coerced to a matrix. For replacement a logical matrix (only) can be used to select the elements to be replaced in the same way as for a matrix.

Both `[` and `[[` extraction methods partially match row names. By default neither partially match column names, but `[[` will unless `exact=TRUE`. If you want to do exact matching on row names use `match` as in the examples.

### Value

For `[` a data frame, list or a single column (the latter two only when dimensions have been dropped). If matrix indexing is used for extraction a matrix results. If the result would be a data frame an error results if undefined columns are selected (as there is no general concept of a 'missing' column in a data frame). Otherwise if a single column is selected and this is undefined the result is `NULL`.

For `[[` a column of the data frame or `NULL` (extraction with one index) or a length-one vector (extraction with two indices).

For `$`, a column of the data frame (or `NULL`).

For `[<-`, `[[<-` and `$<-`, a data frame.

### Coercion

The story over when replacement values are coerced is a complicated one, and one that has changed during R's development. This section is a guide only.

When `[` and `[[` are used to add or replace a whole column, no coercion takes place but `value` will be replicated (by calling the generic function `rep`) to the right length if an exact number of repeats can be used.

When `[` is used with a logical matrix, each value is coerced to the type of the column into which it is to be placed.

When `[` and `[[` are used with two indices, the column will be coerced as necessary to accommodate the value.

Note that when the replacement value is an array (including a matrix) it is *not* treated as a series of columns (as `data.frame` and `as.data.frame` do) but inserted as a single column.

### Warning

The default behaviour when only one *row* is left is equivalent to specifying `drop = FALSE`. To drop from a data frame to a list, `drop = TRUE` has to be specified explicitly.

Arguments other than `drop` and `exact` should not be named: there is a warning if they are and the behaviour differs from the description here.

**See Also**

`subset` which is often easier for extraction, `data.frame`, `Extract`.

**Examples**

```
sw <- swiss[1:5, 1:4] # select a manageable subset

sw[1:3]           # select columns
sw[, 1:3]         # same
sw[4:5, 1:3]     # select rows and columns
sw[1]             # a one-column data frame
sw[, 1, drop = FALSE] # the same
sw[, 1]          # a (unnamed) vector
sw[[1]]          # the same

sw[1,]           # a one-row data frame
sw[1,, drop=TRUE] # a list

sw["C", ] # partially matches
sw[match("C", row.names(sw)), ] # no exact match

swiss[ c(1, 1:2), ] # duplicate row, unique row names are created

sw[sw <= 6] <- 6 # logical matrix indexing
sw

## adding a column
sw["new1"] <- LETTERS[1:5] # adds a character column
sw[["new2"]] <- letters[1:5] # ditto
sw[, "new3"] <- LETTERS[1:5] # ditto
sw$new4 <- 1:5
sapply(sw, class)
sw$new4 <- NULL # delete the column
sw
sw[6:8] <- list(letters[10:14], NULL, aa=1:5)
# delete col7, update 6, append
sw

## matrices in a data frame
A <- data.frame(x=1:3, y=I(matrix(4:6)), z=I(matrix(letters[1:9],3,3)))
A[1:3, "y"] # a matrix
A[1:3, "z"] # a matrix
A[, "y"]    # a matrix
```

---

Extract.factor

*Extract or Replace Parts of a Factor*

---

**Description**

Extract or replace subsets of factors.

## Usage

```
## S3 method for class 'factor':  
x[... , drop = FALSE]  
## S3 method for class 'factor':  
x[[...]]  
## S3 replacement method for class 'factor':  
x[...] <- value
```

## Arguments

x	a factor
...	a specification of indices – see <a href="#">Extract</a> .
drop	logical. If true, unused levels are dropped.
value	character: a set of levels. Factor values are coerced to character.

## Details

When unused levels are dropped the ordering of the remaining levels is preserved.

If `value` is not in `levels(x)`, a missing value is assigned with a warning.

Any [contrasts](#) assigned to the factor are preserved unless `drop=TRUE`.

The `[ [` method supports argument `exact`.

## Value

A factor with the same set of levels as `x` unless `drop=TRUE`.

## See Also

[factor](#), [Extract](#).

## Examples

```
## following example(factor)  
(ff <- factor(substring("statistics", 1:10, 1:10), levels=letters))  
ff[, drop=TRUE]  
factor(letters[7:10])[2:3, drop = TRUE]
```

## Description

Returns the (parallel) maxima and minima of the input values.

**Usage**

```

max(..., na.rm = FALSE)
min(..., na.rm = FALSE)

pmax(..., na.rm = FALSE)
pmin(..., na.rm = FALSE)

pmax.int(..., na.rm = FALSE)
pmin.int(..., na.rm = FALSE)

```

**Arguments**

`...` numeric or character arguments (see Note).  
`na.rm` a logical indicating whether missing values should be removed.

**Details**

`max` and `min` return the maximum or minimum of *all* the values present in their arguments, as [integer](#) if all are logical or integer, as [double](#) if all are numeric, and character otherwise. If `na.rm` is `FALSE` an NA value in any of the arguments will cause a value of NA to be returned, otherwise NA values are ignored.

The minimum and maximum of a numeric empty set are `+Inf` and `-Inf` (in this order!) which ensures *transitivity*, e.g., `min(x1, min(x2)) == min(x1, x2)`. For numeric `x` `max(x) == -Inf` and `min(x) == +Inf` whenever `length(x) == 0` (after removing missing values if requested). However, `pmax` and `pmin` return NA if all the parallel elements are NA even for `na.rm = TRUE`.

`pmax` and `pmin` take one or more vectors (or matrices) as arguments and return a single vector giving the ‘parallel’ maxima (or minima) of the vectors. The first element of the result is the maximum (minimum) of the first elements of all the arguments, the second element of the result is the maximum (minimum) of the second elements of all the arguments and so on. Shorter inputs are recycled if necessary. [attributes](#) (such as [names](#) or [dim](#)) are transferred from the first argument (if applicable).

`pmax.int` and `pmin.int` are faster internal versions only used when all arguments are atomic vectors and there are no classes: they drop all attributes. (Note that all versions fail for raw and complex vectors since these have no ordering.)

`max` and `min` are generic functions: methods can be defined for them individually or via the [Summary](#) group generic. For this to work properly, the arguments `...` should be unnamed, and dispatch is on the first argument.

By definition the min/max of a numeric vector containing an NaN is NaN, except that the min/max of any vector containing an NA is NA even if it also contains an NaN. Note that `max(NA, Inf) == NA` even though the maximum would be `Inf` whatever the missing value actually is.

Character versions are sorted lexicographically, and this depends on the collating sequence of the locale in use: the help for [‘Comparison’](#) gives details. The max/min of an empty character vector is defined to be a character NA. (One could argue that as `" "` is the smallest character element, the maximum should be `" "`, but there is no obvious candidate for the minimum.)

**Value**

For `min` or `max`, a length-one vector. For `pmin` or `pmax`, a vector of length the longest of the input vectors.

The type of the result will be that of the highest of the inputs in the hierarchy integer < real < character.

For `min` and `max` if there are only numeric inputs and all are empty (after possible removal of NAs), the result is double (`Inf` or `-Inf`).

### S4 methods

`max` and `min` are part of the S4 [Summary](#) group generic. Methods for them must use the signature `x, ..., na.rm`.

### Note

'Numeric' arguments are vectors of type integer and numeric, and logical (coerced to integer). For historical reasons, `NULL` is accepted as equivalent to `integer(0)`.

`pmax` and `pmin` will also work on classed objects with appropriate methods for comparison, `is.na` and `rep` (if recycling of arguments is needed).

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[range](#) (both `min` and `max`) and [which.min](#) ([which.max](#)) for the *arg min*, i.e., the location where an extreme value occurs.

'[plotmath](#)' for the use of `min` in plot annotation.

### Examples

```
require(stats); require(graphics)
min(5:1, pi) #-> one number
pmin(5:1, pi) #-> 5 numbers

x <- sort(rnorm(100)); cH <- 1.35
pmin(cH, quantile(x)) # no names
pmin(quantile(x), cH) # has names
plot(x, pmin(cH, pmax(-cH, x)), type='b', main= "Huber's function")
```

---

factor

*Factors*

---

### Description

The function `factor` is used to encode a vector as a factor (the terms 'category' and 'enumerated type' are also used for factors). If `ordered` is `TRUE`, the factor levels are assumed to be ordered. For compatibility with `S` there is also a function `ordered`.

`is.factor`, `is.ordered`, `as.factor` and `as.ordered` are the membership and coercion functions for these classes.

**Usage**

```

factor(x = character(), levels, labels = levels,
       exclude = NA, ordered = is.ordered(x))

ordered(x, ...)

is.factor(x)
is.ordered(x)

as.factor(x)
as.ordered(x)

addNA(x, ifany=FALSE)

```

**Arguments**

<code>x</code>	a vector of data, usually taking a small number of distinct values.
<code>levels</code>	an optional vector of the values that <code>x</code> might have taken. The default is the unique set of values taken by <code>as.character(x)</code> , sorted into increasing order of <code>x</code> . Note that this set can be smaller than <code>sort(unique(x))</code> .
<code>labels</code>	<i>either</i> an optional vector of labels for the levels (in the same order as <code>levels</code> after removing those in <code>exclude</code> ), <i>or</i> a character string of length 1.
<code>exclude</code>	a vector of values to be excluded when forming the set of levels. This should be of the same type as <code>x</code> , and will be coerced if necessary.
<code>ordered</code>	logical flag to determine if the levels should be regarded as ordered (in the order given).
<code>...</code>	(in <code>ordered(.)</code> ): any of the above, apart from <code>ordered</code> itself.
<code>ifany</code>	(in <code>addNA</code> ): Only add an NA level if it is used, i.e. if <code>any(is.na(x))</code> .

**Details**

The type of the vector `x` is not restricted; it only must have an `as.character` method and be sortable (by `sort.list`).

Ordered factors differ from factors only in their class, but methods and the model-fitting functions treat the two classes quite differently.

The encoding of the vector happens as follows. First all the values in `exclude` are removed from `levels`. If `x[i]` equals `levels[j]`, then the *i*-th element of the result is *j*. If no match is found for `x[i]` in `levels`, then the *i*-th element of the result is set to `NA`.

Normally the ‘levels’ used as an attribute of the result are the reduced set of levels after removing those in `exclude`, but this can be altered by supplying `labels`. This should either be a set of new labels for the levels, or a character string, in which case the levels are that character string with a sequence number appended.

`factor(x, exclude=NULL)` applied to a factor is a no-operation unless there are unused levels: in that case, a factor with the reduced level set is returned. If `exclude` is used it should also be a factor with the same level set as `x` or a set of codes for the levels to be excluded.

The codes of a factor may contain `NA`. For a numeric `x`, set `exclude=NULL` to make `NA` an extra level (prints as `<NA>`); by default, this is the last level.

If `NA` is a level, the way to set a code to be missing (as opposed to the code of the missing level) is to use `is.na` on the left-hand-side of an assignment (as in `is.na(f)[i] <- TRUE`; indexing

inside `is.na` does not work). Under those circumstances missing values are currently printed as `<NA>`, i.e., identical to entries of level NA.

`is.factor` is generic: you can write methods to handle specific classes of objects, see [Internal-Methods](#).

## Value

`factor` returns an object of class `"factor"` which has a set of integer codes the length of `x` with a `"levels"` attribute of mode `character` and unique (`!anyDuplicated(.)`) entries. If `ordered` is true (or `ordered` is used) the result has class `c("ordered", "factor")`.

Applying `factor` to an ordered or unordered factor returns a factor (of the same type) with just the levels which occur: see also `[.factor]` for a more transparent way to achieve this.

`is.factor` returns TRUE or FALSE depending on whether its argument is of type factor or not. Correspondingly, `is.ordered` returns TRUE when its argument is ordered and FALSE otherwise.

`as.factor` coerces its argument to a factor. It is an abbreviated form of `factor`.

`as.ordered(x)` returns `x` if this is ordered, and `ordered(x)` otherwise.

`addNA` modifies a factor by turning NA into an extra level (so that NA values are counted in tables, for instance).

## Warning

The interpretation of a factor depends on both the codes and the `"levels"` attribute. Be careful only to compare factors with the same set of levels (in the same order). In particular, `as.numeric` applied to a factor is meaningless, and may happen by implicit coercion. To transform a factor `f` to approximately its original numeric values, `as.numeric(levels(f))[f]` is recommended and slightly more efficient than `as.numeric(as.character(f))`.

The levels of a factor are by default sorted, but the sort order may well depend on the locale at the time of creation, and should not be assumed to be ASCII.

There are some anomalies associated with factors that have NA as a level. It is suggested to use them sparingly, e.g., only for tabulation purposes.

## Comparison operators and group generic methods

There are `"factor"` and `"ordered"` methods for the [group generic Ops](#), which provide methods for the [Comparison](#) operators. (The rest of the group and the [Math](#) and [Summary](#) groups generate an error as they are not meaningful for factors.)

Only `==` and `!=` can be used for factors: a factor can only be compared to another factor with an identical set of levels (not necessarily in the same ordering) or to a character vector. Ordered factors are compared in the same way, but the general dispatch mechanism precludes comparing ordered and unordered factors.

All the comparison operators are available for ordered factors. Sorting is done by the levels of the operands: if both operands are ordered factors they must have the same level set.

## Note

In earlier versions of R, storing character data as a factor was more space efficient if there is even a small proportion of repeats. Since R 2.6.0 identical character strings share storage, so the difference is now small in most cases. (Integer values are stored in 4 bytes whereas each reference to a character string needs a pointer of 4 or 8 bytes.)



## References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

## See Also

[.factor for subsetting of factors.

gl for construction of balanced factors and C for factors with specified contrasts. levels and nlevels for accessing the levels, and unclass to get integer codes.

## Examples

```
(ff <- factor(substring("statistics", 1:10, 1:10), levels=letters))
as.integer(ff) # the internal codes
factor(ff)     # drops the levels that do not occur
ff[, drop=TRUE] # the same, more transparently

factor(letters[1:20], labels="letter")

class(ordered(4:1)) # "ordered", inheriting from "factor"

## suppose you want "NA" as a level, and to allow missing values.
(x <- factor(c(1, 2, NA), exclude = NULL))
is.na(x)[2] <- TRUE
x # [1] 1 <NA> <NA>
is.na(x)
# [1] FALSE TRUE FALSE

## Using addNA()
Month <- airquality$Month
table(addNA(Month))
table(addNA(Month, ifany=TRUE))
```

---

file.access

*Ascertain File Accessibility*

---

## Description

Utility function to access information about files on the user's file systems.

## Usage

```
file.access(names, mode = 0)
```

## Arguments

names	character vector containing file names.
mode	integer specifying access mode required.

## Details

Tilde-expansion is done on names: see [path.expand](#).

The mode value can be the exclusive or of the following values

- 0** test for existence.
- 1** test for execute permission.
- 2** test for write permission.
- 4** test for read permission.

Permission will be computed for real user ID and real group ID (rather than the effective IDs).

Please note that it is not good to use this function to test before trying to open a file. On a multi-tasking system, it is possible that the accessibility of a file will change between the time you call `file.access()` and the time you try to open the file. It is better to wrap file open attempts in [try](#).

## Value

An integer vector with values 0 for success and -1 for failure.

## Note

This is intended as a replacement for the S-PLUS function `access`, a wrapper for the C function of the same name, which explains the return value encoding. Note that the return value is **false** for **success**.

## See Also

[file.info](#) for more details on permissions, [Sys.chmod](#) to change permissions, and [try](#) for a 'test it and see' approach.

[file\\_test](#) for shell-style file tests.

## Examples

```
fa <- file.access(dir("."))
table(fa) # count successes & failures
```

---

file.choose

*Choose a File Interactively*

---

## Description

Choose a file interactively.

## Usage

```
file.choose(new = FALSE)
```

## Arguments

`new` Logical: choose the style of dialog box presented to the user: at present only `new = FALSE` is used.

**Value**

A character vector of length one giving the file path.

**See Also**

[list.files](#) for non-interactive selection.

---

 file.info

*Extract File Information*


---

**Description**

Utility function to extract information about files on the user's file systems.

**Usage**

```
file.info(...)
```

**Arguments**

... character vectors containing file paths.

**Details**

The file paths are tilde-expanded: see [path.expand](#).

The file 'mode' follows POSIX conventions, giving three octal digits summarizing the permissions for the file owner, the owner's group and for anyone respectively. Each digit is the logical *or* of read (4), write (2) and execute/search (1) permissions.

On most systems symbolic links are followed, so information is given about the file to which the link points rather than about the link.

**Value**

A data frame with row names the file names and columns

size	double: File size in bytes.
isdir	logical: Is the file a directory?
mode	integer of class "octmode". The file permissions, printed in octal, for example 644.
mtime, ctime, atime	integer of class "POSIXct": file modification, 'last status change' and last access times.
uid	integer: the user ID of the file's owner.
gid	integer: the group ID of the file's group.
uname	character: uid interpreted as a user name.
grname	character: gid interpreted as a group name.

Unknown user and group names will be NA.

Entries for non-existent or non-readable files will be NA. The `uid`, `gid`, `uname` and `grname` columns may not be supplied on a non-POSIX Unix-alike system.

What is meant by the three file times depends on the OS and file system. On Windows native file systems `ctime` is the file creation time. What is meant by ‘file access’ and hence the ‘last access time’ is system-dependent.

### Note

Some systems allow files of more than 2Gb to be created but not accessed by the `stat` system call. Such files will show up as non-readable (and very likely not be readable by any of R’s input functions) – fortunately such file systems are becoming rare.

### See Also

[Sys.readlink](#) to find out about symbolic links, [files](#), [file.access](#), [list.files](#), and [DateTimeClasses](#) for the date formats.

[Sys.chmod](#) to change permissions.

### Examples

```
ncol(finf <- file.info(dir()))# at least six
## Not run: finf # the whole list
## Those that are more than 100 days old :
finf[diffftime(Sys.time(), finf[,"mtime"], units="days") > 100 , 1:4]

file.info("no-such-file-exists")
```

---

file.path

*Construct Path to File*

---

### Description

Construct the path to a file from components in a platform-independent way.

### Usage

```
file.path(..., fsep = .Platform$file.sep)
```

### Arguments

...                    character vectors.  
fsep                    the path separator to use.

### Value

A character vector of the arguments concatenated term-by-term and separated by `fsep` if all arguments have positive length; otherwise, an empty character vector.

### Note

The components are separated by / (not \) on Windows.

---

file.show

*Display One or More Files*


---

### Description

Display one or more files.

### Usage

```
file.show(..., header = rep("", nfiles),
          title = "R Information",
          delete.file = FALSE, pager = getOption("pager"),
          encoding = "")
```

### Arguments

...	one or more character vectors containing the names of the files to be displayed. These will be tilde-expanded: see <a href="#">path.expand</a> .
header	character vector (of the same length as the number of files specified in ...) giving a header for each file being displayed. Defaults to empty strings.
title	an overall title for the display. If a single separate window is used for the display, title will be used as the window title. If multiple windows are used, their titles should combine the title and the file-specific header.
delete.file	should the files be deleted after display? Used for temporary files.
pager	the pager to be used: not used on all platforms
encoding	character string giving the encoding to be assumed for the file(s).

### Details

This function provides the core of the R help system, but it can be used for other purposes as well, such as [page](#).

How the pager is implemented is highly system-dependent.

The basic Unix version concatenates the files (using the headers) to a temporary file, and displays it in the pager selected by the `pager` argument, which is a character vector specifying a system command to run on the set of files. The ‘factory-fresh’ default is to use ‘`R_HOME/bin/pager`’, which is a shell script running the command specified by the environment variable `PAGER` whose default is set at configuration, usually to `less`. On a Unix-alike `more` is used if `pager` is empty.

Most GUI systems will use a separate pager window for each file, and let the user leave it up while R continues running. The selection of such pagers could either be done using special pager names being intercepted by lower-level code (such as `"internal"` and `"console"` on Windows), or by letting `pager` be an R function which will be called with the same first four arguments as `file.show` and take care of interfacing to the GUI.

The R.app Mac OS X GUI uses its internal pager irrespective of the setting of `pager`.

Not all implementations will honour `delete.file`. In particular, using an external pager on Windows does not, as there is no way to know when the external application has finished with the file.

**Author(s)**

Ross Ihaka, Brian Ripley.

**See Also**

[files](#), [list.files](#), [help](#).

**Examples**

```
file.show(file.path(R.home("doc"), "COPYRIGHTS"))
```

---

files

*File Manipulation*


---

**Description**

These functions provide a low-level interface to the computer's file system.

**Usage**

```
file.create(..., showWarnings = TRUE)
file.exists(...)
file.remove(...)
file.rename(from, to)
file.append(file1, file2)
file.copy(from, to, overwrite = recursive, recursive = FALSE)
file.symlink(from, to)
```

**Arguments**

<code>...</code>	<code>file1</code> , <code>file2</code>	character vectors, containing file names or paths.
<code>from</code> , <code>to</code>		character string, containing a file name or path.
<code>overwrite</code>		logical; should the destination files be overwritten?
<code>showWarnings</code>		logical; should the warnings on failure be shown?
<code>recursive</code>		logical. If <code>to</code> is a directory, should directories in <code>from</code> be copied (and their contents).

**Details**

The `...` arguments are concatenated to form one character string: you can specify the files separately or as one vector. All of these functions expand path names: see [path.expand](#).

`file.create` creates files with the given names if they do not already exist and truncates them if they do. They are created with the maximal permissions allowed by the `umask` setting.

`file.exists` returns a logical vector indicating whether the files named by its argument exist. (Here 'exists' is in the sense of the system's `stat` call: a file will be reported as existing only if you have the permissions needed by `stat`. Existence can also be checked by [file.access](#), which might use different permissions and so obtain a different result. Note that the existence of a file does not imply that it is readable: for that use [file.access](#).) Note that if the file is a symbolic link, the result indicates if the link points to an actual file, not just if the link exists.

`file.remove` attempts to remove the files named in its argument. On most Unix platforms ‘file’ includes *empty* directories, symbolic links, fifos and sockets. On Windows, ‘file’ means a regular file and not, say, an empty directory.

`file.rename` attempts to rename a single file. Where file permissions allow this will first remove an existing file `to`. This is subject to the limitations of the OS’s corresponding system call: in particular in the interpretation of ‘file’: also most platforms will not rename files across file systems.

`file.append` attempts to append the files named by its second argument to those named by its first. The R subscript recycling rule is used to align names given in vectors of different lengths.

`file.copy` works in a similar way to `file.append` but with the arguments in the natural order for copying. Copying to existing destination files is skipped unless `overwrite = TRUE`. The `to` argument can specify a single existing directory.

`file.symlink` makes symbolic links on those Unix-like platforms which support them. The `to` argument can specify a single existing directory.

### Value

`file.rename` and `file.symlink` returns a logical value, true for success.

The remaining functions return a logical vector indicating which operation succeeded for each of the files attempted. Using a missing value for a file or path name will always be regarded as a failure.

If `showWarnings = TRUE`, `file.create` will give a warning for an unexpected failure.

### Author(s)

Ross Ihaka, Brian Ripley

### See Also

[file.info](#), [file.access](#), [file.path](#), [file.show](#), [list.files](#), [unlink](#), [basename](#), [path.expand](#).

[dir.create](#).

[Sys.glob](#) to expand wildcards in file specifications.

[file\\_test](#), [Sys.readlink](#).

### Examples

```
cat("file A\n", file="A")
cat("file B\n", file="B")
file.append("A", "B")
file.create("A")
file.append("A", rep("B", 10))
if(interactive()) file.show("A")
file.copy("A", "C")
dir.create("tmp")
file.copy(c("A", "B"), "tmp")
list.files("tmp")
setwd("tmp")
file.remove("B")
file.symlink(file.path("../", c("A", "B")), ".")
setwd("../")
unlink("tmp", recursive=TRUE)
file.remove("A", "B", "C")
```

## Description

These functions provide a low-level interface to the computer's file system.

## Usage

```
dir.create(path, showWarnings = TRUE, recursive = FALSE, mode = "0777")
Sys.chmod(paths, mode = "0777")
Sys.umask(mode = "0000")
```

## Arguments

<code>path</code>	a character vector containing a single path name.
<code>paths</code>	character vectors containing file or directory paths.
<code>showWarnings</code>	logical; should the warnings on failure be shown?
<code>recursive</code>	logical. Should elements of the path other than the last be created? If true, like Unix's <code>mkdir -p</code> .
<code>mode</code>	the file mode to be used on Unix-alikes: it will be coerced by <code>as.octmode</code> .

## Details

`dir.create` creates the last element of the path, unless `recursive = TRUE`. Trailing path separators are removed. The mode will be modified by the `umask` setting in the same way as for the system function `mkdir`. What modes can be set is OS-dependent, and it is unsafe to assume that more than three octal digits will be used. For more details see your OS's documentation on the system call `mkdir` (and not that on the command-line utility of that name).

`Sys.chmod` sets the file permissions of one or more files. It may not be supported (when a warning is issued). See the comments for `dir.create` for how modes are interpreted. Changing mode on a symbolic link is unlikely to work (nor be necessary). For more details see your OS's documentation on the system call `chmod` (and not that on the command-line utility of that name).

`Sys.umask` sets the `umask`. It may not be supported (when a warning is issued and `"0000"` returned). For more details see your OS's documentation on the system call `umask`.

## Value

`dir.create` and `Sys.chmod` return invisibly a logical vector indicating if the operation succeeded for each of the files attempted. Using a missing value for a path name will always be regarded as a failure. `dir.create` indicates failure if the directory already exists. If `showWarnings = TRUE`, `dir.create` will give a warning for an unexpected failure (e.g. not for a missing value nor for an already existing component for `recursive = TRUE`).

`Sys.umask` returns the previous value of the `umask`, invisibly, as a length-one object of class `"octmode"`.

## Author(s)

Ross Ihaka, Brian Ripley



**See Also**

`file.info`, `file.exists`, `file.path`, `list.files`, `unlink`, `basename`,  
`path.expand`.

---

findInterval

*Find Interval Numbers or Indices*

---

**Description**

Find the indices of `x` in `vec`, where `vec` must be sorted (non-decreasingly); i.e., if `i <- findInterval(x, v)`, we have  $v_{i_j} \leq x_j < v_{i_j+1}$  where  $v_0 := -\infty$ ,  $v_{N+1} := +\infty$ , and  $N <- \text{length}(\text{vec})$ . At the two boundaries, the returned index may differ by 1, depending on the optional arguments `rightmost.closed` and `all.inside`.

**Usage**

```
findInterval(x, vec, rightmost.closed = FALSE, all.inside = FALSE)
```

**Arguments**

<code>x</code>	numeric.
<code>vec</code>	numeric, sorted (weakly) increasingly, of length <code>N</code> , say.
<code>rightmost.closed</code>	logical; if true, the rightmost interval, <code>vec[N-1] .. vec[N]</code> is treated as <i>closed</i> , see below.
<code>all.inside</code>	logical; if true, the returned indices are coerced into $1, \dots, N-1$ , i.e., 0 is mapped to 1 and $N$ to $N-1$ .

**Details**

The function `findInterval` finds the index of one vector `x` in another, `vec`, where the latter must be non-decreasing. Where this is trivial, equivalent to `apply(outer(x, vec, ">="), 1, sum)`, as a matter of fact, the internal algorithm uses interval search ensuring  $O(n \log N)$  complexity where  $n <- \text{length}(x)$  (and  $N <- \text{length}(vec)$ ). For (almost) sorted `x`, it will be even faster, basically  $O(n)$ .

This is the same computation as for the empirical distribution function, and indeed, `findInterval(t, sort(X))` is *identical* to  $nF_n(t; X_1, \dots, X_n)$  where  $F_n$  is the empirical distribution function of  $X_1, \dots, X_n$ .

When `rightmost.closed = TRUE`, the result for `x[j] = vec[N]` ( $= \max vec$ ), is  $N - 1$  as for all other values in the last interval.

**Value**

vector of length `length(x)` with values in  $0:N$  (and NA) where  $N <- \text{length}(vec)$ , or values coerced to  $1:(N-1)$  if and only if `all.inside = TRUE` (equivalently coercing all `x` values *inside* the intervals). Note that NAs are propagated from `x`, and `Inf` values are allowed in both `x` and `vec`.

**Author(s)**

Martin Maechler

**See Also**

`approx`(\*, method = "constant") which is a generalization of `findInterval()`, `ecdf` for computing the empirical distribution function which is (up to a factor of  $n$ ) also basically the same as `findInterval()`.

**Examples**

```
N <- 100
X <- sort(round(stats::rt(N, df=2), 2))
tt <- c(-100, seq(-2,2, len=201), +100)
it <- findInterval(tt, X)
tt[it < 1 | it >= N] # only first and last are outside range(X)
```

force

*Force Evaluation of an Argument***Description**

Forces the evaluation of a function argument.

**Usage**

```
force(x)
```

**Arguments**

`x` a formal argument of the enclosing function.

**Details**

`force` forces the evaluation of a formal argument. This can be useful if the argument will be captured in a closure by the lexical scoping rules and will later be altered by an explicit assignment or an implicit assignment in a loop or an apply function.

**Note**

This is semantic sugar: just evaluating the symbol will do the same thing (see the examples).

`force` does not force the evaluation of other [promises](#). (It works by forcing the promise that is created when the actual arguments of a call are matched to the formal arguments of a closure, the mechanism which implements *lazy evaluation*.)

**Examples**

```
f <- function(y) function() y
lf <- vector("list", 5)
for (i in seq_along(lf)) lf[[i]] <- f(i)
lf[[1]]() # returns 5

g <- function(y) { force(y); function() y }
lg <- vector("list", 5)
for (i in seq_along(lg)) lg[[i]] <- g(i)
lg[[1]]() # returns 1
```

```
## This is identical to
g <- function(y) { y; function() y }
```

Foreign

*Foreign Function Interface***Description**

Functions to make calls to compiled code that has been loaded into R.

**Usage**

```
.C(name, ..., NAOK = FALSE, DUP = TRUE, PACKAGE, ENCODING)
.Fortran(name, ..., NAOK = FALSE, DUP = TRUE, PACKAGE, ENCODING)
.External(name, ..., PACKAGE)
.Call(name, ..., PACKAGE)
```

**Arguments**

name	a character string giving the name of a C function or Fortran subroutine, or an object of class " <code>NativeSymbolInfo</code> ", " <code>RegisteredNativeSymbol</code> " or " <code>NativeSymbol</code> " referring to such a name.
...	arguments to be passed to the foreign function.
NAOK	if TRUE then any <code>NA</code> or <code>NaN</code> or <code>Inf</code> values in the arguments are passed on to the foreign function. If FALSE, the presence of <code>NA</code> or <code>NaN</code> or <code>Inf</code> values is regarded as an error.
DUP	if TRUE then arguments are duplicated before their address is passed to C or Fortran.
PACKAGE	if supplied, confine the search for the name to the DLL given by this argument (plus the conventional extension, <code>‘.so’</code> , <code>‘.sl’</code> , <code>‘.dll’</code> , ...). This is intended to add safety for packages, which can ensure by using this argument that no other package can override their external symbols. Use <code>PACKAGE="base"</code> for symbols linked in to R.
ENCODING	optional name for an encoding to be assumed for character vectors. See <code>‘Details’</code> .

**Details**

The functions `.C` and `.Fortran` can be used to make calls to compiled C and Fortran code.

`.Call` can be used to call compiled code which makes use of internal R objects, passing the arguments to the C code as a sequence of R objects.

`.External` can be used to call compiled code that uses R objects in the same way as internal R functions: this allows for a variable number of arguments.

Specifying `ENCODING` overrides any declared encodings (see [Encoding](#)) which are otherwise used to translate to the current locale before passing the strings to the compiled code.

These functions are all [primitive](#), and `name` is always matched to the first argument supplied (which if named must partially match `name`). The other named arguments follow `...` and so cannot be abbreviated.

For details about how to write code to use with `.Call` and `.External`, see the chapter on “System and foreign language interfaces” in the “Writing R Extensions” manual.

**Value**

The functions `.C` and `.Fortran` return a list similar to the `...` list of arguments passed in, but reflecting any changes made by the C or Fortran code.

`.External` and `.Call` return an (arbitrary) R object.

These calls are typically made in conjunction with `dyn.load` which links DLLs to R.

**Argument types**

The mapping of the types of R arguments to C or Fortran arguments in `.C` or `.Fortran` is

R	C	Fortran
integer	int *	integer
numeric	double *	double precision
– or –	float *	real
complex	Rcomplex *	double complex
logical	int *	integer
character	char **	[see below]
raw	unsigned char *	not allowed
list	SEXP *	not allowed
other	SEXP	not allowed

Numeric vectors in R will be passed as type `double *` to C (and as `double precision` to Fortran) unless (i) `.C` or `.Fortran` is used, (ii) `DUP` is true and (iii) the argument has attribute `Csingle` set to `TRUE` (use `as.single` or `single`). This mechanism is only intended to be used to facilitate the interfacing of existing C and Fortran code.

The C type `Rcomplex` is defined in ‘Complex.h’ as a `typedef struct {double r; double i;}`. Fortran type `double complex` is an extension to the Fortran standard, and the availability of a mapping of `complex` to Fortran may be compiler dependent.

Logical values are sent as 0 (`FALSE`), 1 (`TRUE`) or `INT_MIN = -2147483648` (`NA`, but only if `NAOK = TRUE`), and the compiled code should return one of these three values.

*Note:* The C types corresponding to `integer` and `logical` are `int`, not `long` as in S. This difference matters on most 64-bit platforms, where `int` is 32-bit and `long` is 64-bit (but not on 64-bit Windows).

*Note:* The Fortran type corresponding to `logical` is `integer`, not `logical`: the difference matters on some older Fortran compilers.

The first character string of a character vector is passed as a C character array to Fortran: that string may be usable as `character*255` if its true length is passed separately. Only up to 255 characters of the string are passed back. (How well this works, or even if it works at all, depends on the C and Fortran compilers and the platform.)

Missing (`NA`) string values are passed to `.C` as the string "NA". As the C `char` type can represent all possible bit patterns there appears to be no way to distinguish missing strings from the string "NA". If this distinction is important use `.Call`.

Functions, expressions, environments and other language elements are passed as the internal R pointer type `SEXP`. This type is defined in ‘Rinternals.h’ or the arguments can be declared as generic pointers, `void *`. Lists are passed as C arrays of `SEXP` and can be declared as `void *` or `SEXP *`. Note that you cannot assign values to the elements of the list within the C routine. Assigning values to elements of the array corresponding to the list bypasses R’s memory management/garbage collection and will cause problems. Essentially, the array corresponding to the list is read-only. If you need to return S objects created within the C routine, use the `.Call` interface.

R functions can be invoked using `call_S` or `call_R` and can be passed lists or the simple types as arguments.

### Warning

`DUP=FALSE` is dangerous.

There are two dangers with using `DUP=FALSE`.

The first is that if you pass a local variable to `.C/.Fortran` with `DUP=FALSE`, your compiled code can alter the local variable and not just the copy in the return list. Worse, if you pass a local variable that is a formal parameter of the calling function, you may be able to change not only the local variable but the variable one level up. This will be very hard to trace.

The second is that lists are passed as a single R SEXP with `DUP=FALSE`, not as an array of SEXP. This means the accessor macros in ‘`Rinternals.h`’ are needed to get at the list elements and the lists cannot be passed to `call_S/call_R`. New code using R objects should be written using `.Call` or `.External`, so this is now only a minor issue.

In addition, character vectors and lists cannot be used with `DUP=FALSE`.

It is safe and useful to set `DUP=FALSE` if you do not change any of the variables that might be affected, e.g.,

```
.C("Cfunction", input=x, output=numeric(10)).
```

In this case the output variable did not exist before the call so it cannot cause trouble. If the input variable is not changed in the C code of `Cfunction` you are safe.

Neither `.Call` nor `.External` copy their arguments. You should treat arguments you receive through these interfaces as read-only.

### Fortran symbol names

All Fortran compilers that can be used to compile R map symbol names to lower case, and so does `.Fortran`.

Symbol names containing underscores are not valid Fortran 77 (although they are valid in Fortran 9x). Many Fortran 77 compilers will allow them but may translate them in a different way to names not containing underscores. Such names will often work with `.Fortran` (since how they are translated is detected when R is built and the information used by `.Fortran`), but portable code should not use Fortran names containing underscores.

Use `.Fortran` with care for compiled Fortran 9x code: it may not work if the Fortran 9x compiler used differs from the Fortran compiler used when configuring R, especially if the subroutine name is not lower-case or includes an underscore. It is also possible to use `.C` and do any necessary symbol-name translation yourself.

### Header files for external code

Writing code for use with `.External` and `.Call` will need to use internal R structures. If possible use just those defined in ‘`Rinternals.h`’ and/or the macros in ‘`Rdefines.h`’, as other header files are not installed and are even more likely to be changed.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (`.C` and `.Fortran`.)

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer. (`.Call`.)

**See Also**

[dyn.load](#).

---

formals

*Access to and Manipulation of the Formal Arguments*

---

**Description**

Get or set the formal arguments of a function.

**Usage**

```
formals(fun = sys.function(sys.parent()))
formals(fun, envir = environment(fun)) <- value
```

**Arguments**

fun	a function object, or see ‘Details’.
envir	environment in which the function should be defined.
value	a list (or pairlist) of R expressions.

**Details**

For the first form, `fun` can also be a character string naming the function to be manipulated, which is searched for from the parent environment. If it is not specified, the function calling `formals` is used.

Only *closures* have formals, not primitive functions.

**Value**

`formals` returns the formal argument list of the function specified, as a [pairlist](#), or NULL for a non-function or primitive.

The replacement form sets the formals of a function to the list/pairlist on the right hand side, and (potentially) resets the environment of the function.

**See Also**

[args](#) for a human-readable version, [alist](#), [body](#), [function](#).

**Examples**

```
require(stats); require(graphics)
length(formals(lm))      # the number of formal arguments
names(formals(boxplot)) # formal arguments names

f <- function(x) a+b
formals(f) <- alist(a=,b=3) # function(a,b=3)a+b
f(2) # result = 5
```

format

*Encode in a Common Format***Description**

Format an R object for pretty printing.

**Usage**

```
format(x, ...)

## Default S3 method:
format(x, trim = FALSE, digits = NULL, nsmall = 0L,
       justify = c("left", "right", "centre", "none"),
       width = NULL, na.encode = TRUE, scientific = NA,
       big.mark = "", big.interval = 3L,
       small.mark = "", small.interval = 5L,
       decimal.mark = ".", zero.print = NULL, drop0trailing = FALSE, ...)

## S3 method for class 'data.frame':
format(x, ..., justify = "none")

## S3 method for class 'factor':
format(x, ...)

## S3 method for class 'AsIs':
format(x, width = 12, ...)
```

**Arguments**

<code>x</code>	any R object (conceptually); typically numeric.
<code>trim</code>	logical; if FALSE, logical, numeric and complex values are right-justified to a common width: if TRUE the leading blanks for justification are suppressed.
<code>digits</code>	how many significant digits are to be used for numeric and complex <code>x</code> . The default, NULL, uses <code>getOption(digits)</code> . This is a suggestion: enough decimal places will be used so that the smallest (in magnitude) number has this many significant digits, and also to satisfy <code>nsmall</code> . (For the interpretation for complex numbers see <a href="#">signif.</a> )
<code>nsmall</code>	the minimum number of digits to the right of the decimal point in formatting real/complex numbers in non-scientific formats. Allowed values are $0 \leq nsmall \leq 20$ .
<code>justify</code>	should a <i>character</i> vector be left-justified (the default), right-justified, centred or left alone.
<code>width</code>	default method: the <i>minimum</i> field width or NULL or 0 for no restriction. AsIs method: the <i>maximum</i> field width for non-character objects. NULL corresponds to the default 12.
<code>na.encode</code>	logical: should NA strings be encoded? Note this only applies to elements of character vectors, not to numerical or logical NAs, which are always encoded as "NA".

`scientific` Either a logical specifying whether elements of a real or complex vector should be encoded in scientific format, or an integer penalty (see `options("scipen")`). Missing values correspond to the current default penalty.

`...` further arguments passed to or from other methods.

`big.mark`, `big.interval`, `small.mark`, `small.interval`, `decimal.mark`, `zero.print`, `dr` used for prettying (longish) decimal sequences, passed to `prettyNum`: that help page explains the details.

## Details

`format` is a generic function. Apart from the methods described here there are methods for dates (see `format.Date`), date-times (see `format.POSIXct`) and for other classes such as `format.octmode` and `format.dist`.

`format.data.frame` formats the data frame column by column, applying the appropriate method of `format` for each column. Methods for columns are often similar to `as.character` but offer more control. Matrix and data-frame columns will be converted to separate columns in the result, and character columns (normally all) will be given class `"AsIs"`.

`format.factor` converts the factor to a character vector and then calls the default method (and so `justify` applies).

`format.AsIs` deals with columns of complicated objects that have been extracted from a data frame. Character objects are passed to the default method (and so `width` does not apply). Otherwise it calls `toString` to convert the object to character (if a vector or list, element by element) and then right-justifies the result.

Justification for character vectors (and objects converted to character vectors by their methods) is done on display width (see `nchar`), taking double-width characters and the rendering of special characters (as escape sequences, including escaping backslash: see `print.default`) into account. Character strings are padded with blanks to the display width of the widest. (If `na.encode = FALSE` missing character strings are not included in the width computations and are not encoded.)

Numeric vectors are encoded with the minimum number of decimal places needed to display all the elements to at least the `digit` significant digits. However, if all the elements then have trailing zeroes, the number of decimal places is reduced until at least one element has a non-zero final digit; see also the argument documentation for `big.*`, `small.*` etc, above.

Raw vectors are converted to their 2-digit hexadecimal representation by `as.character`.

## Value

An object of similar structure to `x` containing character representations of the elements of the first argument `x` in a common format, and in the current locale's encoding.

For character, numeric, complex or factor `x`, `dims` and `dimnames` are preserved on matrices/arrays and names on vectors: no other attributes are copied.

If `x` is a list, the result is a character vector obtained by applying `format.default(x, ...)` to each element of the list (after `unlisting` elements which are themselves lists), and then collapsing the result for each element with `paste(collapse = ", ")`. The defaults in this case are `trim = TRUE`, `justify = "none"` since one does not usually want alignment in the collapsed strings.



## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

`format.info` indicates how an atomic vector would be formatted.

`formatC`, `paste`, `as.character`, `sprintf`, `print`, `prettyNum`, `toString`, `encodeString`.

## Examples

```
format(1:10)
format(1:10, trim = TRUE)

zz <- data.frame("(row names)"= c("aaaaa", "b"), check.names=FALSE)
format(zz)
format(zz, justify = "left")

## use of nsmall
format(13.7)
format(13.7, nsmall = 3)
format(c(6.0, 13.1), digits = 2)
format(c(6.0, 13.1), digits = 2, nsmall = 1)

## use of scientific
format(2^31-1)
format(2^31-1, scientific = TRUE)

## a list
z <- list(a=letters[1:3], b=(-pi+0i)^((-2:2)/2), c=c(1,10,100,1000),
          d=c("a", "longer", "character", "string"))
format(z, digits = 2)
format(z, digits = 2, justify = "left", trim = FALSE)
```

---

format.Date

*Date Conversion Functions to and from Character*

---

## Description

Functions to convert between character representations and objects of class "Date" representing calendar dates.

## Usage

```
as.Date(x, ...)
## S3 method for class 'character':
as.Date(x, format = "", ...)
## S3 method for class 'numeric':
as.Date(x, origin, ...)

## S3 method for class 'Date':
```

```
format(x, ...)

## S3 method for class 'Date':
as.character(x, ...)
```

### Arguments

<code>x</code>	An object to be converted.
<code>format</code>	A character string. If not specified, it will try "%Y-%m-%d" then "%Y/%m/%d" on the first non-NA element, and give an error if neither works.
<code>origin</code>	a Date object, or something which can be coerced by <code>as.Date(origin, ...)</code> to such an object.
<code>...</code>	Further arguments to be passed from or to other methods, including <code>format</code> for <code>as.character</code> and <code>as.Date</code> methods.

### Details

The usual vector re-cycling rules are applied to `x` and `format` so the answer will be of length that of the longer of the vectors.

Locale-specific conversions to and from character strings are used where appropriate and available. This affects the names of the days and months.

The `as.Date` methods accept character strings, factors, logical NA and objects of classes "POSIXlt" and "POSIXct". (The last is converted to days by ignoring the time after midnight in the representation of the time in UTC.) Also objects of class "date" (from package **date**) and "dates" (from package **chron**). Character strings are processed as far as necessary for the format specified: any trailing characters are ignored.

`as.Date` will accept numeric data (the number of days since an epoch), but *only* if `origin` is supplied.

The `format` and `as.character` methods ignore any fractional part of the date.

### Value

The `format` and `as.character` methods return a character vector representing the date. NA dates are returned as `NA_character_`.

The `as.Date` methods return an object of class "Date".

### Note

The default formats follow the rules of the ISO 8601 international standard which expresses a day as "2001-02-03".

If the date string does not specify the date completely, the returned answer may be system-specific. The most common behaviour is to assume that a missing year, month or day is the current one. If it specifies a date incorrectly, reliable implementations will give an error and the date is reported as NA. Unfortunately some common implementations (such as 'glibc') are unreliable and guess at the intended meaning.

Years before 1CE (aka 1AD) will probably not be handled correctly.

## References

International Organization for Standardization (2004, 1988, 1997, ...) *ISO 8601. Data elements and interchange formats – Information interchange – Representation of dates and times*. For links to versions available on-line see (at the time of writing) <http://www.qsl.net/g1smd/isopdf.htm>; for information on the current official version, see <http://www.iso.org/iso/en/prods-services/popstds/datesandtime.html>.

## See Also

[Date](#) for details of the date class; [locales](#) to query or set a locale.

Your system's help pages on `strftime` and `strptime` to see how to specify their formats. Windows users will find no help page for `strptime`: code based on 'glibc' is used (with corrections), so all the format specifiers described here are supported, but with no alternative number representation nor era available in any locale.

## Examples

```
## locale-specific version of the date
format(Sys.Date(), "%a %b %d")

## read in date info in format 'ddmmmyyyy'
## This will give NA(s) in some locales; setting the C locale
## as in the commented lines will overcome this on most systems.
## lct <- Sys.getlocale("LC_TIME"); Sys.setlocale("LC_TIME", "C")
x <- c("1jan1960", "2jan1960", "31mar1960", "30jul1960")
z <- as.Date(x, "%d%b%Y")
## Sys.setlocale("LC_TIME", lct)
z

## read in date/time info in format 'm/d/y'
dates <- c("02/27/92", "02/27/92", "01/14/92", "02/28/92", "02/01/92")
as.Date(dates, "%m/%d/%y")

## date given as number of days since 1900-01-01 (a date in 1989)
as.Date(32768, origin="1900-01-01")

## Excel is said to use 1900-01-01 as day 1 (Windows default) or
## 1904-01-01 as day 0 (Mac default), but this is complicated by Excel
## thinking 1900 was a leap year.
## So for recent dates from Windows Excel
as.Date(35981, origin="1899-12-30") # 1998-07-05
## and Mac Excel
as.Date(34519, origin="1904-01-01") # 1998-07-05
```

---

format.info

*format(.) Information*

---

## Description

Information is returned on how `format(x, digits, nsmall)` would be formatted.

**Usage**

```
format.info(x, digits = NULL, nsmall = 0)
```

**Arguments**

`x` an atomic vector; a potential argument of `format(x, ...)`.

`digits` how many significant digits are to be used for numeric and complex `x`. The default, `NULL`, uses `getOption(digits)`.

`nsmall` (see `format(..., nsmall)`).

**Value**

An [integer vector](#) of length 1, 3 or 6, say `r`.

For logical, integer and character vectors a single element, the width which would be used by `format` if `width = NULL`.

For numeric vectors:

`r[1]` width (in characters) used by `format(x)`

`r[2]` number of digits after decimal point.

`r[3]` in `0:2`; if  $\geq 1$ , *exponential* representation would be used, with exponent length of `r[3]+1`.

For a complex vector the first three elements refer to the real parts, and there are three further elements corresponding to the imaginary parts.

**See Also**

[format](#), [formatC](#).

**Examples**

```
dd <- options("digits") ; options(digits = 7) #-- for the following
format.info(123) # 3 0 0
format.info(pi) # 8 6 0
format.info(1e8) # 5 0 1 - exponential "1e+08"
format.info(1e222) # 6 0 2 - exponential "1e+222"

x <- pi*10^c(-10,-2,0:2,8,20)
names(x) <- formatC(x, width=1, digits=3, format="g")
cbind(sapply(x,format))
t(sapply(x, format.info))

## using at least 8 digits right of "."
t(sapply(x, format.info, nsmall = 8))

# Reset old options:
options(dd)
```

---

format.pval	<i>Format P Values</i>
-------------	------------------------

---

### Description

format.pval is intended for formatting p-values.

### Usage

```
format.pval(pv, digits = max(1, getOption("digits") - 2),  
            eps = .Machine$double.eps, na.form = "NA")
```

### Arguments

pv	a numeric vector.
digits	how many significant digits are to be used.
eps	a numerical tolerance: see ‘Details’.
na.form	character representation of NAs.

### Details

format.pval is mainly an auxiliary function for [print.summary.lm](#) etc., and does separate formatting for fixed, floating point and very small values; those less than eps are formatted as "<[eps]" (where ‘[eps]’ stands for `format(eps, digits)`).

### Value

A character vector.

### Examples

```
format.pval(c(stats::runif(5), pi^-100, NA))  
format.pval(c(0.1, 0.0001, 1e-27))
```

---

formatC	<i>Formatting Using C-style Formats</i>
---------	---

---

### Description

Formatting numbers individually and flexibly, using C style format specifications.

**Usage**

```
formatC(x, digits = NULL, width = NULL,
        format = NULL, flag = "", mode = NULL,
        big.mark = "", big.interval = 3L,
        small.mark = "", small.interval = 5L,
        decimal.mark = ".", preserve.width = "individual",
        zero.print = NULL, drop0trailing = FALSE)

prettyNum(x, big.mark = "", big.interval = 3L,
          small.mark = "", small.interval = 5L,
          decimal.mark = ".",
          preserve.width = c("common", "individual", "none"),
          zero.print = NULL, drop0trailing = FALSE, is.cmplx = NA, ...)
```

**Arguments**

x	an atomic numerical or character object, possibly <code>complex</code> only for <code>prettyNum()</code> , typically a vector of real numbers.
digits	the desired number of digits after the decimal point ( <code>format = "f"</code> ) or <i>significant</i> digits ( <code>format = "g", "e" or "fg"</code> ). Default: 2 for integer, 4 for real numbers. If less than 0, the C default of 6 digits is used. If specified as more than 50, 50 will be used with a warning unless <code>format = "f"</code> where it is limited to typically 324. (Not more than 15–21 digits need be accurate, depending on the OS and compiler used. This limit is just a precaution against segfaults in the underlying C runtime.)
width	the total field width; if both <code>digits</code> and <code>width</code> are unspecified, <code>width</code> defaults to 1, otherwise to <code>digits + 1</code> . <code>width = 0</code> will use <code>width = digits</code> , <code>width &lt; 0</code> means left justify the number in this field (equivalent to <code>flag = "-"</code> ). If necessary, the result will have more characters than <code>width</code> . For character data this is interpreted in characters (not bytes nor display width).
format	equal to "d" (for integers), "f", "e", "E", "g", "G", "fg" (for reals), or "s" (for strings). Default is "d" for integers, "g" for reals. "f" gives numbers in the usual xxx.xxx format; "e" and "E" give n.ddde+nn or n.dddE+nn (scientific format); "g" and "G" put x[i] into scientific format only if it saves space to do so. "fg" uses fixed format as "f", but <code>digits</code> as the minimum number of <i>significant</i> digits. This can lead to quite long result strings, see examples below. Note that unlike <code>signif</code> this prints large numbers with more significant digits than <code>digits</code> . Trailing zeros are <i>dropped</i> in this format, unless <code>flag</code> contains "#".
flag	For <code>formatC</code> , a character string giving a format modifier as in Kernighan and Ritchie (1988, page 243). "0" pads leading zeros; "-" does left adjustment, others are "+", " ", and "#". There can be more than one of these, in any order.
mode	"double" (or "real"), "integer" or "character". Default: Determined from the storage mode of x.
big.mark	character; if not empty used as mark between every <code>big.interval</code> decimals <i>before</i> (hence <code>big</code> ) the decimal point.
big.interval	see <code>big.mark</code> above; defaults to 3.
small.mark	character; if not empty used as mark between every <code>small.interval</code> decimals <i>after</i> (hence <code>small</code> ) the decimal point.

<code>small.interval</code>	see <code>small.mark</code> above; defaults to 5.
<code>decimal.mark</code>	the character to be used to indicate the numeric decimal point.
<code>preserve.width</code>	string specifying if the string widths should be preserved where possible in those cases where marks ( <code>big.mark</code> or <code>small.mark</code> ) are added. "common", the default, corresponds to <code>format</code> -like behavior whereas "individual" is the default in <code>formatC()</code> .
<code>zero.print</code>	logical, character string or NULL specifying if and how <i>zeros</i> should be formatted specially. Useful for pretty printing 'sparse' objects.
<code>drop0trailing</code>	logical, indicating if trailing zeros, i.e., "0" <i>after</i> the decimal mark, should be removed; also drops "e+00" in exponential formats.
<code>is.cmplx</code>	optional logical, to be used when <code>x</code> is "character" to indicate if it stems from <code>complex</code> vector or not. By default (NA), <code>x</code> is checked to 'look like' complex.
<code>...</code>	arguments passed to <code>format</code> .

### Details

If you set `format` it overrides the setting of `mode`, so `formatC(123.45, mode="double", format="d")` gives 123.

The rendering of scientific format is platform-dependent: some systems use `n.ddde+nnn` or `n.ddden` rather than `n.ddde+nn`.

`formatC` does not necessarily align the numbers on the decimal point, so `formatC(c(6.11, 13.1), digits=2, format="fg")` gives `c("6.1", " 13")`. If you want common formatting for several numbers, use `format`.

`prettyNum` is the utility function for prettifying `x`. `x` can be complex (or `format(<complex>)`, here. If `x` is not a character, `format(x[i], ...)` is applied to each element, and then it is left unchanged if all the other arguments are at their defaults. Note that `prettyNum(x)` may behave unexpectedly if `x` is a character vector not resulting from something like `format(<number>)`: in particular it assumes that a period is a decimal mark.

### Value

A character object of same size and attributes as `x`, in the current locale's encoding. Unlike `format`, each number is formatted individually. Looping over each element of `x`, the C function `sprintf(...)` is called for numeric inputs (inside the C function `str_signif`).

`formatC`: for character `x`, do simple (left or right) padding with white space.

### Author(s)

`formatC` was originally written by Bill Dunlap, later much improved by Martin Maechler. It was first adapted for R by Friedrich Leisch.

### References

Kernighan, B. W. and Ritchie, D. M. (1988) *The C Programming Language*. Second edition. Prentice Hall.

**See Also**

[format](#).

[sprintf](#) for more general C like formatting.

**Examples**

```
xx <- pi * 10^(-5:4)
cbind(format(xx, digits=4), formatC(xx))
cbind(formatC(xx, width = 9, flag = "-"))
cbind(formatC(xx, digits = 5, width = 8, format = "f", flag = "0"))
cbind(format(xx, digits=4), formatC(xx, digits = 4, format = "fg"))

formatC(  c("a", "Abc", "no way"), width = -7) # <=> flag = "-"
formatC(c((-1:1)/0,c(1,100)*pi), width=8, digits=1)

xx <- c(1e-12, -3.98765e-10, 1.45645e-69, 1e-70, pi*1e37, 3.44e4)
##      1          2          3          4          5          6
formatC(xx)
formatC(xx, format="fg")          # special "fixed" format.
formatC(xx[1:4], format="f", digits=75) #>> even longer strings

formatC(c(3.24, 2.3e-6), format="f", digits=11, drop0trailing=TRUE)

r <- c("76491283764.97430", "29.12345678901", "-7.1234", "-100.1", "1123")
## American:
prettyNum(r, big.mark = ",")
## Some Europeans:
prettyNum(r, big.mark = "'", decimal.mark = ",")

(dd <- sapply(1:10, function(i)paste((9:0)[1:i],collapse="")))
prettyNum(dd, big.mark="'")

## examples of 'small.mark'
pN <- stats::pnorm(1:7, lower.tail = FALSE)
cbind(format (pN, small.mark = " ", digits = 15))
cbind(formatC(pN, small.mark = " ", digits = 17, format = "f"))

cbind(ff <- format(1.2345 + 10^(0:5), width = 11, big.mark = "'"))
## all with same width (one more than the specified minimum)

## individual formatting to common width:
fc <- formatC(1.234 + 10^(0:8), format="fg", width=11, big.mark = "'")
cbind(fc)

## complex numbers:
r <- 10.0000001; rv <- (r/10)^(1:10)
(zv <- (rv + 1i*rv))
op <- options(digits=7) ## (system default)
(pnv <- prettyNum(zv))
stopifnot(pnv == "1+1i", pnv == format(zv),
          pnv == prettyNum(zv, drop0trailing=TRUE))
## more digits change the picture:
options(digits=8)
head(fv <- format(zv), 3)
prettyNum(fv)
prettyNum(fv, drop0trailing=TRUE) # a bit nicer
```



options(op)

---

formatDL

*Format Description Lists*

---

### Description

Format vectors of items and their descriptions as 2-column tables or LaTeX-style description lists.

### Usage

```
formatDL(x, y, style = c("table", "list"),
         width = 0.9 * getOption("width"), indent = NULL)
```

### Arguments

<code>x</code>	a vector giving the items to be described, or a list of length 2 or a matrix with 2 columns giving both items and descriptions.
<code>y</code>	a vector of the same length as <code>x</code> with the corresponding descriptions. Only used if <code>x</code> does not already give the descriptions.
<code>style</code>	a character string specifying the rendering style of the description information. If "table", a two-column table with items and descriptions as columns is produced (similar to Texinfo's @table environment. If "list", a LaTeX-style tagged description list is obtained.
<code>width</code>	a positive integer giving the target column for wrapping lines in the output.
<code>indent</code>	a positive integer specifying the indentation of the second column in table style, and the indentation of continuation lines in list style. Must not be greater than <code>width/2</code> , and defaults to <code>width/3</code> for table style and <code>width/9</code> for list style.

### Details

After extracting the vectors of items and corresponding descriptions from the arguments, both are coerced to character vectors.

In table style, items with more than `indent - 3` characters are displayed on a line of their own.

### Value

a character vector with the formatted entries.

### Examples

```
## Not run:
## Use R to create the 'INDEX' for package 'splines' from its 'CONTENTS'
x <- read.dcf(file = system.file("CONTENTS", package = "splines"),
              fields = c("Entry", "Description"))
x <- as.data.frame(x)
writeLines(formatDL(x$Entry, x$Description))
## or equivalently: writeLines(formatDL(x))
## Same information in tagged description list style:
writeLines(formatDL(x$Entry, x$Description, style = "list"))
## or equivalently: writeLines(formatDL(x, style = "list"))

## End(Not run)
```

---

function	<i>Function Definition</i>
----------	----------------------------

---

**Description**

These functions provide the base mechanisms for defining new functions in the R language.

**Usage**

```
function( arglist ) expr
return(value)
```

**Arguments**

arglist	Empty or one or more name or name=expression terms.
value	An expression.

**Details**

The names in an argument list can be back-quoted non-standard names (see ‘[backquote](#)’).

If `value` is missing, `NULL` is returned. If it is a single expression, the value of the evaluated expression is returned. (The expression is evaluated as soon as `return` is called, in the evaluation frame of the function and before any `on.exit` expression is evaluated.)

If the end of a function is reached without calling `return`, the value of the last evaluated expression is returned.

**Warning**

Prior to R 1.8.0, `value` could be a series of non-empty expressions separated by commas. In that case the value returned is a list of the evaluated expressions, with names set to the expressions where these are the names of R objects. That is, `a=foo()` names the list component `a` and gives it the value which results from evaluating `foo()`.

This has been deprecated (and a warning is given), as it was never documented in S, and whether or not the list is named differs by S versions. Supply a (named) list `value` instead.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[args](#) and [body](#) for accessing the arguments and body of a function.

[debug](#) for debugging; using [invisible](#) inside `return(.)` for returning *invisibly*.

**Examples**

```
norm <- function(x) sqrt(x**x)
norm(1:4)

## An anonymous function:
(function(x,y){ z <- x^2 + y^2; x+y+z })(0:7, 1)
```

funprog

---

*Common Higher-Order Functions in Functional Programming Languages*


---

### Description

Reduce uses a binary function to successively combine the elements of a given vector and a possibly given initial value. Filter extracts the elements of a vector for which a predicate (logical) function gives true. Find and Position give the first or last such element and its position in the vector, respectively. Map applies a function to the corresponding elements of given vectors. Negate creates the negation of a given function.

### Usage

```
Reduce(f, x, init, right = FALSE, accumulate = FALSE)
Filter(f, x)
Find(f, x, right = FALSE, nomatch = NULL)
Map(f, ...)
Negate(f)
Position(f, x, right = FALSE, nomatch = NA_integer_)
```

### Arguments

f	a function of the appropriate arity (binary for Reduce, unary for Filter, Find and Position, $k$ -ary for Map if this is called with $k$ arguments). An arbitrary predicate function for Negate.
x	a vector.
init	an R object of the same kind as the elements of x.
right	a logical indicating whether to proceed from left to right (default) or from right to left.
accumulate	a logical indicating whether the successive reduce combinations should be accumulated. By default, only the final combination is used.
nomatch	the value to be returned in the case when “no match” (no element satisfying the predicate) is found.
...	vectors.

### Details

If `init` is given, Reduce logically adds it to the start (when proceeding left to right) or the end of `x`, respectively. If this possibly augmented vector  $v$  has  $n > 1$  elements, Reduce successively applies  $f$  to the elements of  $v$  from left to right or right to left, respectively. I.e., a left reduce computes  $l_1 = f(v_1, v_2)$ ,  $l_2 = f(l_1, v_3)$ , etc., and returns  $l_{n-1} = f(l_{n-2}, v_n)$ , and a right reduce does  $r_{n-1} = f(v_{n-1}, v_n)$ ,  $r_{n-2} = f(v_{n-2}, r_{n-1})$  and returns  $r_1 = f(v_1, r_2)$ . (E.g., if  $v$  is the sequence (2, 3, 4) and  $f$  is division, left and right reduce give  $(2/3)/4 = 1/6$  and  $2/(3/4) = 8/3$ , respectively.) If  $v$  has only a single element, this is returned; if there are no elements, NULL is returned. Thus, it is ensured that `f` is always called with 2 arguments.

The current implementation is non-recursive to ensure stability and scalability.

Reduce is patterned after Common Lisp's `reduce`. A reduce is also known as a fold (e.g., in Haskell) or an accumulate (e.g., in the C++ Standard Template Library). The accumulative version corresponds to Haskell's scan functions.

Filter applies the unary predicate function `f` to each element of `x`, coercing to logical if necessary, and returns the subset of `x` for which this gives true. Note that possible NA values are currently always taken as false; control over NA handling may be added in the future. Filter corresponds to `filter` in Haskell or `remove-if-not` in Common Lisp.

Find and Position are patterned after Common Lisp's `find-if` and `position-if`, respectively. If there is an element for which the predicate function gives true, then the first or last such element or its position is returned depending on whether `right` is false (default) or true, respectively. If there is no such element, the value specified by `nomatch` is returned. The current implementation is not optimized for performance.

Map is a simple wrapper to `mapply` which does not attempt to simplify the result, similar to Common Lisp's `mapcar` (with arguments being recycled, however). Future versions may allow some control of the result type.

Negate corresponds to Common Lisp's `complement`. Given a (predicate) function `f`, it creates a function which returns the logical negation of what `f` returns.

## Examples

```
## A general-purpose adder:
add <- function(x) Reduce("+", x)
add(list(1, 2, 3))
## Like sum(), but can also be used for adding matrices etc., as it will
## use the appropriate '+' method in each reduction step.
## More generally, many generics meant to work on arbitrarily many
## arguments can be defined via reduction:
FOO <- function(...) Reduce(FOO2, list(...))
FOO2 <- function(x, y) UseMethod("FOO2")
## FOO() methods can then be provided via FOO2() methods.

## A general-purpose cumulative adder:
cadd <- function(x) Reduce("+", x, accumulate = TRUE)
cadd(seq_len(7))

## A simple function to compute continued fractions:
cfrac <- function(x) Reduce(function(u, v) u + 1 / v, x, right = TRUE)
## Continued fraction approximation for pi:
cfrac(c(3, 7, 15, 1, 292))
## Continued fraction approximation for Euler's number (e):
cfrac(c(2, 1, 2, 1, 1, 4, 1, 1, 6, 1, 1, 8))

## Iterative function application:
Funcall <- function(f, ...) f(...)
## Compute log(exp(acos(cos(0))))
Reduce(Funcall, list(log, exp, acos, cos), 0, right = TRUE)
## n-fold iterate of a function, functional style:
Iterate <- function(f, n = 1)
  function(x) Reduce(Funcall, rep.int(list(f), n), x, right = TRUE)
## Continued fraction approximation to the golden ratio:
Iterate(function(x) 1 + 1 / x, 30)(1)
## which is the same as
cfrac(rep.int(1, 31))
## Computing square root approximations for x as fixed points of the
```

```
## function t |-> (t + x / t) / 2, as a function of the initial value:
asqrt <- function(x, n) Iterate(function(t) (t + x / t) / 2, n)
asqrt(2, 30)(10) # Starting from a positive value => +sqrt(2)
asqrt(2, 30)(-1) # Starting from a negative value => -sqrt(2)

## A list of all functions in the base environment:
funs <- Filter(is.function, sapply(ls(baseenv()), get, baseenv()))
## Functions in base with more than 10 arguments:
names(Filter(function(f) length(formals(args(f))) > 10, funs))
## Number of functions in base with a '...' argument:
length(Filter(function(f)
              any(names(formals(args(f))) %in% "..."),
              funs))

## Find all objects in the base environment which are *not* functions:
Filter(Negate(is.function), sapply(ls(baseenv()), get, baseenv()))
```

---

gc

### *Garbage Collection*

---

#### Description

A call of `gc` causes a garbage collection to take place. `gcinfo` sets a flag so that automatic collection is either silent (`verbose=FALSE`) or prints memory usage statistics (`verbose=TRUE`).

#### Usage

```
gc(verbose = getOption("verbose"), reset=FALSE)
gcinfo(verbose)
```

#### Arguments

<code>verbose</code>	logical; if <code>TRUE</code> , the garbage collection prints statistics about cons cells and the space allocated for vectors.
<code>reset</code>	logical; if <code>TRUE</code> the values for maximum space used are reset to the current values.

#### Details

A call of `gc` causes a garbage collection to take place. This will also take place automatically without user intervention, and the primary purpose of calling `gc` is for the report on memory usage.

However, it can be useful to call `gc` after a large object has been removed, as this may prompt R to return memory to the operating system.

R allocates space for vectors in multiples of 8 bytes: hence the report of "Vcells", a relict of an earlier allocator (that used a vector heap).

When `gcinfo(TRUE)` is in force, messages are sent to the message connection at each garbage collection of the form

```
Garbage collection 12 = 10+0+2 (level 0) ...
6.4 Mbytes of cons cells used (58%)
2.0 Mbytes of vectors used (32%)
```

Here the last two lines give the current memory usage rounded up to the next 0.1Mb and as a percentage of the current trigger value. The first line gives a breakdown of the number of garbage collections at various levels (for an explanation see the ‘R Internals’ manual).

### Value

gc returns a matrix with rows "Ncells" (*cons cells*), usually 28 bytes each on 32-bit systems and 56 bytes on 64-bit systems, and "Vcells" (*vector cells*, 8 bytes each), and columns "used" and "gc trigger", each also interpreted in megabytes (rounded up to the next 0.1Mb).

If maxima have been set for either "Ncells" or "Vcells", a fifth column is printed giving the current limits in Mb (with NA denoting no limit).

The final two columns show the maximum space used since the last call to gc(reset=TRUE) (or since R started).

gcinfo returns the previous value of the flag.

### See Also

The ‘R Internals’ manual.

[Memory](#) on R’s memory management, and [gctorture](#) if you are an R developer.

[reg.finalizer](#) for actions to happen at garbage collection.

### Examples

```
gc() #- do it now
gcinfo(TRUE) #-- in the future, show when R does it
x <- integer(100000); for(i in 1:18) x <- c(x,i)
gcinfo(verbose = FALSE) #-- don't show it anymore

gc(TRUE)

gc(reset=TRUE)
```

---

gc.time

*Report Time Spent in Garbage Collection*

---

### Description

This function reports the time spent in garbage collection so far in the R session while GC timing was enabled.

### Usage

```
gc.time(on = TRUE)
```

### Arguments

on                    logical; if TRUE, GC timing is enabled.

**Value**

A numerical vector of length 5 giving the user CPU time, the system CPU time, the elapsed time and children's user and system CPU times (normally both zero), of time spent doing garbage collection whilst GC timing was enabled.

Times of child processes are not available on Windows and will always be given as NA.

**Warnings**

This is experimental functionality, likely to be removed as soon as the next release.

The timings are rounded up by the sampling interval for timing processes, and so are likely to be over-estimates.

It is a [primitive](#).

**See Also**

[gc](#), [proc.time](#) for the timings for the session.

**Examples**

```
gc.time()
```

---

gctorture

*Torture Garbage Collector*

---

**Description**

Provokes garbage collection on (nearly) every memory allocation. Intended to ferret out memory protection bugs. Also makes R run *very* slowly, unfortunately.

**Usage**

```
gctorture(on = TRUE)
```

**Arguments**

on                   logical; turning it on/off.

**Value**

Previous value.

**Author(s)**

Peter Dalgaard

---

`get`*Return the Value of a Named Object*

---

### Description

Search for an R object with a given name and return it.

### Usage

```
get(x, pos = -1, envir = as.environment(pos), mode = "any",
    inherits = TRUE)

mget(x, envir, mode = "any",
      ifnotfound = list(function(x)
        stop(paste("value for '", x, "' not found", sep = "")),
        call. = FALSE),
      inherits = FALSE)
```

### Arguments

<code>x</code>	a variable name (given as a character string).
<code>pos</code>	where to look for the object (see the details section); if omitted, the function will search as if the name of the object appeared unquoted in an expression.
<code>envir</code>	an alternative way to specify an environment to look in; see the ‘Details’ section.
<code>mode</code>	the mode or type of object sought: see the ‘Details’ section.
<code>inherits</code>	should the enclosing frames of the environment be searched?
<code>ifnotfound</code>	A <a href="#">list</a> of values to be used if the item is not found: it will be coerced to list if necessary.

### Details

The `pos` argument can specify the environment in which to look for the object in any of several ways: as an integer (the position in the [search](#) list); as the character string name of an element in the search list; or as an [environment](#) (including using `sys.frame` to access the currently active function calls). The `envir` argument is an alternative way to specify an environment, but is primarily there for back compatibility.

This function looks to see if the name `x` has a value bound to it in the specified environment. If `inherits` is `TRUE` and a value is not found for `x` in the specified environment, the enclosing frames of the environment are searched until the name `x` is encountered. See [environment](#) and the ‘R Language Definition’ manual for details about the structure of environments and their enclosures.

**Warning:** `inherits = TRUE` is the default behaviour for R but not for S.

If `mode` is specified then only objects of that type are sought. The `mode` may specify one of the collections `"numeric"` and `"function"` (see [mode](#)): any member of the collection will suffice.

Using a `NULL` environment is equivalent to using the current environment.

For `mget` multiple values are returned in a named `list`. This is true even if only one value is requested. The value in `mode` and `ifnotfound` can be either the same length as the number of requested items or of length 1. The argument `ifnotfound` must be a list containing either the



value to use if the requested item is not found or a function of one argument which will be called if the item is not found, with argument the name of the item being requested. The default value for `inherits` is `FALSE`, in contrast to the default behavior for `get`.

`mode` here is a mixture of the meanings of `typeof` and `mode`: "function" covers primitive functions and operators, "numeric", "integer", "real" and "double" all refer to any numeric type, "symbol" and "name" are equivalent *but* "language" must be used.

### Value

The object found. (If no object is found an error results.)

### Note

The reverse of `a <- get(nam)` is `assign(nam, a)`.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

`exists`, `assign`.

### Examples

```
get("%o%")

##test mget
e1 <- new.env()
mget(letters, e1, ifnotfound = as.list(LETTERS))
```

---

getDLLRegisteredRoutines

*Reflectance Information for C/Fortran routines in a DLL*

---

### Description

This function allows us to query the set of routines in a DLL that are registered with R to enhance dynamic lookup, error handling when calling native routines, and potentially security in the future. This function provides a description of each of the registered routines in the DLL for the different interfaces, i.e. `.C`, `.Call`, `.Fortran` and `.External`.

### Usage

```
getDLLRegisteredRoutines(dll, addNames = TRUE)
```

**Arguments**

dll	a character string or <code>DLLInfo</code> object. The character string specifies the file name of the DLL of interest, and is given without the file name extension (e.g., the <code>.dll</code> or <code>.so</code> ) and with no directory/path information. So a file <code>'MyPackage/libs/MyPackage.so'</code> would be specified as <code>'MyPackage'</code> . The <code>DLLInfo</code> objects can be obtained directly in calls to <code>dyn.load</code> and <code>library.dynam</code> , or can be found after the DLL has been loaded using <code>getLoadedDLLs</code> , which returns a list of <code>DLLInfo</code> objects (index-able by DLL file name). The <code>DLLInfo</code> approach avoids any ambiguities related to two DLLs having the same name but corresponding to files in different directories.
addNames	a logical value. If this is <code>TRUE</code> , the elements of the returned lists are named using the names of the routines (as seen by R via registration or raw name). If <code>FALSE</code> , these names are not computed and assigned to the lists. As a result, the call should be quicker. The name information is also available in the <code>NativeSymbolInfo</code> objects in the lists.

**Details**

This takes the registration information after it has been registered and processed by the R internals. In other words, it uses the extended information

**Value**

A list with four elements corresponding to the routines registered for the `.C`, `.Call`, `.Fortran` and `.External` interfaces. Each element is a list with as many elements as there were routines registered for that interface. Each element identifies a routine and is an object of class `NativeSymbolInfo`. An object of this class has the following fields:

name	the registered name of the routine (not necessarily the name in the C code).
address	the memory address of the routine as resolved in the loaded DLL. This may be <code>NULL</code> if the symbol has not yet been resolved.
dll	an object of class <code>DLLInfo</code> describing the DLL. This is same for all elements returned.
numParameters	the number of arguments the native routine is to be called with. In the future, we will provide information about the types of the parameters also.

**Author(s)**

Duncan Temple Lang <duncan@wald.ucdavis.edu>

**References**

"Writing R Extensions Manual" for symbol registration. R News, Volume 1/3, September 2001. "In search of C/C++ & Fortran Symbols"

**See Also**

[getLoadedDLLs](#)

**Examples**

```
dlls <- getLoadedDLLs()
getDLLRegisteredRoutines(dlls[["base"]])

getDLLRegisteredRoutines("stats")
```

---

getLoadedDLLs            *Get DLLs Loaded in Current Session*

---

**Description**

This function provides a way to get a list of all the DLLs (see [dyn.load](#)) that are currently loaded in the R session.

**Usage**

```
getLoadedDLLs()
```

**Details**

This queries the internal table that manages the DLLs.

**Value**

An object of class "DLLInfoList" which is a list with an element corresponding to each DLL that is currently loaded in the session. Each element is an object of class "DLLInfo" which has the following entries.

name	the abbreviated name.
path	the fully qualified name of the loaded DLL.
dynamicLookup	a logical value indicating whether R uses only the registration information to resolve symbols or whether it searches the entire symbol table of the DLL.
handle	a reference to the C-level data structure that provides access to the contents of the DLL. This is an object of class "DLLHandle".

Note that the class `DLLInfo` has an overloaded method for `$` which can be used to resolve native symbols within that DLL. Therefore, one must access the R-level elements described above using `[, e.g. x[["name"]]` or `x[["handle"]]`.

**Note**

We are starting to use the `handle` elements in the DLL object to resolve symbols more directly in R.

**Author(s)**

Duncan Temple Lang <duncan@wald.ucdavis.edu>.

**See Also**

[getDLLRegisteredRoutines](#), [getNativeSymbolInfo](#)

**Examples**

```
getLoadedDLLs ()
```

---

```
getNativeSymbolInfo
```

*Obtain a Description of one or more Native (C/Fortran) Symbols*

---

**Description**

This finds and returns as comprehensive a description of one or more dynamically loaded or ‘exported’ built-in native symbols. For each name, it returns information about the name of the symbol, the library in which it is located and, if available, the number of arguments it expects and by which interface it should be called (i.e. `.Call`, `.C`, `.Fortran`, or `.External`). Additionally, it returns the address of the symbol and this can be passed to other C routines which can invoke. Specifically, this provides a way to explicitly share symbols between different dynamically loaded package libraries. Also, it provides a way to query where symbols were resolved, and aids diagnosing strange behavior associated with dynamic resolution.

This is vectorized in the `name` argument so can process multiple symbols in a single call. The result is a list that can be indexed by the given symbol names.

**Usage**

```
getNativeSymbolInfo(name, PACKAGE, unlist = TRUE,
                    withRegistrationInfo = FALSE)
```

**Arguments**

<code>name</code>	the name(s) of the native symbol(s) as used in a call to <code>is.loaded</code> , etc. Note that Fortran symbols should be supplied as-is, not wrapped in <code>symbol.FOR</code> .
<code>PACKAGE</code>	an optional argument that specifies to which DLL we restrict the search for this symbol. If this is "base", we search in the R executable itself.
<code>unlist</code>	a logical value which controls how the result is returned if the function is called with the name of a single symbol. If <code>unlist</code> is <code>TRUE</code> and the number of symbol names in <code>name</code> is one, then the <code>NativeSymbolInfo</code> object is returned. If it is <code>FALSE</code> , then a list of <code>NativeSymbolInfo</code> objects is returned. This is ignored if the number of symbols passed in <code>name</code> is more than one. To be compatible with earlier versions of this function, this defaults to <code>TRUE</code> .
<code>withRegistrationInfo</code>	a logical value indicating whether, if <code>TRUE</code> , to return information that was registered with R about the symbol and its parameter types if such information is available, or if <code>FALSE</code> to return the address of the symbol.

**Details**

This uses the same mechanism for resolving symbols as is used in all the native interfaces (`.Call`, etc.). If the symbol has been explicitly registered by the DLL in which it is contained, information about the number of arguments and the interface by which it should be called will be returned. Otherwise, a generic native symbol object is returned.

**Value**

Generally, a list of `NativeSymbolInfo` elements whose elements can be indexed by the elements of `name` in the call. Each `NativeSymbolInfo` object is a list containing the following elements:

<code>name</code>	the name of the symbol, as given by the <code>name</code> argument.
<code>address</code>	if <code>withRegistrationInfo</code> is <code>FALSE</code> , this is the native memory address of the symbol which can be used to invoke the routine, and also to compare with other symbol addresses. This is an external pointer object and of class <code>NativeSymbol</code> . If <code>withRegistrationInfo</code> is <code>TRUE</code> and registration information is available for the symbol, then this is an object of class <code>RegisteredNativeSymbol</code> and is a reference to an internal data type that has access to the routine pointer and registration information. This too can be used in calls to <code>.Call</code> , <code>.C</code> , <code>.Fortran</code> and <code>.External</code> .
<code>package</code>	a list containing 3 elements: <b>name</b> the short form of the library name which can be used as the value of the <code>PACKAGE</code> argument in the different native interface functions. <b>path</b> the fully qualified name of the DLL. <b>dynamicLookup</b> a logical value indicating whether dynamic resolution is used when looking for symbols in this library, or only registered routines can be located.

If the routine was explicitly registered by the dynamically loaded library, the list contains a fourth field

<code>numParameters</code>	the number of arguments that should be passed in a call to this routine.
----------------------------	--

Additionally, the list will have an additional class, being `CRoutine`, `CallRoutine`, `FortranRoutine` or `ExternalRoutine` corresponding to the R interface by which it should be invoked.

If any of the symbols is not found, an error is immediately raised.

If `name` contains only one symbol name and `unlist` is `TRUE`, then the single `NativeSymbolInfo` is returned rather than the list containing that one element.

**Note**

One motivation for accessing this reflectance information is to be able to pass native routines to C routines as function pointers in C. This allows us to treat native routines and R functions in a similar manner, such as when passing an R function to C code that makes callbacks to that function at different points in its computation (e.g., `nls`). Additionally, we can resolve the symbol just once and avoid resolving it repeatedly or using the internal cache. In the future, one may be able to treat `NativeSymbol` objects directly as callback objects.

**Author(s)**

Duncan Temple Lang

**References**

For information about registering native routines, see “In Search of C/C++ & FORTRAN Routines”, R-News, volume 1, number 3, 2001, p20–23 (<http://CRAN.R-project.org/doc/Rnews/>).

**See Also**

`getDLLRegisteredRoutines`, `is.loaded`, `.C`, `.Fortran`, `.External`, `.Call`, `dyn.load`.

**Examples**

```
library(stats) # normally loaded
getNativeSymbolInfo("dansari")

getNativeSymbolInfo("hcass2") # a Fortran symbol
```

---

gettext

*Translate Text Messages*

---

**Description**

If Native Language Support was enabled in this build of R, attempt to translate character vectors or set where the translations are to be found.

**Usage**

```
gettext(..., domain = NULL)

ngettext(n, msg1, msg2, domain = NULL)

bindtextdomain(domain, dirname = NULL)
```

**Arguments**

<code>...</code>	One or more character vectors.
<code>domain</code>	The ‘domain’ for the translation.
<code>n</code>	a non-negative integer.
<code>msg1</code>	the message to be used in English for $n = 1$ .
<code>msg2</code>	the message to be used in English for $n = 0, 2, 3, \dots$
<code>dirname</code>	The directory in which to find translated message catalogs for the domain.

**Details**

If `domain` is `NULL` or `"`, a domain is searched for based on the name space which contains the function calling `gettext` or `ngettext`. If a suitable domain can be found, each character string is offered for translation, and replaced by its translation into the current language if one is found.

Conventionally the domain for R warning/error messages in package **pkg** is `"R-pkg"`, and that for C-level messages is `"pkg"`.

For `gettext`, leading and trailing whitespace is ignored when looking for the translation.

`ngettext` is used where the message needs to vary by a single integer. Translating such messages is subject to very specific rules for different languages: see the GNU Gettext Manual. The string will often contain a single instance of `%d` to be used in `sprintf`. If English is used, `msg1` is returned if  $n == 1$  and `msg2` in all other cases.

**Value**

For `gettext`, a character vector, one element per string in . . . . If translation is not enabled or no domain is found or no translation is found in that domain, the original strings are returned.

For `ngettext`, a character string.

For `bindtextdomain`, a character string giving the current base directory, or `NULL` if setting it failed.

**See Also**

[stop](#) and [warning](#) make use of `gettext` to translate messages.

[xgettext](#) for extracting translatable strings from R source files.

**Examples**

```
bindtextdomain("R") # non-null if and only if NLS is enabled

for(n in 0:3)
  print(sprintf(ngettext(n, "%d variable has missing values",
                        "%d variables have missing values"),
              n))

## Not run: ## for translation, those strings should appear in R-pkg.pot as
msgid      "%d variable has missing values"
msgid_plural "%d variables have missing values"
msgstr[0] ""
msgstr[1] ""

## End(Not run)

miss <- c("one", "or", "another")
cat(ngettext(length(miss), "variable", "variables"),
    paste(sQuote(miss), collapse=", "),
    ngettext(length(miss), "contains", "contain"), "missing values\n")

## better for translators would be to use
cat(sprintf(ngettext(length(miss),
                    "variable %s contains missing values\n",
                    "variables %s contain missing values\n"),
          paste(sQuote(miss), collapse=", ")))
```

---

getwd

*Get or Set Working Directory*


---

**Description**

`getwd` returns an absolute filename representing the current working directory of the R process; `setwd(dir)` is used to set the working directory to `dir`.

**Usage**

```
getwd()
setwd(dir)
```

**Arguments**

`dir`                    A character string.

**Value**

`getwd` returns a character vector, or `NULL` if the working directory is not available. On Windows the path returned will use `/` as the path separator. The path will not have a trailing `/` unless it is the root directory (of a drive or share on Windows).

`setwd` returns the current directory before the change, invisibly. It will give an error if it does not succeed.

**Note**

These functions are not implemented on all platforms.

**See Also**

[list.files](#) for the *contents* of a directory.

**Examples**

```
(WD <- getwd())
if (!is.null(WD)) setwd(WD)
```

---

gl

*Generate Factor Levels*


---

**Description**

Generate factors by specifying the pattern of their levels.

**Usage**

```
gl(n, k, length = n*k, labels = 1:n, ordered = FALSE)
```

**Arguments**

`n`                    an integer giving the number of levels.  
`k`                    an integer giving the number of replications.  
`length`            an integer giving the length of the result.  
`labels`            an optional vector of labels for the resulting factor levels.  
`ordered`           a logical indicating whether the result should be ordered or not.

**Value**

The result has levels from 1 to `n` with each value replicated in groups of length `k` out to a total length of `length`.

`gl` is modelled on the *GLIM* function of the same name.



**See Also**

The underlying `factor()`.

**Examples**

```
## First control, then treatment:
gl(2, 8, labels = c("Control", "Treat"))
## 20 alternating 1s and 2s
gl(2, 1, 20)
## alternating pairs of 1s and 2s
gl(2, 2, 20)
```

---

 grep

*Pattern Matching and Replacement*


---

**Description**

`grep`, `grepl`, `regexpr` and `gregexpr` search for matches to argument `pattern` within a character vector: they differ in the format of and amount of detail in the results.

`sub` and `gsub` perform replacement of the first and all matches respectively.

**Usage**

```
grep(pattern, x, ignore.case = FALSE, perl = FALSE, value = FALSE,
      fixed = FALSE, useBytes = FALSE, invert = FALSE)
```

```
grepl(pattern, x, ignore.case = FALSE, perl = FALSE, fixed = FALSE,
       useBytes = FALSE)
```

```
sub(pattern, replacement, x, ignore.case = FALSE, perl = FALSE,
     fixed = FALSE, useBytes = FALSE)
```

```
gsub(pattern, replacement, x, ignore.case = FALSE, perl = FALSE,
      fixed = FALSE, useBytes = FALSE)
```

```
regexpr(pattern, text, ignore.case = FALSE, perl = FALSE,
        fixed = FALSE, useBytes = FALSE)
```

```
gregexpr(pattern, text, ignore.case = FALSE, perl = FALSE,
         fixed = FALSE, useBytes = FALSE)
```

**Arguments**

`pattern` character string containing a [regular expression](#) (or character string for `fixed = TRUE`) to be matched in the given character vector. Coerced by `as.character` to a character string if possible. If a character vector of length 2 or more is supplied, the first element is used with a warning. Missing values are allowed except for `regexpr` and `gregexpr`.

`x`, `text` a character vector where matches are sought, or an object which can be coerced by `as.character` to a character vector.

<code>ignore.case</code>	if <code>FALSE</code> , the pattern matching is <i>case sensitive</i> and if <code>TRUE</code> , case is ignored during matching.
<code>perl</code>	logical. Should perl-compatible regexps be used? Has priority over <code>extended</code> .
<code>value</code>	if <code>FALSE</code> , a vector containing the ( <i>integer</i> ) indices of the matches determined by <code>grep</code> is returned, and if <code>TRUE</code> , a vector containing the matching elements themselves is returned.
<code>fixed</code>	logical. If <code>TRUE</code> , <code>pattern</code> is a string to be matched as is. Overrides all conflicting arguments.
<code>useBytes</code>	logical. If <code>TRUE</code> the matching is done byte-by-byte rather than character-by-character. See ‘Details’.
<code>invert</code>	logical. If <code>TRUE</code> return indices or values for elements that do <i>not</i> match.
<code>replacement</code>	a replacement for matched pattern in <code>sub</code> and <code>gsub</code> . Coerced to character if possible. For <code>fixed = FALSE</code> this can include backreferences " <code>\1</code> " to " <code>\9</code> " to parenthesized subexpressions of <code>pattern</code> . For <code>perl = TRUE</code> only, it can also contain " <code>\U</code> " or " <code>\L</code> " to convert the rest of the replacement to upper or lower case and " <code>\E</code> " to end case conversion. If a character vector of length 2 or more is supplied, the first element is used with a warning. If <code>NA</code> , all elements in the result corresponding to matches will be set to <code>NA</code> .

## Details

Arguments which should be character strings or character vectors are coerced to character if possible.

Each of these functions operates in one of three modes:

1. `fixed = TRUE`: use exact matching.
2. `perl = TRUE`: use Perl-style regular expressions.
3. `fixed = FALSE`, `perl = FALSE`: use POSIX 1003.2 extended regular expressions.

See the help pages on [regular expression](#) for details of the different types of regular expressions.

The two `*sub` functions differ only in that `sub` replaces only the first occurrence of a `pattern` whereas `gsub` replaces all occurrences.

For `regexpr` and `gregexpr` it is an error for `pattern` to be `NA`, otherwise `NA` is permitted and gives an `NA` match.

The main effect of `useBytes` is to avoid errors/warnings about invalid inputs and spurious matches in multibyte locales, but for `regexpr` it changes the interpretation of the output. As from R 2.10.0 it inhibits the conversion of inputs with marked encodings.

Caseless matching does not make much sense for bytes in a multibyte locale, and you should expect it only to work for ASCII characters if `useBytes = TRUE`.

## Value

`grep(value = FALSE)` returns an integer vector of the indices of the elements of `x` that yielded a match (or not, for `invert = TRUE`).

`grep(value = TRUE)` returns a character vector containing the selected elements of `x` (after coercion, preserving names but no other attributes).

`grepl` returns a logical vector (match or not for each element of `x`).

For `sub` and `gsub` return a character vector of the same length and with the same attributes as `x` (after possible coercion to character). Elements of character vectors `x` which are not substituted will

be returned unchanged (including any declared encoding). If `useBytes = FALSE` a non-ASCII substituted result will often be in UTF-8 with a marked encoding (e.g. if there is a UTF-8 input, and in a multibyte locale unless `fixed = TRUE`).

`regexpr` returns an integer vector of the same length as `text` giving the starting position of the first match or `-1` if there is none, with attribute `"match.length"`, an integer vector giving the length of the matched text (or `-1` for no match). The match positions and lengths are in characters unless `useBytes = TRUE` is used, when they are in bytes.

`gregexpr` returns a list of the same length as `text` each element of which is of the same form as the return value for `regexpr`, except that the starting positions of every (disjoint) match are given.

### Warning

POSIX 1003.2 mode of `gsub` and `gregexpr` does not work correctly with repeated word-boundaries (e.g. `pattern = "\\b"`). Use `perl = TRUE` for such matches (but that may not work as expected with non-ASCII inputs, as the meaning of ‘word’ is system-dependent).

### Performance considerations

If you are doing a lot of regular expression matching, including on very long strings, you will want to consider the options used. Generally PCRE will be faster than the default regular expression engine, and `fixed = TRUE` faster still (especially when each pattern is matched only a few times).

If you are working in a single-byte locale and have marked UTF-8 strings that are representable in that locale, convert them first as just one UTF-8 string will force all the matching to be done in Unicode, which attracts a penalty of around  $3 \times$  for the default POSIX 1003.2 mode.

If you can make use of `useBytes = TRUE`, the strings will not be checked before matching, and the actual matching will be faster. Often byte-based matching suffices in a UTF-8 locale since byte patterns of one character never match part of another.

### Note

Prior to R 2.11.0 there was an argument `extended` which could be used to select ‘basic’ regular expressions: this was often used when `fixed = TRUE` would be preferable. In the actual implementation (as distinct from the POSIX standard) the only difference was that ‘?’, ‘+’, ‘{’, ‘|’, ‘(’, and ‘)’ were not interpreted as metacharacters.

### Source

The C code for POSIX-style regular expression matching has changed over the years. As from R 2.10.0 the TRE library of Ville Laurikari (<http://laurikari.net/tre/>) is used. From 2005 to R 2.9.2, code based on `glibc` was used (and before that, code from GNU `grep`). The POSIX standard does give some room for interpretation, especially in the handling of invalid regular expressions and the collation of character ranges, so the results will have changed slightly.

For Perl-style matching PCRE (<http://www.pcre.org>) is used.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole (`grep`)

**See Also**

[regular expression](#) (aka [regexp](#)) for the details of the pattern specification.

[glob2rx](#) to turn wildcard matches into regular expressions.

[agrep](#) for approximate matching.

[enc2native](#) to re-encode the result of `sub`.

[tolower](#), [toupper](#) and [chartr](#) for character translations. [charmatch](#), [pmatch](#), [match](#).

[apropos](#) uses regexps and has more examples.

**Examples**

```
grep("[a-z]", letters)

txt <- c("arm", "foot", "lefroo", "bafoobar")
if(length(i <- grep("foo", txt)))
  cat("'foo' appears at least once in\n\t", txt, "\n")
i # 2 and 4
txt[i]

## Double all 'a' or 'b's; "\" must be escaped, i.e., 'doubled'
gsub("[ab]", "\\1_\\1_", "abc and ABC")

txt <- c("The", "licenses", "for", "most", "software", "are",
  "designed", "to", "take", "away", "your", "freedom",
  "to", "share", "and", "change", "it.",
  "", "By", "contrast", "the", "GNU", "General", "Public", "License",
  "is", "intended", "to", "guarantee", "your", "freedom", "to",
  "share", "and", "change", "free", "software", "--",
  "to", "make", "sure", "the", "software", "is",
  "free", "for", "all", "its", "users")
(i <- grep("[gu]", txt)) # indices
stopifnot(txt[i] == grep("[gu]", txt, value = TRUE))

## Note that in locales such as en_US this includes B as the
## collation order is aAbBcCdEe ...
(ot <- sub("[b-e]", ".", txt))
txt[ot != gsub("[b-e]", ".", txt)] # gsub does "global" substitution

txt[gsub("g", "#", txt) !=
  gsub("g", "#", txt, ignore.case = TRUE)] # the "G" words

regexpr("en", txt)

gregexpr("e", txt)

## trim trailing white space
str <- 'Now is the time      '
sub(' +$', '', str) ## spaces only
sub('[:space:]+$ ', '', str) ## white space, POSIX-style
sub('\\s+$ ', '', str, perl = TRUE) ## Perl-style white space

## capitalizing
txt <- "a test of capitalizing"
gsub("(\\w)(\\w*)", "\\U\\1\\L\\2", txt, perl=TRUE)
gsub("\\b(\\w)", "\\U\\1", txt, perl=TRUE)
```

```
txt2 <- "useRs may fly into JFK or laGuardia"
gsub("(\\w)(\\w*)(\\w)", "\\U\\1\\E\\2\\U\\3", txt2, perl=TRUE)
sub("(\\w)(\\w*)(\\w)", "\\U\\1\\E\\2\\U\\3", txt2, perl=TRUE)
```

---

groupGeneric

*S3 Group Generic Functions*


---

## Description

Group generic methods can be defined for four pre-specified groups of functions, `Math`, `Ops`, `Summary` and `Complex`. (There are no objects of these names in base R, but there are in the **methods** package.)

A method defined for an individual member of the group takes precedence over a method defined for the group as a whole.

## Usage

```
## S3 methods for group generics have prototypes:
Math(x, ...)
Ops(e1, e2)
Complex(z)
Summary(..., na.rm = FALSE)
```

## Arguments

`x`, `z`, `e1`, `e2` objects.  
`...` further arguments passed to methods.  
`na.rm` logical: should missing values be removed?

## Details

There are four *groups* for which S3 methods can be written, namely the "Math", "Ops", "Summary" and "Complex" groups. These are not R objects, but methods can be supplied for them and base R contains `factor`, `data.frame` and `difftime` methods for the first three groups. (There is also a `ordered` method for Ops, `POSIXt` and `Date` methods for Math and Ops, `package_version` methods for Ops and Summary, as well as a `ts` method for Ops in package `stats`.)

### 1. Group "Math":

- `abs`, `sign`, `sqrt`,  
`floor`, `ceiling`, `trunc`,  
`round`, `signif`
- `exp`, `log`, `expm1`, `log1p`,  
`cos`, `sin`, `tan`,  
`acos`, `asin`, `atan`  
`cosh`, `sinh`, `tanh`,  
`acosh`, `asinh`, `atanh`
- `lgamma`, `gamma`, `digamma`, `trigamma`
- `cumsum`, `cumprod`, `cummax`, `cummin`

Members of this group dispatch on `x`. Most members accept only one argument, but members `log`, `round` and `signif` accept one or two arguments, and `trunc` accepts one or more.

## 2. Group "Ops":

- "+", "-", "\*", "/", "^", "%%", "%/%"
- "&", "|", "!"
- "==", "!=", "<", "<=", ">=", ">"

This group contains both binary and unary operators (+, - and !): when a unary operator is encountered the `Ops` method is called with one argument and `e2` is missing.

The classes of both arguments are considered in dispatching any member of this group. For each argument its vector of classes is examined to see if there is a matching specific (preferred) or `Ops` method. If a method is found for just one argument or the same method is found for both, it is used. If different methods are found, there is a warning about 'incompatible methods': in that case or if no method is found for either argument the internal method is used.

If the members of this group are called as functions, any argument names are removed to ensure that positional matching is always used.

## 3. Group "Summary":

- all, any
- sum, prod
- min, max
- range

Members of this group dispatch on the first argument supplied.

## 4. Group "Complex":

- Arg, Conj, Im, Mod, Re

Members of this group dispatch on `z`.

Note that a method will be used for either one of these groups or one of its members *only* if it corresponds to a "class" attribute, as the internal code dispatches on `oldClass` and not on `class`. This is for efficiency: having to dispatch on, say, `Ops.integer` would be too slow.

The number of arguments supplied for primitive members of the "Math" group generic methods is not checked prior to dispatch.

There is no lazy evaluation of arguments for group-generic functions.

## Technical Details

These functions are all primitive and [internal generic](#).

The details of method dispatch and variables such as `.Generic` are discussed in the help for [UseMethod](#). There are a few small differences:

- For the operators of group `Ops`, the object `.Method` is a length-two character vector with elements the methods selected for the left and right arguments respectively. (If no method was selected, the corresponding element is `" "`.)
- Object `.Group` records the group used for dispatch (if a specific method is used this is `" "`).

## References

Appendix A, *Classes and Methods* of  
Chambers, J. M. and Hastie, T. J. eds (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

**See Also**

[methods](#) for methods of non-internal generic functions.

[S4groupGeneric](#) for group generics for S4 methods.

**Examples**

```
require(utils)

d.fr <- data.frame(x=1:9, y=stats::rnorm(9))
class(1 + d.fr) == "data.frame" ##-- add to d.f. ...

methods("Math")
methods("Ops")
methods("Summary")
methods("Complex") # none in base R
```

---

gzcon

*(De)compress I/O Through Connections*


---

**Description**

`gzcon` provides a modified connection that wraps an existing connection, and decompresses reads or compresses writes through that connection. Standard `gzip` headers are assumed.

**Usage**

```
gzcon(con, level = 6, allowNonCompressed = TRUE)
```

**Arguments**

<code>con</code>	a connection.
<code>level</code>	integer between 0 and 9, the compression level when writing.
<code>allowNonCompressed</code>	logical. When reading, should non-compressed input be allowed?

**Details**

If `con` is open then the modified connection is opened. Closing the wrapper connection will also close the underlying connection.

Reading from a connection which does not supply a `gzip` magic header is equivalent to reading from the original connection if `allowNonCompressed` is true, otherwise an error.

Compressed output will contain embedded NUL bytes, and so `con` is not permitted to be a [textConnection](#) opened with `open="w"`. Use a writable [rawConnection](#) to compress data into a variable.

The original connection becomes unusable: any object pointing to it will now refer to the modified connection.

**Value**

An object inheriting from class `"connection"`. This is the same connection *number* as supplied, but with a modified internal structure. It has binary mode.

**See Also**[gzfile](#)**Examples**

```
## Uncompress a data file from a URL
z <- gzcon(url("http://www.stats.ox.ac.uk/pub/datasets/csb/ch12.dat.gz"))
# read.table can only read from a text-mode connection.
raw <- textConnection(readLines(z))
close(z)
dat <- read.table(raw)
close(raw)
dat[1:4, ]

## gzfile and gzcon can inter-work.
## Of course here one would used gzfile, but file() can be replaced by
## any other connection generator.
zz <- gzfile("ex.gz", "w")
cat("TITLE extra line", "2 3 5 7", "", "11 13 17", file = zz, sep = "\n")
close(zz)
readLines(zz <- gzcon(file("ex.gz", "rb")))
close(zz)
unlink("ex.gz")

zz <- gzcon(file("ex2.gz", "wb"))
cat("TITLE extra line", "2 3 5 7", "", "11 13 17", file = zz, sep = "\n")
close(zz)
readLines(zz <- gzfile("ex2.gz"))
close(zz)
unlink("ex2.gz")
```

hexmode

*Display Numbers in Hexadecimal***Description**

Convert or print integers in hexadecimal format, with as many digits as are needed to display the largest, using leading zeroes as necessary.

**Usage**

```
as.hexmode(x)

## S3 method for class 'hexmode':
as.character(x, ...)

## S3 method for class 'hexmode':
format(x, width = NULL, upper.case = FALSE, ...)

## S3 method for class 'hexmode':
print(x, ...)
```



**Arguments**

<code>x</code>	An object, for the methods inheriting from class "hexmode".
<code>width</code>	NULL or a positive integer specifying the minimum field width to be used, with padding by leading zeroes.
<code>upper.case</code>	a logical indicating whether to use upper-case letters or lower-case letters (default).
<code>...</code>	further arguments passed to or from other methods.

**Details**

Class "hexmode" consists of integer vectors with that class attribute, used merely to ensure that they are printed in hex.

If `width = NULL` (the default), the output is padded with leading zeroes to the smallest width needed for all the non-missing elements.

`as.hexmode` can convert integers (of [type](#) "integer" or "double") and character vectors whose elements contain only 0-9, a-f, A-F (or are NA) to class "hexmode".

**See Also**

[octmode](#), [sprintf](#) for other options in converting integers to hex, [strtoi](#) to convert hex strings to integers.

---

Hyperbolic

*Hyperbolic Functions*

---

**Description**

These functions give the obvious hyperbolic functions. They respectively compute the hyperbolic cosine, sine, tangent, and their inverses, arc-cosine, arc-sine, arc-tangent (or 'area cosine', etc).

**Usage**

```
cosh(x)
sinh(x)
tanh(x)
acosh(x)
asinh(x)
atanh(x)
```

**Arguments**

<code>x</code>	a numeric or complex vector
----------------	-----------------------------

**Details**

These are [internal generic primitive](#) functions: methods can be defined for them individually or via the [Math](#) group generic.

Branch cuts are consistent with the inverse trigonometric functions `asin()` et seq, and agree with those defined in Abramowitz and Stegun, figure 4.7, page 86.

## S4 methods

All are S4 generic functions: methods can be defined for them individually or via the [Math](#) group generic.

## References

Abramowitz, M. and Stegun, I. A. (1972) *Handbook of Mathematical Functions*. New York: Dover. Chapter 4. Elementary Transcendental Functions: Logarithmic, Exponential, Circular and Hyperbolic Functions

## See Also

The trigonometric functions, [cos](#), [sin](#), [tan](#), and their inverses [acos](#), [asin](#), [atan](#).

The logistic distribution function [plogis](#) is a shifted version of `tanh()` for numeric `x`.

---

iconv

*Convert Character Vector between Encodings*

---

## Description

This uses system facilities to convert a character vector between encodings: the ‘i’ stands for ‘internationalization’.

## Usage

```
iconv(x, from = "", to = "", sub = NA, mark = TRUE)
```

```
iconvlist()
```

## Arguments

<code>x</code>	A character vector, or an object to be converted to a character vector by <a href="#">as.character</a> .
<code>from</code>	A character string describing the current encoding.
<code>to</code>	A character string describing the target encoding.
<code>sub</code>	character string. If not <code>NA</code> it is used to replace any non-convertible bytes in the input. (This would normally be a single character, but can be more.) If <code>"byte"</code> , the indication is <code>"&lt;xx&gt;"</code> with the hex code of the byte.
<code>mark</code>	logical, for expert use. Should encodings be marked?

## Details

The names of encodings and which ones are available are platform-dependent. All R platforms support `" "` (for the encoding of the current locale), `"latin1"` and `"UTF-8"`. Generally case is ignored when specifying an encoding.

On many platforms, including Windows, `iconvlist` provides an alphabetical list of the supported encodings. On others, the information is on the man page for `iconv(5)` or elsewhere in the man pages (but beware that the system command `iconv` may not support the same set of encodings as the C functions R calls). Unfortunately, the names are rarely common across platforms.

Elements of `x` which cannot be converted (perhaps because they are invalid or because they cannot be represented in the target encoding) will be returned as NA unless `sub` is specified.

Most versions of `iconv` will allow transliteration by appending `'//TRANSLIT'` to the `to` encoding: see the examples.

Encoding "ASCII" is also accepted, but prior to R 2.10.0 conversion to "ASCII" on Windows might have involved dropping accents.

Any encoding bits (see [Encoding](#)) on elements of `x` are ignored: they will always be translated as if from `from` even if declared otherwise.

"UTF8" will be accepted as meaning the (more correct) "UTF-8".

## Value

A character vector of the same length and the same attributes as `x` (after conversion).

If `mark = TRUE` (the default) the elements of the result have a declared encoding if `from` is "latin1" or "UTF-8", or if `from = ""` and the current locale's encoding is detected as Latin-1 or UTF-8.

## Implementation Details

`iconv` was optional before R 2.10.0, but its absence was deprecated in R 2.5.0.

There are three main implementations of `iconv` in use. `'glibc'` (as used on Linux) contains one. Several platforms supply GNU `'libiconv'`, including Mac OS X and Cygwin. On Windows we use a version of Yukihiro Nakadaira's `'win_iconv'`, which is based on Windows' codepages (but `'libiconv'` can be used by swapping a DLL). All three have `iconvlist`, ignore case in encoding names and support `'//TRANSLIT'` (but with different results, and for `'win_iconv'` currently a 'best fit' strategy is used except for `to = "ASCII"`).

Most commercial Unixes contain an implementation of `iconv` but none we have encountered have supported the encoding names we need: the "R Installation and Administration Manual" recommends installing `'libiconv'` on Solaris and AIX, for example.

There are other implementations, e.g. NetBSD uses one from the Citrus project (which does not support `'//TRANSLIT'`) and there is an older FreeBSD port (`'libiconv'` is usually used there): it has not been reported whether or not these work with R.

## See Also

[localeToCharset](#), [file](#).

## Examples

```
## not all systems have iconvlist
try(utils::head(iconvlist(), n = 50))

## Not run:
## convert from Latin-2 to UTF-8: two of the glibc iconv variants.
iconv(x, "ISO_8859-2", "UTF-8")
iconv(x, "LATIN2", "UTF-8")

## End(Not run)

## Both x below are in latin1 and will only display correctly in a
## locale that can represent and display latin1.
x <- "fa\xe7ile"
```

```

Encoding(x) <- "latin1"
x
charToRaw(xx <- iconv(x, "latin1", "UTF-8"))
xx

iconv(x, "latin1", "ASCII")           # NA
iconv(x, "latin1", "ASCII", "?")     # "fa?ile"
iconv(x, "latin1", "ASCII", "")      # "faile"
iconv(x, "latin1", "ASCII", "byte")  # "fa<e7>ile"

# Extracts from R help files
x <- c("Ekstr\xfbm", "J\xfbreskog", "bi\xfdchen Z\xfdcher")
Encoding(x) <- "latin1"
x
try(iconv(x, "latin1", "ASCII//TRANSLIT")) # platform-dependent
iconv(x, "latin1", "ASCII", sub="byte")

```

---

icuSetCollate                      *Setup Collation by ICU*

---

## Description

Controls the way collation is done by ICU (an optional part of the R build).

## Usage

```
icuSetCollate(...)
```

## Arguments

...                      Named arguments, see ‘Details’.

## Details

Optionally, R can be built to collate character strings by ICU (<http://site.icu-project.org>). For such systems, `icuSetCollate` can be used to tune the way collation is done. On other builds calling this function does nothing, with a warning.

Possible arguments are

**locale:** A character string such as "da\_DK" giving the country whose collation rules are to be used. If present, this should be the first argument.

**case\_first:** "upper", "lower" or "default", asking for upper- or lower-case characters to be sorted first. The default is usually lower-case first, but not in all languages (see the Danish example).

**alternate\_handling:** Controls the handling of ‘variable’ characters (mainly punctuation and symbols). Possible values are "non\_ignorable" (primary strength) and "shifted" (quaternary strength).

**strength:** Which components should be used? Possible values "primary", "secondary", "tertiary" (default), "quaternary" and "identical".

**french\_collation:** In a French locale the way accents affect collation is from right to left, whereas in most other locales it is from left to right. Possible values "on", "off" and "default".

**normalization:** Should strings be normalized? Possible values "on" and "off" (default). This affects the collation of composite characters.

**case\_level:** An additional level between secondary and tertiary, used to distinguish large and small Japanese Kana characters. Possible values "on" and "off" (default).

**hiragana\_quaternary:** Possible values "on" (sort Hiragana first at quaternary level) and "off".

Only the first three are likely to be of interest except to those with a detailed understanding of collation and specialized requirements.

Some examples are `case_level="on"`, `strength="primary"` to ignore accent differences and `alternate_handling="shifted"` to ignore space and punctuation characters.

Note that these settings have no effect if collation is set to the C locale, unless `locale` is specified.

### Note

As from R 2.9.0, ICU is used by default wherever it is available: this include Mac OS >= 10.4 and many Linux installations.

### See Also

[Comparison, sort](#)

The ICU user guide chapter on collation (<http://userguide.icu-project.org/collation>).

### Examples

```
## these examples depend on having ICU available, and on the locale
x <- c("Aarhus", "aarhus", "safe", "test", "Zoo")
sort(x)
icuSetCollate(case_first="upper"); sort(x)
icuSetCollate(case_first="lower"); sort(x)

icuSetCollate(locale="da_DK", case_first="default"); sort(x)
icuSetCollate(locale="et_EE"); sort(x)
```

---

identical

*Test Objects for Exact Equality*

---

### Description

The safe and reliable way to test two objects for being *exactly* equal. It returns TRUE in this case, FALSE in every other case.

### Usage

```
identical(x, y, num.eq = TRUE, single.NA = TRUE, attrib.as.set = TRUE)
```

**Arguments**

<code>x, y</code>	any R objects.
<code>num.eq</code>	logical indicating if ( <code>double</code> and <code>complex</code> non-NA) numbers should be compared using <code>==</code> ('equal'), or by bitwise comparison. The latter (non-default) differentiates between <code>-0</code> and <code>+0</code> .
<code>single.NA</code>	logical indicating if there is conceptually just one numeric NA and one NaN; <code>single.NA = FALSE</code> differentiates bit patterns.
<code>attrib.as.set</code>	logical indicating if <code>attributes</code> of <code>x</code> and <code>y</code> should be treated as <i>unordered</i> tagged pairlists ("sets"); this currently also applies to <code>slots</code> of S4 objects. It may well be too strict to set <code>attrib.as.set = FALSE</code> .

**Details**

A call to `identical` is the way to test exact equality in `if` and `while` statements, as well as in logical expressions that use `&&` or `||`. In all these applications you need to be assured of getting a single logical value.

Users often use the comparison operators, such as `==` or `!=`, in these situations. It looks natural, but it is not what these operators are designed to do in R. They return an object like the arguments. If you expected `x` and `y` to be of length 1, but it happened that one of them wasn't, you will *not* get a single `FALSE`. Similarly, if one of the arguments is NA, the result is also NA. In either case, the expression `if(x == y) ...` won't work as expected.

The function `all.equal` is also sometimes used to test equality this way, but was intended for something different: it allows for small differences in numeric results.

The computations in `identical` are also reliable and usually fast. There should never be an error. The only known way to kill `identical` is by having an invalid pointer at the C level, generating a memory fault. It will usually find inequality quickly. Checking equality for two large, complicated objects can take longer if the objects are identical or nearly so, but represent completely independent copies. For most applications, however, the computational cost should be negligible.

If `single.NA` is true, as by default, `identical` sees NaN as different from `NA_real_`, but all NaNs are equal (and all NA of the same type are equal).

Character strings are regarded as identical if they are in different marked encodings but would agree when translated to UTF-8.

If `attrib.as.set` is true, as by default, comparison of attributes view them as a set (and not a vector, so order is not tested).

Note that `identical(x, y, FALSE, FALSE, FALSE)` pickily tests for very exact equality.

**Value**

A single logical value, `TRUE` or `FALSE`, never NA and never anything other than a single value.

**Author(s)**

John Chambers and R Core

**References**

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

**See Also**

[all.equal](#) for descriptions of how two objects differ; [Comparison](#) for operators that generate elementwise comparisons. `isTRUE` is a simple wrapper based on `identical`.

**Examples**

```
identical(1, NULL) ## FALSE -- don't try this with ==
identical(1, 1.)  ## TRUE in R (both are stored as doubles)
identical(1, as.integer(1)) ## FALSE, stored as different types

x <- 1.0; y <- 0.999999999999
## how to test for object equality allowing for numeric fuzz :
(E <- all.equal(x,y))
isTRUE(E) # which is simply defined to just use
identical(TRUE, E)
## If all.equal thinks the objects are different, it returns a
## character string, and the above expression evaluates to FALSE

## even for unusual R objects :
identical(.GlobalEnv, environment())

### ----- Pickyness Flags : -----

## the infamous example:
identical(0., -0.) # TRUE, i.e. not differentiated
identical(0., -0., num.eq = FALSE)
## similar:
identical(NaN, -NaN) # TRUE
identical(NaN, -NaN, single.NA=FALSE) # differ on bit-level
```

---

identity

*Identity Function*

---

**Description**

A trivial identity function returning its argument.

**Usage**

```
identity(x)
```

**Arguments**

`x` an R object.

**Description**

`ifelse` returns a value with the same shape as `test` which is filled with elements selected from either `yes` or `no` depending on whether the element of `test` is TRUE or FALSE.

**Usage**

```
ifelse(test, yes, no)
```

**Arguments**

<code>test</code>	an object which can be coerced to logical mode.
<code>yes</code>	return values for true elements of <code>test</code> .
<code>no</code>	return values for false elements of <code>test</code> .

**Details**

If `yes` or `no` are too short, their elements are recycled. `yes` will be evaluated if and only if any element of `test` is true, and analogously for `no`.

Missing values in `test` give missing values in the result.

**Value**

A vector of the same length and attributes (including dimensions and "class") as `test` and data values from the values of `yes` or `no`. The mode of the answer will be coerced from logical to accommodate first any values taken from `yes` and then any values taken from `no`.

**Warning**

The mode of the result may depend on the value of `test` (see the examples), and the class attribute (see `oldClass`) of the result is taken from `test` and may be inappropriate for the values selected from `yes` and `no`.

Sometimes it is better to use a construction such as `(tmp <- yes; tmp[!test] <- no[!test]; tmp)`, possibly extended to handle missing values in `test`.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[if](#).



**Examples**

```
x <- c(6:-4)
sqrt(x) #- gives warning
sqrt(iffelse(x >= 0, x, NA)) # no warning

## Note: the following also gives the warning !
iffelse(x >= 0, sqrt(x), NA)

## example of different return modes:
yes <- 1:3
no <- pi^(0:3)
typeof(iffelse(NA, yes, no)) # logical
typeof(iffelse(TRUE, yes, no)) # integer
typeof(iffelse(FALSE, yes, no)) # double
```

integer

*Integer Vectors***Description**

Creates or tests for objects of type "integer".

**Usage**

```
integer(length = 0)
as.integer(x, ...)
is.integer(x)
```

**Arguments**

length	desired length.
x	object to be coerced or tested.
...	further arguments passed to or from other methods.

**Details**

Integer vectors exist so that data can be passed to C or Fortran code which expects them, and so that (small) integer data can be represented exactly and compactly.

Note that current implementations of R use 32-bit integers for integer vectors, so the range of representable integers is restricted to about  $\pm 2 \times 10^9$ : `doubles` can hold much larger integers exactly.

**Value**

`integer` creates a integer vector of the specified length. Each element of the vector is equal to 0. `as.integer` attempts to coerce its argument to be of integer type. The answer will be `NA` unless the coercion succeeds. Real values larger in modulus than the largest integer are coerced to `NA` (unlike S which gives the most extreme integer of the same sign). Non-integral numeric values are truncated towards zero (i.e., `as.integer(x)` equals `trunc(x)` there), and imaginary parts of complex numbers are discarded (with a warning). Character strings containing optional whitespace followed by either a decimal representation or a hexadecimal representation (starting with `0x` or

0X) can be converted, as well as any allowed by the platform for real numbers. Like `as.vector` it strips attributes including names. (To ensure that an object `x` is of integer type without stripping attributes, use `storage.mode(x) <- "integer"`.)

`is.integer` returns TRUE or FALSE depending on whether its argument is of integer type or not, unless it is a factor when it returns FALSE.

### Note

`is.integer(x)` does **not** test if `x` contains integer numbers! For that, use `round`, as in the function `is.wholenumber(x)` in the examples.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

`numeric`, `storage.mode`.

`round` (and `ceiling` and `floor` on that help page) to convert to integral values.

### Examples

```
## as.integer() truncates:
x <- pi * c(-1:1,10)
as.integer(x)

is.integer(1) # is FALSE !

is.wholenumber <-
  function(x, tol = .Machine$double.eps^0.5) abs(x - round(x)) < tol
is.wholenumber(1) # is TRUE
(x <- seq(1,5, by=0.5) )
is.wholenumber( x ) #--> TRUE FALSE TRUE ...
```

---

interaction

*Compute Factor Interactions*

---

### Description

`interaction` computes a factor which represents the interaction of the given factors. The result of `interaction` is always unordered.

### Usage

```
interaction(..., drop = FALSE, sep = ".", lex.order = FALSE)
```

**Arguments**

<code>...</code>	the factors for which interaction is to be computed, or a single list giving those factors.
<code>drop</code>	if <code>drop</code> is <code>TRUE</code> , unused factor levels are dropped from the result. The default is to retain all factor levels.
<code>sep</code>	string to construct the new level labels by joining the constituent ones.
<code>lex.order</code>	logical indicating if the order of factor concatenation should be lexically ordered.

**Value**

A factor which represents the interaction of the given factors. The levels are labelled as the levels of the individual factors joined by `sep` which is `.` by default.

By default, when `lex.order = FALSE`, the levels are ordered so the level of the first factor varies fastest, then the second and so on. This is the reverse of lexicographic ordering (which you can get by `lex.order = TRUE`), and differs from `:.`  (It is done this way for compatibility with S.)

**References**

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

**See Also**

`factor`; `:` where `f:g` is similar to `interaction(f, g, sep=":")` when `f` and `g` are factors.

**Examples**

```
a <- gl(2, 4, 8)
b <- gl(2, 2, 8, labels = c("ctrl", "treat"))
s <- gl(2, 1, 8, labels = c("M", "F"))
interaction(a, b)
interaction(a, b, s, sep = ":")
stopifnot(identical(a:s,
                    interaction(a, s, sep = ":", lex.order = TRUE)),
          identical(a:s:b,
                    interaction(a, s, b, sep = ":", lex.order = TRUE)))
```

---

interactive

*Is R Running Interactively?*

---

**Description**

Return `TRUE` when `R` is being used interactively and `FALSE` otherwise.

**Usage**

```
interactive()
```

## Details

An interactive R session is one in which it is assumed that there is a human operator to interact with, so for example R can prompt for corrections to incorrect input or ask what to do next or if it is OK to move to the next plot.

GUI consoles will arrange to start R in an interactive session. When R is run in a terminal (via `Rterm.exe` on Windows), it assumes that it is interactive if `'stdin'` is connected to a (pseudo-)terminal and not if `'stdin'` is redirected to a file or pipe. Command-line options `'--interactive'` (Unix) and `'--ess'` (Windows, `Rterm.exe`) override the default assumption. (On a Unix-alike, whether the `readline` command-line editor is used is **not** overridden by `'--interactive'`.)

Embedded uses of R can set a session to be interactive or not.

Internally, whether a session is interactive determines

- how some errors are handled and reported, e.g. see [stop](#) and [options\("showWarnCalls"\)](#).
- whether one of `'--save'`, `'--no-save'` or `'--vanilla'` is required, and if R ever asks whether to save the workspace.
- the choice of default graphics device launched when needed and by [dev.new](#): see [options\("device"\)](#)
- whether graphics devices ever ask for confirmation of a new page.

In addition, R's own R code makes use of `interactive()`: for example [help](#), [debugger](#) and [install.packages](#) do.

## Note

This is a [primitive](#) function.

## See Also

[source](#), [.First](#)

## Examples

```
.First <- function() if(interactive()) x11()
```

---

Internal

*Call an Internal Function*

---

## Description

`.Internal` performs a call to an internal code which is built in to the R interpreter.

Only true R wizards should even consider using this function, and only R developers can add to the list of internal functions.

## Usage

```
.Internal(call)
```

**Arguments**

`call`            a call expression

**See Also**

`.Primitive`, `.External` (the nearest equivalent available to users).

---

InternalMethods      *Internal Generic Functions*

---

**Description**

Many R-internal functions are *generic* and allow methods to be written for.

**Details**

The following primitive and internal functions are *generic*, i.e., you can write `methods` for them:

`[`, `[[`, `$`, `[<-`, `[[<-`, `$<-`,  
`length`, `length<-`, `dimnames`, `dimnames<-`, `dim`, `dim<-`, `names`, `names<-`,  
`levels<-`,  
`c`, `unlist`, `cbind`, `rbind`,  
`as.character`, `as.complex`, `as.double`, `as.integer`, `as.logical`, `as.raw`,  
`as.vector`, `is.array`, `is.matrix`, `is.na`, `is.nan`, `is.numeric`, `rep`, `seq.int`  
(which dispatches methods for "seq") and `xtfrm`

In addition, `is.name` is a synonym for `is.symbol` and dispatches methods for the latter.

Note that all of the `group generic` functions are also internal/primitive and allow methods to be written for them.

`.S3PrimitiveGenerics` is a character vector listing the primitives which are internal generic and not `group generic`. Currently `as.vector`, `cbind`, `rbind` and `unlist` are the internal non-primitive functions which are internally generic.

For efficiency, internal dispatch only occurs on *objects*, that is those for which `is.object` returns true.

**See Also**

`methods` for the methods which are available.

---

`invisible`*Change the Print Mode to Invisible*

---

**Description**

Return a (temporarily) invisible copy of an object.

**Usage**

```
invisible(x)
```

**Arguments**

`x` an arbitrary R object.

**Details**

This function can be useful when it is desired to have functions return values which can be assigned, but which do not print when they are not assigned.

This is a [primitive](#) function.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[withVisible](#), [return](#), [function](#).

**Examples**

```
# These functions both return their argument
f1 <- function(x) x
f2 <- function(x) invisible(x)
f1(1) # prints
f2(1) # does not
```

---

`is.finite`*Finite, Infinite and NaN Numbers*

---

**Description**

`is.finite` and `is.infinite` return a vector of the same length as `x`, indicating which elements are finite (not infinite and not missing) or infinite.

`Inf` and `-Inf` are positive and negative infinity whereas `NaN` means 'Not a Number'. (These apply to numeric values and real and imaginary parts of complex values but not to values of integer vectors.) `Inf` and `NaN` are [reserved](#) words in the R language.

**Usage**

```
is.finite(x)
is.infinite(x)
Inf
NaN
is.nan(x)
```

**Arguments**

`x` R object to be tested: the default methods handle atomic vectors, lists and pairlists.

**Details**

`is.finite` returns a vector of the same length as `x` the `j`th element of which is `TRUE` if `x[j]` is finite (i.e., it is not one of the values `NA`, `NaN`, `Inf` or `-Inf`) and `FALSE` otherwise. All elements of types other than logical, integer, numeric and complex vectors are false. Complex numbers are finite if both the real and imaginary parts are.

`is.infinite` returns a vector of the same length as `x` the `j`th element of which is `TRUE` if `x[j]` is infinite (i.e., equal to one of `Inf` or `-Inf`) and `FALSE` otherwise. This will be false unless `x` is numeric or complex. Complex numbers are infinite if either the real or the imaginary part is.

`is.nan` tests if a numeric value is `NaN`. Do not test equality to `NaN`, or even use `identical`, since systems typically have many different `NaN` values. One of these is used for the numeric missing value `NA`, and `is.nan` is false for that value. A complex number is regarded as `NaN` if either the real or imaginary part is `NaN` but not `NA`. All elements of logical, integer and raw vectors are considered not to be `NaN`, and elements of lists and pairlists are also unless the element is a length-one numeric or complex vector whose single element is `NaN`.

All three functions are generic: you can write methods to handle specific classes of objects, see [InternalMethods](#). The default methods handle atomic vectors.

**Value**

A logical vector of the same length as `x`: `dim`, `dimnames` and `names` attributes are preserved.

**Note**

In R, basically all mathematical functions (including basic [Arithmetic](#)), are supposed to work properly with `+/- Inf` and `NaN` as input or output.

The basic rule should be that calls and relations with `Infs` really are statements with a proper mathematical *limit*.

**References**

The IEC 60559 standard, also known as the ANSI/IEEE 754 Floating-Point Standard.

D. Goldberg (1991) *What Every Computer Scientist Should Know about Floating-Point Arithmetic* ACM Computing Surveys, **23**(1).

Postscript version available at <http://www.validlab.com/goldberg/paper.ps> Extended PDF version at <http://www.validlab.com/goldberg/paper.pdf>

<http://grouper.ieee.org/groups/754/> for accessible information.

The C99 function `isfinite` is used for `is.finite` if available.

**See Also**

`NA`, ‘*Not Available*’ which is not a number as well, however usually used for missing values and applies to many modes, not just numeric.

**Examples**

```
pi / 0 ## = Inf a non-zero number divided by zero creates infinity
0 / 0 ## = NaN

1/0 + 1/0# Inf
1/0 - 1/0# NaN

stopifnot(
  1/0 == Inf,
  1/Inf == 0
)
sin(Inf)
cos(Inf)
tan(Inf)
```

---

is.function

*Is an Object of Type (Primitive) Function?*


---

**Description**

Checks whether its argument is a (primitive) function.

**Usage**

```
is.function(x)
is.primitive(x)
```

**Arguments**

`x` an R object.

**Details**

`is.primitive(x)` tests if `x` is a primitive function (either a "builtin" or "special" as described for `typeof`)? It is a [primitive](#) function.

**Value**

TRUE if `x` is a (primitive) function, and FALSE otherwise.

**Examples**

```
is.function(1) # FALSE
is.function(is.primitive) # TRUE: it is a function, but ..
is.primitive(is.primitive) # FALSE:it's not a primitive one, whereas
is.primitive(is.function) # TRUE: that one *is*
```



---

`is.language`*Is an Object a Language Object?*

---

**Description**

`is.language` returns TRUE if `x` is a variable [name](#), a [call](#), or an [expression](#).

**Usage**

```
is.language(x)
```

**Arguments**

`x` object to be tested.

**Note**

This is a [primitive](#) function.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**Examples**

```
ll <- list(a = expression(x^2 - 2*x + 1), b = as.name("Jim"),
          c = as.expression(exp(1)), d = call("sin", pi))
sapply(ll, typeof)
sapply(ll, mode)
stopifnot(sapply(ll, is.language))
```

---

`is.object`*Is an Object "internally classed"?*

---

**Description**

A function rather for internal use. It returns TRUE if the object `x` has the R internal OBJECT bit set, and FALSE otherwise. The OBJECT bit is set when a "class" attribute is added and removed when that attribute is removed, so this is a very efficient way to check if an object has a class attribute. (S4 objects always should.)

**Usage**

```
is.object(x)
```

**Arguments**

`x` object to be tested.

**Note**

This is a [primitive](#) function.

**See Also**

[class](#), and [methods](#).

[isS4](#).

**Examples**

```
is.object(1) # FALSE
is.object(as.factor(1:3)) # TRUE
```

---

is.R

*Are we using R, rather than S?*

---

**Description**

Test if running under R.

**Usage**

```
is.R()
```

**Details**

The function has been written such as to correctly run in all versions of R, S and S-PLUS. In order for code to be runnable in both R and S dialects previous to S-PLUS 8.0, your code must either define `is.R` or use it as

```
if (exists("is.R") && is.function(is.R) && is.R()) {
  ## R-specific code
} else {
  ## S-version of code
}
```

**Value**

`is.R` returns TRUE if we are using R and FALSE otherwise.

**See Also**

[R.version](#), [system](#).

**Examples**

```
x <- stats::runif(20); small <- x < 0.4
## In the early years of R, 'which()' only existed in R:
if(is.R()) which(small) else seq(along=small)[small]
```

---

is.recursive

*Is an Object Atomic or Recursive?*


---

### Description

is.atomic returns TRUE if x is an atomic vector (or NULL) and FALSE otherwise.

is.recursive returns TRUE if x has a recursive (list-like) structure and FALSE otherwise.

### Usage

```
is.atomic(x)
is.recursive(x)
```

### Arguments

x                    object to be tested.

### Details

is.atomic is true for the atomic vector types ("logical", "integer", "numeric", "complex", "character" and "raw") and NULL.

Most types of objects are regarded as recursive, except for atomic vector types, NULL and symbols (as given by [as.name](#)).

These are [primitive](#) functions.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[is.list](#), [is.language](#), etc, and the demo ("is.things").

### Examples

```
require(stats)

is.a.r <- function(x) c(is.atomic(x), is.recursive(x))

is.a.r(c(a=1,b=3))            # TRUE FALSE
is.a.r(list())                # FALSE TRUE - a list is a list
is.a.r(list(2))              # FALSE TRUE
is.a.r(lm)                    # FALSE TRUE
is.a.r(y ~ x)                # FALSE TRUE
is.a.r(expression(x+1))     # FALSE TRUE (nowadays)
```

---

`is.single`*Is an Object of Single Precision Type?*

---

**Description**

`is.single` reports an error. There are no single precision values in R.

**Usage**

```
is.single(x)
```

**Arguments**

`x` object to be tested.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

---

`is.unsorted`*Test if an Object is Not Sorted*

---

**Description**

Test if an object is not sorted, without the cost of sorting it.

**Usage**

```
is.unsorted(x, na.rm = FALSE, strictly = FALSE)
```

**Arguments**

`x` an R object with a class or a numeric, complex, character or logical vector.  
`na.rm` logical. Should missing values be removed before checking?  
`strictly` logical indicating if the check should be for *strictly* increasing values.

**Value**

A length-one logical value. All objects of length 0 or 1 are sorted: the result will be `NA` for objects of length 2 or more except for atomic vectors and objects with a class (where the `>=` or `>` method is used).

**See Also**

[sort](#), [order](#).

---

 ISOdatetime

*Date-time Conversion Functions from Numeric Representations*


---

**Description**

Convenience wrappers to create Date-times from numeric representations.

**Usage**

```
ISOdatetime(year, month, day, hour, min, sec, tz = "")
ISOdate(year, month, day, hour = 12, min = 0, sec = 0, tz = "GMT")
```

**Arguments**

`year, month, day`  
numerical values to specify a day.

`hour, min, sec`  
numerical values for a time within a day. Fractional seconds are allowed.

`tz`  
A [timezone](#) specification to be used for the conversion. "" is the current time zone and "GMT" is UTC.

**Details**

ISOdatetime and ISOdate are convenience wrappers for `strptime` that differ only in their defaults and that ISOdate sets UTC as the timezone. For dates without times it would normally be better to use the `"Date"` class.

**Value**

An object of class `"POSIXct"`.

**See Also**

[DateTimeClasses](#) for details of the date-time classes; [strptime](#) for conversions from character strings.

---

 isS4

*Test for an S4 object*


---

**Description**

Tests whether the object is an instance of an S4 class.

**Usage**

```
isS4(object)

asS4(object, flag = TRUE, complete = TRUE)
```

**Arguments**

object	Any R object.
flag	A single logical value; not NA, whether to turn the S4 object flag on or off.
complete	How to complete the transformation to/from S4. Only currently used when flag is FALSE. If 1, the object must convert to a valid S3 object, or an error results. If 2, a non-valid S3 object is left alone, silently. If 0, no conversion is made other than setting the internal bit (used internally but not recommended, since it can result in an invalid object).

**Details**

Note that `isS4` does not rely on the **methods** package, so in particular it can be used to detect the need to `require` that package. (But `asS4` does depend on **methods**.)

When `asS4` is called with `flag == FALSE`, the value of `complete` controls whether an attempt is made to transform `object` into a valid object of the implied S3 class. If so, then an object from an S4 class extending an S3 class will be transformed into an S3 object with the corresponding S3 class (see [S3Part](#)). This includes classes extending the pseudo-classes `array` and `matrix`: such objects will have their class attribute set to `NULL`.

**Value**

`isS4` always returns `TRUE` or `FALSE` according to whether the internal flag marking an S4 object has been turned on for this object.

`asS4` will turn this flag on or off, according to argument `flag`, and in the latter case `complete` the conversion as described under argument `complete`. Note that with `flag FALSE`, an S4 object will *not* but turned into an S3 object unless there is a valid conversion; that is, an object of type other than "S4" for which the S4 object is an extension, unless argument `complete` is 0.

**See Also**

`is.object` for a more general test; [Methods](#) for general information on S4.

**Examples**

```
isS4(pi) # FALSE
isS4(getClass("MethodDefinition")) # TRUE
```

---

`isSymmetric`                      *Test if a Matrix or other Object is Symmetric*

---

**Description**

Generic function to test if `object` is symmetric or not. Currently only a matrix method is implemented.

**Usage**

```
isSymmetric(object, ...)
## S3 method for class 'matrix':
isSymmetric(object, tol = 100 * .Machine$double.eps, ...)
```

**Arguments**

object	any R object; a <code>matrix</code> for the matrix method.
tol	numeric scalar $\geq 0$ . Smaller differences are not considered, see <code>all.equal.numeric</code> .
...	further arguments passed to methods; the matrix method passes these to <code>all.equal</code> .

**Details**

The `matrix` method is used inside `eigen` by default to test symmetry of matrices *up to rounding error*, using `all.equal`. It might not be appropriate in all situations.

Note that a matrix is only symmetric if its `rownames` and `colnames` are identical.

**Value**

logical indicating if `object` is symmetric or not.

**See Also**

`eigen` which calls `isSymmetric` when its `symmetric` argument is missing.

**Examples**

```
isSymmetric(D3 <- diag(3)) # -> TRUE

D3[2,1] <- 1e-100
D3
isSymmetric(D3) # TRUE
isSymmetric(D3, tol = 0) # FALSE for zero-tolerance
```

---

jitter

*'Jitter' (Add Noise) to Numbers*


---

**Description**

Add a small amount of noise to a numeric vector.

**Usage**

```
jitter(x, factor=1, amount = NULL)
```

**Arguments**

x	numeric vector to which <i>jitter</i> should be added.
factor	numeric
amount	numeric; if positive, used as <i>amount</i> (see below), otherwise, if = 0 the default is <code>factor * z/50</code> . Default (NULL): <code>factor * d/5</code> where <code>d</code> is about the smallest difference between <code>x</code> values.

**Details**

The result, say `r`, is `r <- x + runif(n, -a, a)` where `n <- length(x)` and `a` is the `amount` argument (if specified).

Let `z <- max(x) - min(x)` (assuming the usual case). The amount `a` to be added is either provided as *positive* argument `amount` or otherwise computed from `z`, as follows:

If `amount == 0`, we set `a <- factor * z/50` (same as `S`).

If `amount` is `NULL` (*default*), we set `a <- factor * d/5` where `d` is the smallest difference between adjacent unique (apart from fuzz) `x` values.

**Value**

`jitter(x, ...)` returns a numeric of the same length as `x`, but with an amount of noise added in order to break ties.

**Author(s)**

Werner Stahel and Martin Maechler, ETH Zurich

**References**

Chambers, J. M., Cleveland, W. S., Kleiner, B. and Tukey, P.A. (1983) *Graphical Methods for Data Analysis*. Wadsworth; figures 2.8, 4.22, 5.4.

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

**See Also**

[rug](#) which you may want to combine with `jitter`.

**Examples**

```
round(jitter(c(rep(1,3), rep(1.2, 4), rep(3,3))), 3)
## These two 'fail' with S-plus 3.x:
jitter(rep(0, 7))
jitter(rep(10000,5))
```

---

kappa

---

*Compute or Estimate the Condition Number of a Matrix*


---

**Description**

The condition number of a regular (square) matrix is the product of the *norm* of the matrix and the norm of its inverse (or pseudo-inverse), and hence depends on the kind of matrix-norm.

`kappa()` computes by default (an estimate of) the 2-norm condition number of a matrix or of the *R* matrix of a *QR* decomposition, perhaps of a linear fit. The 2-norm condition number can be shown to be the ratio of the largest to the smallest *non-zero* singular value of the matrix.

`rcond()` computes an approximation of the reciprocal **condition** number, see the details.



**Usage**

```

kappa(z, ...)
## Default S3 method:
kappa(z, exact = FALSE,
      norm = NULL, method = c("qr", "direct"), ...)
## S3 method for class 'lm':
kappa(z, ...)
## S3 method for class 'qr':
kappa(z, ...)

kappa.tri(z, exact = FALSE, LINPACK = TRUE, norm=NULL, ...)

rcond(x, norm = c("O", "I", "1"), triangular = FALSE, ...)

```

**Arguments**

<code>z, x</code>	A matrix or a the result of <code>qr</code> or a fit from a class inheriting from "lm".
<code>exact</code>	logical. Should the result be exact?
<code>norm</code>	character string, specifying the matrix norm with respect to which the condition number is to be computed, see also <code>norm</code> . For <code>rcond</code> , the default is "O", meaning the <b>One-</b> or 1-norm. The (currently only) other possible value is "I" for the infinity norm.
<code>method</code>	character string, specifying the method to be used; "qr" is default for back-compatibility, mainly.
<code>triangular</code>	logical. If true, the matrix used is just the lower triangular part of <code>z</code> .
<code>LINPACK</code>	logical. If true and <code>z</code> is not complex, the Linpack routine <code>dtrco()</code> is called; otherwise the relevant Lapack routine is.
<code>...</code>	further arguments passed to or from other methods; for <code>kappa.*()</code> , notably <code>LINPACK</code> when <code>norm</code> is not "2".

**Details**

For `kappa()`, if `exact = FALSE` (the default) the 2-norm condition number is estimated by a cheap approximation. Following `S`, by default, this uses the LINPACK routine `dtrco()`. However, in `R` (or `S`) the exact calculation (via `svd`) is also likely to be quick enough.

Note that the 1- and Inf-norm condition numbers are much faster to calculate, and `rcond()` computes these *reciprocal* condition numbers, also for complex matrices, using standard Lapack routines.

`kappa` and `rcond` are different interfaces to *partly* identical functionality.

`kappa.tri` is an internal function called by `kappa.qr`.

**Value**

The condition number, *kappa*, or an approximation if `exact = FALSE`.

**Author(s)**

The design was inspired by (but differs considerably from) the `S` function of the same name described in Chambers (1992).

## References

Chambers, J. M. (1992) *Linear models*. Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

## See Also

`norm`; `svd` for the singular value decomposition and `qr` for the *QR* one.

## Examples

```
kappa(x1 <- cbind(1,1:10))# 15.71
kappa(x1, exact = TRUE)      # 13.68
kappa(x2 <- cbind(x1,2:11))# high! [x2 is singular!]

hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, "+") }
sv9 <- svd(h9 <- hilbert(9))$ d
kappa(h9)# pretty high!
kappa(h9, exact = TRUE) == max(sv9) / min(sv9)
kappa(h9, exact = TRUE) / kappa(h9) # .677 (i.e., rel.error = 32%)
```

---

kronecker

*Kronecker Products on Arrays*


---

## Description

Computes the generalised kronecker product of two arrays, *X* and *Y*. `kronecker(X, Y)` returns an array *A* with dimensions  $\text{dim}(X) * \text{dim}(Y)$ .

## Usage

```
kronecker(X, Y, FUN = "*", make.dimnames = FALSE, ...)
```

`X %x% Y`

## Arguments

<code>X</code>	A vector or array.
<code>Y</code>	A vector or array.
<code>FUN</code>	a function; it may be a quoted string.
<code>make.dimnames</code>	Provide dimnames that are the product of the dimnames of <i>X</i> and <i>Y</i> .
<code>...</code>	optional arguments to be passed to <code>FUN</code> .

## Details

If *X* and *Y* do not have the same number of dimensions, the smaller array is padded with dimensions of size one. The returned array comprises submatrices constructed by taking *X* one term at a time and expanding that term as `FUN(x, Y, ...)`.

`%x%` is an alias for `kronecker` (where `FUN` is hardwired to `"*"`).

**Author(s)**

Jonathan Rougier, <J.C.Rougier@durham.ac.uk>

**References**

Shayle R. Searle (1982) *Matrix Algebra Useful for Statistics*. John Wiley and Sons.

**See Also**

[outer](#), on which `kron` is built and `%*%` for usual matrix multiplication.

**Examples**

```
# simple scalar multiplication
( M <- matrix(1:6, ncol=2) )
kron(4, M)
# Block diagonal matrix:
kron(diag(1, 3), M)

# ask for dimnames

fred <- matrix(1:12, 3, 4, dimnames=list(LETTERS[1:3], LETTERS[4:7]))
bill <- c("happy" = 100, "sad" = 1000)
kron(fred, bill, make.dimnames = TRUE)

bill <- outer(bill, c("cat"=3, "dog"=4))
kron(fred, bill, make.dimnames = TRUE)
```

---

l10n\_info

*Localization Information*


---

**Description**

Report on localization information.

**Usage**

```
l10n_info()
```

**Value**

A list with three logical components:

MBCS	If a multi-byte character set in use?
UTF-8	Is this a UTF-8 locale?
Latin-1	Is this a Latin-1 locale?

**See Also**

[Sys.getlocale](#), [localeconv](#)

**Examples**

```
l10n_info()
```

---

labels	<i>Find Labels from Object</i>
--------	--------------------------------

---

**Description**

Find a suitable set of labels from an object for use in printing or plotting, for example. A generic function.

**Usage**

```
labels(object, ...)
```

**Arguments**

object	Any R object: the function is generic.
...	further arguments passed to or from other methods.

**Value**

A character vector or list of such vectors. For a vector the results is the names or `seq_along(x)` and for a data frame or array it is the `dimnames` (with `NULL` expanded to `seq_len(d[i])`).

**References**

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

---

lapply	<i>Apply a Function over a List or Vector</i>
--------	---

---

**Description**

`lapply` returns a list of the same length as `X`, each element of which is the result of applying `FUN` to the corresponding element of `X`.

`sapply` is a user-friendly version of `lapply` by default returning a vector or matrix if appropriate.

`vapply` is similar to `sapply`, but has a pre-specified type of return value, so it can be safer (and sometimes faster) to use.

`replicate` is a wrapper for the common use of `sapply` for repeated evaluation of an expression (which will usually involve random number generation).

**Usage**

```
lapply(X, FUN, ...)
```

```
sapply(X, FUN, ..., simplify = TRUE, USE.NAMES = TRUE)
```

```
vapply(X, FUN, FUN.VALUE, ..., USE.NAMES = TRUE)
```

```
replicate(n, expr, simplify = TRUE)
```

**Arguments**

X	a vector (atomic or list) or an expressions vector. Other objects (including classed objects) will be coerced by <code>as.list</code> .
FUN	the function to be applied to each element of X: see ‘Details’. In the case of functions like <code>+</code> , <code>%*%</code> , etc., the function name must be backquoted or quoted.
...	optional arguments to FUN.
simplify	logical; should the result be simplified to a vector or matrix if possible?
USE.NAMES	logical; if TRUE and if X is character, use X as <code>names</code> for the result unless it had names already.
FUN.VALUE	a vector; a template for the return value from FUN.
n	number of replications.
expr	expression (language object, usually a call) to evaluate repeatedly.

**Details**

FUN is found by a call to `match.fun` and typically is specified as a function or a symbol (e.g. a backquoted name) or a character string specifying a function to be searched for from the environment of the call to `lapply`.

Function FUN must be able to accept as input any of the elements of X. If the latter is an atomic vector, FUN will always be passed a length-one vector of the same type as X.

Simplification in `sapply` is only attempted if X has length greater than zero and if the return values from all elements of X are all of the same (positive) length. If the common length is one the result is a vector, and if greater than one is a matrix with a column corresponding to each element of X.

Simplification is always done in `vapply`. This function checks that all values of FUN are compatible with the FUN.VALUE, in that they must have the same length and type. (Types may be promoted to a higher type within the ordering `logical < integer < real < complex`, but not demoted.)

Users of S4 classes should pass a list to `lapply`: the internal coercion is done by the system `as.list` in the base namespace and not one defined by a user (e.g. by setting S4 methods on the system function).

`lapply` and `vapply` are **primitive** functions.

**Value**

For `lapply` and `sapply(simplify=FALSE)`, a list.

For `sapply(simplify=TRUE)` and `replicate`: if X has length zero or `n = 0`, an empty list. Otherwise an atomic vector or matrix or list of the same length as X (of length `n` for `replicate`). If simplification occurs, the output type is determined from the highest type of the return values in the hierarchy `NULL < raw < logical < integer < real < complex < character < list < expression`, after coercion of pairlists to lists.

`vapply` returns a vector or matrix of type matching the FUN.VALUE. If `length(FUN.VALUE) != 1` a matrix will be returned with `length(FUN.VALUE)` rows and `length(X)` columns, otherwise a vector of the same length as X. Names of rows in the matrix value are taken from the FUN.VALUE if it is named, otherwise from the result of the first function call. Column names of the matrix value or names of the vector value are set from X as in `sapply`.

**Note**

`sapply(*, simplify = FALSE, USE.NAMES = FALSE)` is equivalent to `lapply(*)`.

For historical reasons, the calls created by `lapply` are unevaluated, and code has been written (e.g. `bquote`) that relies on this. This means that the recorded call is always of the form `FUN(X[[0L]], ...)`, with `0L` replaced by the current integer index. This is not normally a problem, but it can be if `FUN` uses `sys.call` or `match.call` or if it is a primitive function that makes use of the call. This means that it is often safer to call primitive functions with a wrapper, so that e.g. `lapply(l1, function(x) is.numeric(x))` is required in R 2.7.1 to ensure that method dispatch for `is.numeric` occurs correctly.

If `expr` is a function call, be aware of assumptions about where it is evaluated, and in particular what `...` might refer to. You can pass additional named arguments to a function call as additional named arguments to `replicate`: see ‘Examples’.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`apply`, `tapply`, `mapply` for applying a function to multiple arguments, and `rapply` for a recursive version of `lapply()`, `eapply` for applying a function to each entry in an environment.

**Examples**

```
require(stats); require(graphics)

x <- list(a = 1:10, beta = exp(-3:3), logic = c(TRUE,FALSE,FALSE,TRUE))
# compute the list mean for each list element
lapply(x,mean)
# median and quartiles for each list element
lapply(x, quantile, probs = 1:3/4)
sapply(x, quantile)
i39 <- sapply(3:9, seq) # list of vectors
sapply(i39, fivenum)
vapply(i39, fivenum, c(Min.=0, "1st Qu."=0, Median=0, "3rd Qu."=0, Max.=0))

hist(replicate(100, mean(arexp(10))))

## use of replicate() with parameters:
foo <- function(x=1, y=2) c(x,y)
# does not work: bar <- function(n, ...) replicate(n, foo(...))
bar <- function(n, x) replicate(n, foo(x=x))
bar(5, x=3)
```

---

<code>Last.value</code>	<i>Value of Last Evaluated Expression</i>
-------------------------	---

---

**Description**

The value of the internal evaluation of a top-level R expression is always assigned to `.Last.value` (in `package:base`) before further processing (e.g., printing).

**Usage**

```
.Last.value
```

**Details**

The value of a top-level assignment *is* put in `.Last.value`, unlike S.

Do not assign to `.Last.value` in the workspace, because this will always mask the object of the same name in `package:base`.

**See Also**

[eval](#)

**Examples**

```
## These will not work correctly from example(),
## but they will in make check or if pasted in,
## as example() does not run them at the top level
gamma(1:15)          # think of some intensive calculation...
fac14 <- .Last.value # keep them

library("splines") # returns invisibly
.Last.value       # shows what library(.) above returned
```

---

<code>length</code>	<i>Length of an Object</i>
---------------------	----------------------------

---

**Description**

Get or set the length of vectors (including lists) and factors, and of any other R object for which a method has been defined.

**Usage**

```
length(x)
length(x) <- value
```

**Arguments**

<code>x</code>	an R object. For replacement, a vector or factor.
<code>value</code>	an integer.

## Details

Both functions are generic: you can write methods to handle specific classes of objects, see [InternalMethods](#). `length<-` has a "factor" method.

The replacement form can be used to reset the length of a vector. If a vector is shortened, extra values are discarded and when a vector is lengthened, it is padded out to its new length with `NA`s (null for raw vectors).

Both are [primitive](#) functions.

## Value

The default method currently returns an [integer](#) of length 1. Since this may change in the future and may differ for other methods, programmers should not rely on it. (Should the length exceed the maximum representable integer, it is returned as `NA`.)

For vectors (including lists) and factors the length is the number of elements. For an environment it is the number of objects in the environment, and `NULL` has length 0. For expressions and pairlists (including language objects and dotlists) it is the length of the pairlist chain. All other objects (including functions) have length one: note that for functions this differs from `S`.

The replacement form removes all the attributes of `x` except its names.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

`nchar` for counting the number of characters in character vectors.

## Examples

```
length(diag(4))# = 16 (4 x 4)
length(options())# 12 or more
length(y ~ x1 + x2 + x3)# 3
length(expression(x, {y <- x^2; y+2}, x^y)) # 3

## from example(warpbreaks)
require(stats)

fm1 <- lm(breaks ~ wool * tension, data = warpbreaks)
length(fm1$call) # 3, lm() and two arguments.
length(formula(fm1)) # 3, ~ lhs rhs
```

---

levels

*Levels Attributes*

---

## Description

`levels` provides access to the levels attribute of a variable. The first form returns the value of the levels of its argument and the second sets the attribute.



**Usage**

```
levels(x)
levels(x) <- value
```

**Arguments**

<code>x</code>	an object, for example a factor.
<code>value</code>	A valid value for <code>levels(x)</code> . For the default method, <code>NULL</code> or a character vector. For the <code>factor</code> method, a vector of character strings with length at least the number of levels of <code>x</code> , or a named list specifying how to rename the levels.

**Details**

Both the extractor and replacement forms are generic and new methods can be written for them. The most important method for the replacement function is that for `factors`.

For the factor replacement method, a `NA` in `value` causes that level to be removed from the levels and the elements formerly with that level to be replaced by `NA`.

Note that for a factor, replacing the levels via `levels(x) <- value` is not the same as (and is preferred to) `attr(x, "levels") <- value`.

The replacement function is [primitive](#).

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[nlevels](#), [relevel](#), [reorder](#).

**Examples**

```
## assign individual levels
x <- gl(2, 4, 8)
levels(x)[1] <- "low"
levels(x)[2] <- "high"
x

## or as a group
y <- gl(2, 4, 8)
levels(y) <- c("low", "high")
y

## combine some levels
z <- gl(3, 2, 12)
levels(z) <- c("A", "B", "A")
z

## same, using a named list
z <- gl(3, 2, 12)
levels(z) <- list(A=c(1,3), B=2)
z
```

```
## we can add levels this way:
f <- factor(c("a","b"))
levels(f) <- c("c", "a", "b")
f

f <- factor(c("a","b"))
levels(f) <- list(C="C", A="a", B="b")
f
```

---

libPaths

*Search Paths for Packages*


---

## Description

`.libPaths` gets/sets the library trees within which packages are looked for.

## Usage

```
.libPaths(new)

.Library
.Library.site
```

## Arguments

`new` a character vector with the locations of R library trees. Tilde expansion (`path.expand`) is done, and if any element contains one of `*?[]`, globbing is done where supported by the platform: see `Sys.glob`.

## Details

`.Library` is a character string giving the location of the default library, the ‘library’ subdirectory of `R_HOME`.

`.Library.site` is a (possibly empty) character vector giving the locations of the site libraries, by default the ‘site-library’ subdirectory of `R_HOME` (which may not exist).

`.libPaths` is used for getting or setting the library trees that R knows about (and hence uses when looking for packages). If called with argument `new`, the library search path is set to the existing directories in `unique(c(new, .Library.site, .Library))` and this is returned. If given no argument, a character vector with the currently active library trees is returned.

The library search path is initialized at startup from the environment variable `R_LIBS` (which should be a colon-separated list of directories at which R library trees are rooted) followed by those in environment variable `R_LIBS_USER`. Only directories which exist at the time will be included.

By default `R_LIBS` is unset, and `R_LIBS_USER` is set to directory ‘`R/R.version$platform-library/x.y`’ of the home directory (or ‘`Library/R/x.y/library`’ for Mac OS X AQUA builds), for R `x.y.z`.

`.Library.site` can be set via the environment variable `R_LIBS_SITE` (as a colon-separated list of library trees).

Both `R_LIBS_USER` and `R_LIBS_SITE` feature possible expansion of specifiers for R version specific information as part of the startup process. The possible conversion specifiers all start with a

'%' and are followed by a single letter (use '%%' to obtain '%'), with currently available conversion specifications as follows:

'%V' R version number including the patchlevel (e.g., '2.5.0').

'%v' R version number excluding the patchlevel (e.g., '2.5').

'%p' the platform for which R was built, the value of `R.version$platform`.

'%o' the underlying operating system, the value of `R.version$os`.

'%a' the architecture (CPU) R was built on/for, the value of `R.version$arch`.

(See `version` for details on R version information.)

Function `.libPaths` always uses the values of `.Library` and `.Library.site` in the base name space. `.Library.site` can be set by the site in '`Rprofile.site`', which should be followed by a call to `.libPaths(.libPaths())` to make use of the updated value.

### Value

A character vector of file paths.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[library](#)

### Examples

```
.libPaths() # all library trees R knows about
```

---

library	<i>Loading and Listing of Packages</i>
---------	--

---

### Description

`library` and `require` load add-on packages.

`.First.lib` is called when a package is loaded; `.Last.lib` is called when a package is detached.

### Usage

```
library(package, help, pos = 2, lib.loc = NULL,
        character.only = FALSE, logical.return = FALSE,
        warn.conflicts = TRUE,
        keep.source = getOption("keep.source.pkgs"),
        verbose = getOption("verbose"))
```

```
require(package, lib.loc = NULL, quietly = FALSE,
        warn.conflicts = TRUE,
        keep.source = getOption("keep.source.pkgs"),
```

```

character.only = FALSE, save = TRUE)

.First.lib(libname, pkgname)
.Last.lib(libpath)

```

### Arguments

<code>package</code> , <code>help</code>	the name of a package, given as a <a href="#">name</a> or literal character string, or a character string, depending on whether <code>character.only</code> is FALSE (default) or TRUE).
<code>pos</code>	the position on the search list at which to attach the loaded package. Note that <code>.First.lib</code> may attach other packages, and <code>pos</code> is computed <i>after</i> <code>.First.lib</code> has been run. Can also be the name of a position on the current search list as given by <code>search()</code> .
<code>lib.loc</code>	a character vector describing the location of R library trees to search through, or NULL. The default value of NULL corresponds to all libraries currently known. Non-existent library trees are silently ignored.
<code>character.only</code>	a logical indicating whether <code>package</code> or <code>help</code> can be assumed to be character strings.
<code>logical.return</code>	logical. If it is TRUE, FALSE or TRUE is returned to indicate success.
<code>warn.conflicts</code>	logical. If TRUE, warnings are printed about <a href="#">conflicts</a> from attaching the new package, unless that package contains an object <code>.conflicts.OK</code> . A conflict is a function masking a function, or a non-function masking a non-function.
<code>keep.source</code>	logical. If TRUE, functions ‘keep their source’ including comments, see argument <code>keep.source</code> to <a href="#">options</a> . This applies only to the named package, and not to any packages or name spaces which might be loaded to satisfy dependencies or imports. This argument does not apply to packages using lazy-loading. Whether they have kept source is determined when they are installed (and is most likely false).
<code>verbose</code>	a logical. If TRUE, additional diagnostics are printed.
<code>quietly</code>	a logical. If TRUE, no message confirming package loading is printed.
<code>save</code>	logical or environment. If TRUE, a call to <code>require</code> from the source for a package will save the name of the required package in the variable <code>".required"</code> , allowing function <a href="#">detach</a> to warn if a required package is detached. See section ‘Packages that require other packages’ below.
<code>libname</code>	a character string giving the library directory where the package was found.
<code>pkgname</code>	a character string giving the name of the package.
<code>libpath</code>	a character string giving the complete path to the package.

### Details

`library(package)` and `require(package)` both load the package with name `package`. `require` is designed for use inside other functions; it returns FALSE and gives a warning (rather than an error as `library()` does by default) if the package does not exist. Both functions check and update the list of currently loaded packages and do not reload a package which is already loaded. (Furthermore, if the package has a name space and a name space of that name is already

loaded, they work from the existing name space rather than reloading from the file system. If you want to reload a package, call `detach` or `unloadNamespace` first.)

To suppress messages during the loading of packages use `suppressPackageStartupMessages`: this will suppress all messages from R itself but not necessarily all those from package authors.

If `library` is called with no `package` or `help` argument, it lists all available packages in the libraries specified by `lib.loc`, and returns the corresponding information in an object of class `"libraryIQR"`. The structure of this class may change in future versions. In earlier versions of R, only the names of all available packages were returned; use `.packages(all = TRUE)` for obtaining these. Note that `installed.packages()` returns even more information.

`library(help = somename)` computes basic information about the package `somename`, and returns this in an object of class `"packageInfo"`. The structure of this class may change in future versions. When used with the default value (NULL) for `lib.loc`, the loaded packages are searched before the libraries.

`.First.lib` is called when a package without a name space is loaded by `library`. (For packages with name spaces see `.onLoad`.) It is called with two arguments, the name of the library directory where the package was found (i.e., the corresponding element of `lib.loc`), and the name of the package. It is a good place to put calls to `library.dynam` which are needed when loading a package into this function (don't call `library.dynam` directly, as this will not work if the package is not installed in a standard location). `.First.lib` is invoked after the search path interrogated by `search()` has been updated, so `as.environment(match("package:name", search()))` will return the environment in which the package is stored. If calling `.First.lib` gives an error the loading of the package is abandoned, and the package will be unavailable. Similarly, if the option `".First.lib"` has a list element with the package's name, this element is called in the same manner as `.First.lib` when the package is loaded. This mechanism allows the user to set package 'load hooks' in addition to startup code as provided by the package maintainers, but `setHook` is preferred.

`.Last.lib` is called when a package is detached. Beware that it might be called if `.First.lib` has failed, so it should be written defensively. (It is called within `try`, so errors will not stop the package being detached.)

## Value

Normally `library` returns (invisibly) the list of loaded packages, but `TRUE` or `FALSE` if `logical.return` is `TRUE`. When called as `library()` it returns an object of class `"libraryIQR"`, and for `library(help=)`, one of class `"packageInfo"`.

`require` returns (invisibly) a logical indicating whether the required package is available.

## Licenses

Some packages have restrictive licenses, and as from R 2.11.0 there is a mechanism to ensure that users are aware of such licenses. If `getOption("checkPackageLicense") == TRUE`, then at first use of a package with a not-known-to-be-FOSS (see below) license the user is asked to view and accept the license: a list of accepted licenses is stored in file `'~/R/licensed'`. In a non-interactive session it is an error to use such a package whose license has not already been accepted.

Free or Open Source Software (FOSS, e.g., <http://en.wikipedia.org/wiki/FOSS>) packages are determined by the same filters used by `available.packages` but applied to just the current package, not its dependencies.

There can also be a site-wide file `'R_HOME/etc/licensed.site'` of packages (one per line).

### Packages that require other packages

The usual way for a package to require other packages is to list them in the ‘Depends:’ field of the ‘DESCRIPTION’ file. Such packages are checked by `detach`.

An alternative way to record that a package is required is to use a call to `require(save = TRUE)` in the `.First.lib` function of the package (but only for a package without a namespace): this mechanism was used more widely in earlier versions of R.

### Formal methods

`library` takes some further actions when package **methods** is attached (as it is by default). Packages may define formal generic functions as well as re-defining functions in other packages (notably **base**) to be generic, and this information is cached whenever such a package is loaded after **methods** and re-defined functions (**implicit generics**) are excluded from the list of conflicts. The caching and check for conflicts require looking for a pattern of objects; the search may be avoided by defining an object `.noGenerics` (with any value) in the package. Naturally, if the package *does* have any such methods, this will prevent them from being used.

### Note

`library` and `require` can only load an *installed* package, and this is detected by having a ‘DESCRIPTION’ file containing a ‘Built:’ field.

Under Unix-alikes, the code checks that the package was installed under a similar operating system as given by `R.version$platform` (the canonical name of the platform under which R was compiled), provided it contains compiled code. Packages which do not contain compiled code can be shared between Unix-alikes, but not to other OSes because of potential problems with line endings and OS-specific help files. If sub-architectures are used, the OS similarity is not checked since the OS used to build may differ (e.g. `i386-pc-linux-gnu` code can be built on an `x86_64-unknown-linux-gnu` OS).

The package name given to `library` and `require` must match the name given in the package’s ‘DESCRIPTION’ file exactly, even on case-insensitive file systems such as are common on MS Windows and Mac OS X.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

`.libPaths`, `.packages`.

`attach`, `detach`, `search`, `objects`, `autoload`, `library.dynam`, `data`, `install.packages` and `installed.packages`; `INSTALL`, `REMOVE`.

The initial set of packages loaded is set by `options(defaultPackages=)`: see also `Startup`.

### Examples

```
library()                # list all available packages
library(lib.loc = .Library) # list all packages in the default library
library(help = splines)  # documentation on package 'splines'
library(splines)        # load package 'splines'
require(splines)        # the same
```

```

search()                # "splines", too
detach("package:splines")

# if the package name is in a character vector, use
pkg <- "splines"
library(pkg, character.only = TRUE)
detach(pos = match(paste("package", pkg, sep=":"), search()))

require(pkg, character.only = TRUE)
detach(pos = match(paste("package", pkg, sep=":"), search()))

require(nonexistent)    # FALSE
## Not run:
## Suppose a package needs to call a DLL named 'fooEXT',
## where 'EXT' is the system-specific extension. Then you should use
.First.lib <- function(lib, pkg)
  library.dynam("foo", pkg, lib)

## if you want to mask as little as possible, use
library(mypkg, pos = "package:base")

## End(Not run)

```

---

library.dynam      *Loading DLLs from Packages*

---

## Description

Load the specified file of compiled code if it has not been loaded already, or unloads it.

## Usage

```

library.dynam(cname, package = NULL, lib.loc = NULL,
              verbose = getOption("verbose"),
              file.ext = .Platform$dynlib.ext, ...)

library.dynam.unload(cname, libpath,
                    verbose = getOption("verbose"),
                    file.ext = .Platform$dynlib.ext)

.dynLibs(new)

```

## Arguments

cname	a character string naming a DLL (also known as a dynamic shared object or library) to load.
package	a character vector with the names of packages to search through, or NULL. By default, all packages in the search path are used.
lib.loc	a character vector describing the location of R library trees to search through, or NULL. The default value of NULL corresponds to all libraries currently known.
libpath	the path to the loaded package whose DLL is to be unloaded.

verbose	a logical value indicating whether an announcement is printed on the console before loading the DLL. The default value is taken from the verbose entry in the system <a href="#">options</a> .
file.ext	the extension (including '.' if used) to append to the file name to specify the library to be loaded. This defaults to the appropriate value for the operating system.
...	additional arguments needed by some libraries that are passed to the call to <a href="#">dyn.load</a> to control how the library and its dependencies are loaded.
new	a list of "DLLInfo" objects corresponding to the DLLs loaded by packages. Can be missing.

### Details

See [dyn.load](#) for what sort of objects these functions handle.

`library.dynam` is designed to be used inside a package rather than at the command line, and should really only be used inside `.First.lib` or `.onLoad`. The system-specific extension for DLLs (e.g., `.so` or `.sl` on Unix systems, `.so` on Mac OS X, `.dll` on Windows) should not be added.

`library.dynam.unload` is designed for use in `.Last.lib` or `.onUnload`: it unloads the DLL and updates the value of `.dynLibs()`

`.dynLibs` is used for getting (with no argument) or setting the DLLs which are currently loaded by packages (using `library.dynam`).

### Value

If `cname` is not specified, `library.dynam` returns an object of class "DLLInfoList" corresponding to the DLLs loaded by packages.

If `cname` is specified, an object of class "DLLInfo" that identifies the DLL and can be used in future calls is returned invisibly. For packages that have name spaces, a list of these objects is stored in the name space's environment for use at run-time.

Note that the class `DLLInfo` has an overloaded method for `$` which can be used to resolve native symbols within that DLL.

`library.dynam.unload` invisibly returns an object of class "DLLInfo" identifying the DLL successfully unloaded.

`.dynLibs` returns an object of class "DLLInfoList" corresponding corresponding to its current value.

### Warning

Do not use `dyn.unload` on a DLL loaded by `library.dynam`: use `library.dynam.unload` to ensure that `.dynLibs` gets updated. Otherwise a subsequent call to `library.dynam` will be told the object is already loaded.

Note that whether or not it is possible to unload a DLL and then reload a revised version of the same file is OS-dependent: see the 'Value' section of the help for [dyn.unload](#).

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.



**See Also**

`getLoadedDLLs` for information on "DLLInfo" and "DLLInfoList" objects.  
`.First.lib`, `library`, `dyn.load`, `.packages`, `.libPaths`  
`SHLIB` for how to create suitable DLLs.

**Examples**

```
## Which DLLs were "dynamically loaded" by packages?
library.dynam()
```

---

license	<i>The R License Terms</i>
---------	----------------------------

---

**Description**

The license terms under which R is distributed.

**Usage**

```
license()
licence()
```

**Details**

R is distributed under the terms of the GNU GENERAL PUBLIC LICENSE Version 2, June 1991. A copy of this license is in file '[R\\_HOME/COPYING](#)' and can be viewed by `RShowDoc("COPYING")`.

A small number of files (the API header files) are distributed under the LESSER GNU GENERAL PUBLIC LICENSE version 2.1. A copy of this license is in file '`$R_DOC_DIR/COPYING.LIB`' and can be viewed by `RShowDoc("COPYING.LIB")`.

---

list	<i>Lists – Generic and Dotted Pairs</i>
------	---

---

**Description**

Functions to construct, coerce and check for both kinds of R lists.

**Usage**

```
list(...)
pairlist(...)

as.list(x, ...)
## S3 method for class 'environment':
as.list(x, all.names = FALSE, ...)
as.pairlist(x)

is.list(x)
is.pairlist(x)

alist(...)
```

**Arguments**

<code>...</code>	objects, possibly named.
<code>x</code>	object to be coerced or tested.
<code>all.names</code>	a logical indicating whether to copy all values or (default) only those whose names do not begin with a dot.

**Details**

Most lists in R internally are *Generic Vectors*, whereas traditional *dotted pair* lists (as in LISP) are available but rarely seen by users (except as `formals` of functions).

The arguments to `list` or `pairlist` are of the form `value` or `tag=value`. The functions return a list or dotted pair list composed of its arguments with each value either tagged or untagged, depending on how the argument was specified.

`alist` handles its arguments as if they described function arguments. So the values are not evaluated, and tagged arguments with no value are allowed whereas `list` simply ignores them. `alist` is most often used in conjunction with `formals`.

`as.list` attempts to coerce its argument to a list. For functions, this returns the concatenation of the list of formal arguments and the function body. For expressions, the list of constituent elements is returned. `as.list` is generic, and as the default method calls `as.vector(mode="list")` methods for `as.vector` may be invoked. `as.list` turns a factor into a list of one-element factors. All attributes will be dropped unless the argument already is a list. (This is inconsistent with functions such as `as.character`, and is for efficiency since lists can be expensive to copy.)

`is.list` returns TRUE if and only if its argument is a list *or* a pairlist of length > 0. `is.pairlist` returns TRUE if and only if the argument is a pairlist or NULL (see below).

The `"environment"` method for `as.list` copies the name-value pairs (for names not beginning with a dot) from an environment to a named list. The user can request that all named objects are copied. The list is in no particular order (the order depends on the order of creation of objects and whether the environment is hashed). No parent environments are searched. (Objects copied are duplicated so this can be an expensive operation.)

An empty pairlist, `pairlist()` is the same as NULL. This is different from `list()`.

`as.pairlist` is implemented as `as.vector(x, "pairlist")`, and hence will dispatch methods for the generic function `as.vector`.

`list`, `is.list` and `is.pairlist` are **primitive** functions.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`vector("list", length)` for creation of a list with empty components; `c`, for concatenation; `formals`. `unlist` is an approximate inverse to `as.list()`.

`'plotmath'` for the use of `list` in plot annotation.

**Examples**

```

require(graphics)

# create a plotting structure
pts <- list(x=cars[,1], y=cars[,2])
plot(pts)

is.pairlist(.Options) # a user-level pairlist

## "pre-allocate" an empty list of length 5
vector("list", 5)

# Argument lists
f <- function() x
# Note the specification of a "..." argument:
formals(f) <- al <- alist(x=, y=2+3, ...=)
f
al

## environment->list coercion

e1 <- new.env()
e1$a <- 10
e1$b <- 20
as.list(e1)

```

---

list.files

*List the Files in a Directory/Folder*


---

**Description**

These functions produce a character vector of the names of files in the named directory.

**Usage**

```

list.files(path = ".", pattern = NULL, all.files = FALSE,
           full.names = FALSE, recursive = FALSE,
           ignore.case = FALSE)

dir(path = ".", pattern = NULL, all.files = FALSE,
    full.names = FALSE, recursive = FALSE,
    ignore.case = FALSE)

```

**Arguments**

path	a character vector of full path names; the default corresponds to the working directory <code>getwd()</code> . Missing values will be ignored.
pattern	an optional <a href="#">regular expression</a> . Only file names which match the regular expression will be returned.
all.files	a logical value. If FALSE, only the names of visible files are returned. If TRUE, all file names will be returned.

`full.names` a logical value. If `TRUE`, the directory path is prepended to the file names. If `FALSE`, only the file names are returned.

`recursive` logical. Should the listing recurse into directories?

`ignore.case` logical. Should pattern-matching be case-insensitive?

**Value**

A character vector containing the names of the files in the specified directories, or "" if there were no files. If a path does not exist or is not a directory or is unreadable it is skipped, with a warning.

The files are sorted in alphabetical order, on the full path if `full.names = TRUE`. Directories are included only if `recursive = FALSE`.

**Note**

File naming conventions are platform dependent.

`recursive = TRUE` is not supported on all platforms and may be ignored (with a warning).

**Author(s)**

Ross Ihaka, Brian Ripley

**See Also**

[file.info](#), [file.access](#) and [files](#) for many more file handling functions and [file.choose](#) for interactive selection.

[glob2rx](#) to convert wildcards (as used by system file commands and shells) to regular expressions.

[Sys.glob](#) for wildcard expansion on file paths.

**Examples**

```
list.files(R.home())
## Only files starting with a-l or r
## Note that a-l is locale-dependent, but using case-insensitive
## matching makes it unambiguous in English locales
dir("../..", pattern = "[a-lr]",full.names=TRUE, ignore.case = TRUE)
```

---

load

*Reload Saved Datasets*

---

**Description**

Reload datasets written with the function `save`.

**Usage**

```
load(file, envir = parent.frame())
```

**Arguments**

`file` a (readable binary) connection or a character string giving the name of the file to load.

`envir` the environment where the data should be loaded.

## Details

`load` can load R objects saved in the current or any earlier format. It can read a compressed file (see [save](#)) directly from a file or from a suitable connection (including a call to [url](#)).

A not-open connection will be opened in mode `"rb"` and closed after use.

Only R objects saved in the current format (used since R 1.4.0) can be read from a connection. If no input is available on a connection a warning will be given, but any input not in the current format will result in an error.

Loading from an earlier version will give a warning about the ‘magic number’: magic numbers 1971:1977 are from R < 0.99.0, and R [ADX] 1 from R 0.99.0 to R 1.3.1.

## Value

A character vector of the names of objects created, invisibly.

## Warning

Saved R objects are binary files, even those saved with `ascii = TRUE`, so ensure that they are transferred without conversion of end of line markers. `load` tries to detect this case and give an informative error message.

## See Also

[save](#), [download.file](#).

## Examples

```
## save all data
xx <- pi # to ensure there is some data
save(list = ls(all=TRUE), file= "all.Rdata")
rm(xx)

## restore the saved values to the current environment
local({
  load("all.Rdata")
  ls()
})
## restore the saved values to the user's workspace
load("all.Rdata", .GlobalEnv)

unlink("all.Rdata")

## Not run:
con <- url("http://some.where.net/R/data/example.rda")
## print the value to see what objects were created.
print(load(con))
close(con) # url() always opens the connection

## End(Not run)
```

---

 locales

*Query or Set Aspects of the Locale*


---

### Description

Get details of or set aspects of the locale for the R process.

### Usage

```

Sys.getlocale(category = "LC_ALL")
Sys.setlocale(category = "LC_ALL", locale = "")

```

### Arguments

category	character string. The following categories should always be supported: "LC_ALL", "LC_COLLATE", "LC_CTYPE", "LC_MONETARY", "LC_NUMERIC" and "LC_TIME". Some systems (not Windows) will also support "LC_MESSAGES", "LC_PAPER" and "LC_MEASUREMENT".
locale	character string. A valid locale name on the system in use. Normally "" (the default) will pick up the default locale for the system.

### Details

The locale describes aspects of the internationalization of a program. Initially most aspects of the locale of R are set to "C" (which is the default for the C language and reflects North-American usage). R sets "LC\_CTYPE" and "LC\_COLLATE", which allow the use of a different character set and alphabetic comparisons in that character set (including the use of `sort`), "LC\_MONETARY" (for use by `Sys.localeconv`) and "LC\_TIME" may affect the behaviour of `as.POSIXlt` and `strptime` and functions which use them (but not `date`).

R can be built with no support for locales, but it is normally available on Unix and is available on Windows.

The first seven categories described here are those specified by POSIX. "LC\_MESSAGES" will be "C" on systems that do not support message translation, and is not supported on Windows. Trying to use an unsupported category is an error for `Sys.setlocale`.

Note that setting "LC\_ALL" sets only "LC\_COLLATE", "LC\_CTYPE", "LC\_MONETARY" and "LC\_TIME".

Attempts to set an invalid locale are ignored. There may or may not be a warning, depending on the OS.

Attempts to change the character set (by `Sys.setlocale("LC_TYPE", )`, if that implies a different character set) during a session may not work and are likely to lead to some confusion.

### Value

A character string of length one describing the locale in use (after setting for `Sys.setlocale`), or an empty character string if the current locale settings are invalid or NULL if locale information is unavailable.

For `category = "LC_ALL"` the details of the string are system-specific: it might be a single locale name or a set of locale names separated by "/" (Solaris, Mac OS X) or ";" (Windows, Linux). For portability, it is best to query categories individually: it is not necessarily the case

that the result of `foo <- Sys.getlocale()` can be used in `Sys.setlocale("LC_ALL", locale = foo)`.

### Warning

Setting "LC\_NUMERIC" may cause R to function anomalously, so gives a warning. Input conversions in R itself are unaffected, but the reading and writing of ASCII `save` files will be, as may packages. Setting it temporarily to produce graphical or text output may work well enough, but `options(OutDec)` is often preferable.

### Note

Changing the values of locale categories whilst R is running ought to be noticed by the OS services, and usually is but exceptions have been seen (usually in collation services).

### See Also

`strptime` for uses of `category = "LC_TIME"`. `Sys.localeconv` for details of numerical and monetary representations.

`l10n_info` gives some summary facts about the locale and its encoding.

### Examples

```
Sys.getlocale()
Sys.getlocale("LC_TIME")
## Not run:
Sys.setlocale("LC_TIME", "de")      # Solaris: details are OS-dependent
Sys.setlocale("LC_TIME", "de_DE.utf8") # Modern Linux etc.
Sys.setlocale("LC_TIME", "de_DE")   # Mac OS X
Sys.setlocale("LC_TIME", "German")  # Windows

## End(Not run)
Sys.getlocale("LC_PAPER")           # may or may not be set

Sys.setlocale("LC_COLLATE", "C")    # turn off locale-specific sorting, usually
```

---

log

*Logarithms and Exponentials*

---

### Description

`log` computes logarithms, by default natural logarithms, `log10` computes common (i.e., base 10) logarithms, and `log2` computes binary (i.e., base 2) logarithms. The general form `log(x, base)` computes logarithms with base `base`.

`log1p(x)` computes  $\log(1 + x)$  accurately also for  $|x| \ll 1$  (and less accurately when  $x \approx -1$ ).

`exp` computes the exponential function.

`expm1(x)` computes  $\exp(x) - 1$  accurately also for  $|x| \ll 1$ .

## Usage

```
log(x, base = exp(1))
logb(x, base = exp(1))
log10(x)
log2(x)

log1p(x)

exp(x)
expm1(x)
```

## Arguments

`x` a numeric or complex vector.

`base` a positive or complex number: the base with respect to which logarithms are computed. Defaults to  $e = \exp(1)$ .

## Details

All except `logb` are generic functions: methods can be defined for them individually or via the [Math](#) group generic.

`log10` and `log2` are only convenience wrappers, but logs to bases 10 and 2 (whether computed *via* `log` or the wrappers) will be computed more efficiently and accurately where supported by the OS. Methods can be set for them individually (and otherwise methods for `log` will be used).

`logb` is a wrapper for `log` for compatibility with S. If (S3 or S4) methods are set for `log` they will be dispatched. Do not set S4 methods on `logb` itself.

All except `log` are [primitive](#) functions.

## Value

A vector of the same length as `x` containing the transformed values. `log(0)` gives `-Inf`, and negative values give `NaN`.

## S4 methods

`exp`, `expm1`, `log`, `log10`, `log2` and `log1p` are S4 generic and are members of the [Math](#) group generic.

Note that this means that the S4 generic for `log` has a signature with only one argument, `x`, but that `base` can be passed to methods (but will not be used for method selection). On the other hand, if you only set a method for the [Math](#) group generic then `base` argument of `log` will be ignored for your class.

## Note

`log` and `logb` are the same thing in R, but `logb` is preferred if `base` is specified, for S-PLUS compatibility.



**Source**

`log1p` and `expm1` may be taken from the operating system, but if not available there are based on the Fortran subroutine `dlnrel` by W. Fullerton of Los Alamos Scientific Laboratory (see <http://www.netlib.org/slatec/fnlib/dlnrel.f> and (for small  $x$ ) a single Newton step for the solution of  $\log_{1p}(y) = x$  respectively.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (for `log`, `log10` and `exp`.)

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer. (for `logb`.)

**See Also**

[Trig](#), [sqrt](#), [Arithmetic](#).

**Examples**

```
log(exp(3))
log10(1e7) # = 7

x <- 10^-(1+2*1:9)
cbind(x, log(1+x), log1p(x), exp(x)-1, expm1(x))
```

---

Logic

*Logical Operators*

---

**Description**

These operators act on logical and number-like vectors.

**Usage**

```
! x
x & y
x && y
x | y
x || y
xor(x, y)

isTRUE(x)
```

**Arguments**

`x`, `y` logical or ‘number-like’ vectors (i.e., of type `double` (class `numeric`), `integer`, `complex` or `raw`), or objects for which methods have been written.

## Details

`!` indicates logical negation (NOT).

`&` and `&&` indicate logical AND and `|` and `||` indicate logical OR. The shorter form performs elementwise comparisons in much the same way as arithmetic operators. The longer form evaluates left to right examining only the first element of each vector. Evaluation proceeds only until the result is determined. The longer form is appropriate for programming control-flow and typically preferred in `if` clauses.

`xor` indicates elementwise exclusive OR.

`isTRUE(x)` is an abbreviation of `identical(TRUE, x)`, and so is true if and only if `x` is a length-one logical vector whose only element is `TRUE` and which has no attributes (not even names).

Numeric and complex vectors will be coerced to logical values, with zero being false and all non-zero values being true. Raw vectors are handled without any coercion for `!`, `&`, `|` and `xor`, with these operators being applied bitwise (so `!` is the 1s-complement).

The operators `!`, `&` and `|` are generic functions: methods can be written for them individually or via the `Ops` (or `S4 Logic`, see below) group generic function. (See `Ops` for how dispatch is computed.)

`NA` is a valid logical object. Where a component of `x` or `y` is `NA`, the result will be `NA` if the outcome is ambiguous. In other words `NA & TRUE` evaluates to `NA`, but `NA & FALSE` evaluates to `FALSE`. See the examples below.

See `Syntax` for the precedence of these operators: unlike many other languages (including `S`) the AND and OR operators do not have the same precedence (the AND operators are higher than the OR operators).

## Value

For `!`, a logical or raw vector of the same length as `x`.

For `|`, `&` and `xor` a logical or raw vector. The elements of shorter vectors are recycled as necessary (with a `warning` when they are recycled only *fractionally*). The rules for determining the attributes of the result are rather complicated. Most attributes are taken from the longer argument, the first if they are of the same length. Names will be copied from the first if it is the same length as the answer, otherwise from the second if that is. For time series, these operations are allowed only if the series are compatible, when the class and `tsp` attribute of whichever is a time series (the same, if both are) are used. For arrays (and an array result) the dimensions and `dimnames` are taken from first argument if it is an array, otherwise the second.

For `||`, `&&` and `isTRUE`, a length-one logical vector.

## S4 methods

`!`, `&` and `|` are S4 generics, the latter two part of the `Logic` group generic (and hence methods need argument names `e1`, `e2`).

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[TRUE](#) or [logical](#).

[any](#) and [all](#) for OR and AND on many scalar arguments.

[Syntax](#) for operator precedence.

**Examples**

```
y <- 1 + (x <- stats::rpois(50, lambda=1.5) / 4 - 1)
x[(x > 0) & (x < 1)] # all x values between 0 and 1
if (any(x == 0) || any(y == 0)) "zero encountered"

## construct truth tables :

x <- c(NA, FALSE, TRUE)
names(x) <- as.character(x)
outer(x, x, "&")## AND table
outer(x, x, "|")## OR table
```

---

logical

*Logical Vectors*

---

**Description**

Create or test for objects of type "logical", and the basic logical constants.

**Usage**

```
TRUE
FALSE
T; F

logical(length = 0)
as.logical(x, ...)
is.logical(x)
```

**Arguments**

length	desired length.
x	object to be coerced or tested.
...	further arguments passed to or from other methods.

**Details**

TRUE and FALSE are [reserved](#) words denoting logical constants in the R language, whereas T and F are global variables whose initial values set to these. All four are `logical(1)` vectors.

Logical vectors are coerced to integer vectors in contexts where a numerical value is required, with TRUE being mapped to 1L, FALSE to 0L and NA\_LOGICAL\_ to NA\_INTEGER\_.

**Value**

`logical` creates a logical vector of the specified length. Each element of the vector is equal to `FALSE`.

`as.logical` attempts to coerce its argument to be of logical type. For `factors`, this uses the `levels` (labels). Like `as.vector` it strips attributes including names.

`is.logical` returns `TRUE` or `FALSE` depending on whether its argument is of logical type or not.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`NA`, the other logical constant.

---

`lower.tri`*Lower and Upper Triangular Part of a Matrix*

---

**Description**

Returns a matrix of logicals the same size of a given matrix with entries `TRUE` in the lower or upper triangle.

**Usage**

```
lower.tri(x, diag = FALSE)
upper.tri(x, diag = FALSE)
```

**Arguments**

<code>x</code>	a matrix.
<code>diag</code>	logical. Should the diagonal be included?

**See Also**

`diag, matrix`.

**Examples**

```
(m2 <- matrix(1:20, 4, 5))
lower.tri(m2)
m2[lower.tri(m2)] <- NA
m2
```

---

 ls *List Objects*


---

**Description**

`ls` and `objects` return a vector of character strings giving the names of the objects in the specified environment. When invoked with no argument at the top level prompt, `ls` shows what data sets and functions a user has defined. When invoked with no argument inside a function, `ls` returns the names of the functions local variables. This is useful in conjunction with `browser`.

**Usage**

```
ls(name, pos = -1, envir = as.environment(pos),
   all.names = FALSE, pattern)
objects(name, pos = -1, envir = as.environment(pos),
        all.names = FALSE, pattern)
```

**Arguments**

<code>name</code>	which environment to use in listing the available objects. Defaults to the <i>current</i> environment. Although called <code>name</code> for back compatibility, in fact this argument can specify the environment in any form; see the details section.
<code>pos</code>	an alternative argument to <code>name</code> for specifying the environment as a position in the search list. Mostly there for back compatibility.
<code>envir</code>	an alternative argument to <code>name</code> for specifying the environment evaluation environment. Mostly there for back compatibility.
<code>all.names</code>	a logical value. If <code>TRUE</code> , all object names are returned. If <code>FALSE</code> , names which begin with a <code>'.'</code> are omitted.
<code>pattern</code>	an optional <a href="#">regular expression</a> . Only names matching <code>pattern</code> are returned. <code>glob2rx</code> can be used to convert wildcard patterns to regular expressions.

**Details**

The `name` argument can specify the environment from which object names are taken in one of several forms: as an integer (the position in the [search](#) list); as the character string name of an element in the search list; or as an explicit [environment](#) (including using `sys.frame` to access the currently active function calls). By default, the environment of the call to `ls` or `objects` is used. The `pos` and `envir` arguments are an alternative way to specify an environment, but are primarily there for back compatibility.

Note that the *order* of the resulting strings is locale dependent, see [Sys.getlocale](#).

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[glob2rx](#) for converting wildcard patterns to regular expressions.

[ls.str](#) for a long listing based on [str](#). [apropos](#) (or [find](#)) for finding objects in the whole search path; [grep](#) for more details on ‘regular expressions’; [class](#), [methods](#), etc., for object-oriented programming.

**Examples**

```
.Ob <- 1
ls(pattern = "O")
ls(pattern= " O", all.names = TRUE)      # also shows ".[foo]"

# shows an empty list because inside myfunc no variables are defined
myfunc <- function() {ls()}
myfunc()

# define a local variable inside myfunc
myfunc <- function() {y <- 1; ls()}
myfunc()          # shows "y"
```

---

make.names

---

*Make Syntactically Valid Names*


---

**Description**

Make syntactically valid names out of character vectors.

**Usage**

```
make.names(names, unique = FALSE, allow_ = TRUE)
```

**Arguments**

names	character vector to be coerced to syntactically valid names. This is coerced to character if necessary.
unique	logical; if TRUE, the resulting elements are unique. This may be desired for, e.g., column names.
allow_	logical. For compatibility with R prior to 1.9.0.

**Details**

A syntactically valid name consists of letters, numbers and the dot or underline characters and starts with a letter or the dot not followed by a number. Names such as ".2way" are not valid, and neither are the [reserved](#) words.

The definition of a *letter* depends on the current locale, but only ASCII digits are considered to be digits.

The character "X" is prepended if necessary. All invalid characters are translated to ".". A missing value is translated to "NA". Names which match R keywords have a dot appended to them. Duplicated values are altered by [make.unique](#).

**Value**

A character vector of same length as `names` with each changed to a syntactically valid name, in the current locale's encoding.

**Note**

Prior to R version 1.9.0, underscores were not valid in variable names, and code that relies on them being converted to dots will no longer work. Use `allow_ = FALSE` for back-compatibility.

`allow_ = FALSE` is also useful when creating names for export to applications which do not allow underline in names (for example, S-PLUS and some DBMSs).

**See Also**

`make.unique`, `names`, `character`, `data.frame`.

**Examples**

```
make.names(c("a and b", "a-and-b"), unique=TRUE)
# "a.and.b" "a.and.b.1"
make.names(c("a and b", "a_and_b"), unique=TRUE)
# "a.and.b" "a_and_b"
make.names(c("a and b", "a_and_b"), unique=TRUE, allow_=FALSE)
# "a.and.b" "a.and.b.1"

state.name[make.names(state.name) != state.name] # those 10 with a space
```

---

`make.unique`

*Make Character Strings Unique*

---

**Description**

Makes the elements of a character vector unique by appending sequence numbers to duplicates.

**Usage**

```
make.unique(names, sep = ".")
```

**Arguments**

<code>names</code>	a character vector
<code>sep</code>	a character string used to separate a duplicate name from its sequence number.

**Details**

The algorithm used by `make.unique` has the property that `make.unique(c(A, B)) == make.unique(c(make.unique(A), B))`.

In other words, you can append one string at a time to a vector, making it unique each time, and get the same result as applying `make.unique` to all of the strings at once.

If character vector `A` is already unique, then `make.unique(c(A, B))` preserves `A`.

**Value**

A character vector of same length as `names` with duplicates changed, in the current locale's encoding.

**Author(s)**

Thomas P. Minka

**See Also**

[make.names](#)

**Examples**

```
make.unique(c("a", "a", "a"))
make.unique(c(make.unique(c("a", "a")), "a"))

make.unique(c("a", "a", "a.2", "a"))
make.unique(c(make.unique(c("a", "a")), "a.2", "a"))

rbind(data.frame(x=1), data.frame(x=2), data.frame(x=3))
rbind(rbind(data.frame(x=1), data.frame(x=2)), data.frame(x=3))
```

---

mapply

*Apply a Function to Multiple List or Vector Arguments*


---

**Description**

`mapply` is a multivariate version of [sapply](#). `mapply` applies `FUN` to the first elements of each `...` argument, the second elements, the third elements, and so on. Arguments are recycled if necessary.

`Vectorize` returns a new function that acts as if `mapply` was called.

**Usage**

```
mapply(FUN, ..., MoreArgs = NULL, SIMPLIFY = TRUE,
       USE.NAMES = TRUE)

Vectorize(FUN, vectorize.args = arg.names, SIMPLIFY = TRUE,
         USE.NAMES = TRUE)
```

**Arguments**

<code>FUN</code>	function to apply, found via <a href="#">match.fun</a> .
<code>...</code>	arguments to vectorize over (list or vector).
<code>MoreArgs</code>	a list of other arguments to <code>FUN</code> .
<code>SIMPLIFY</code>	logical; attempt to reduce the result to a vector or matrix?
<code>USE.NAMES</code>	logical; use names if the first <code>...</code> argument has names, or if it is a character vector, use that character vector as the names.
<code>vectorize.args</code>	a character vector of arguments which should be vectorized. Defaults to all arguments to <code>FUN</code> .



**Details**

The arguments named in the `vectorize.args` argument to `Vectorize` correspond to the arguments passed in the `...` list to `mapply`. However, only those that are actually passed will be vectorized; default values will not. See the example below.

`Vectorize` cannot be used with primitive functions as they have no formal list.

**Value**

`mapply` returns a list, vector, or matrix.

`Vectorize` returns a function with the same arguments as `FUN`, but wrapping a call to `mapply`.

**See Also**

[sapply](#), [outer](#)

**Examples**

```
require(graphics)

mapply(rep, 1:4, 4:1)

mapply(rep, times=1:4, x=4:1)

mapply(rep, times=1:4, MoreArgs=list(x=42))

# Repeat the same using Vectorize: use rep.int as rep is primitive
vrep <- Vectorize(rep.int)
vrep(1:4, 4:1)
vrep(times=1:4, x=4:1)

vrep <- Vectorize(rep.int, "times")
vrep(times=1:4, x=42)

mapply(function(x,y) seq_len(x) + y,
        c(a= 1, b=2, c= 3), # names from first
        c(A=10, B=0, C=-10))

word <- function(C,k) paste(rep.int(C,k), collapse='')
utils::str(mapply(word, LETTERS[1:6], 6:1, SIMPLIFY = FALSE))

f <- function(x=1:3, y) c(x,y)
vf <- Vectorize(f, SIMPLIFY = FALSE)
f(1:3,1:3)
vf(1:3,1:3)
vf(y=1:3) # Only vectorizes y, not x

# Nonlinear regression contour plot, based on nls() example

SS <- function(Vm, K, resp, conc) {
  pred <- (Vm * conc)/(K + conc)
  sum((resp - pred)^2 / pred)
}
vSS <- Vectorize(SS, c("Vm", "K"))
Treated <- subset(Puromycin, state == "treated")
```

```
Vm <- seq(140, 310, len=50)
K <- seq(0, 0.15, len=40)
SSvals <- outer(Vm, K, vSS, Treated$rate, Treated$conc)
contour(Vm, K, SSvals, levels=(1:10)^2, xlab="Vm", ylab="K")
```

---

margin.table	<i>Compute table margin</i>
--------------	-----------------------------

---

### Description

For a contingency table in array form, compute the sum of table entries for a given index.

### Usage

```
margin.table(x, margin=NULL)
```

### Arguments

x	an array
margin	index number (1 for rows, etc.)

### Details

This is really just `apply(x, margin, sum)` packaged up for newbies, except that if `margin` has length zero you get `sum(x)`.

### Value

The relevant marginal table. The class of `x` is copied to the output table, except in the summation case.

### Author(s)

Peter Dalgaard

### See Also

[prop.table](#) and [addmargins](#).

### Examples

```
m <- matrix(1:4, 2)
margin.table(m, 1)
margin.table(m, 2)
```

---

<code>mat.or.vec</code>	<i>Create a Matrix or a Vector</i>
-------------------------	------------------------------------

---

**Description**

`mat.or.vec` creates an `nr` by `nc` zero matrix if `nc` is greater than 1, and a zero vector of length `nr` if `nc` equals 1.

**Usage**

```
mat.or.vec(nr, nc)
```

**Arguments**

`nr`, `nc`            numbers of rows and columns.

**Examples**

```
mat.or.vec(3, 1)
mat.or.vec(3, 2)
```

---

<code>match</code>	<i>Value Matching</i>
--------------------	-----------------------

---

**Description**

`match` returns a vector of the positions of (first) matches of its first argument in its second.

`%in%` is a more intuitive interface as a binary operator, which returns a logical vector indicating if there is a match or not for its left operand.

**Usage**

```
match(x, table, nomatch = NA_integer_, incomparables = NULL)
```

```
x %in% table
```

**Arguments**

`x`                    vector or `NULL`: the values to be matched.

`table`                vector or `NULL`: the values to be matched against.

`nomatch`             the value to be returned in the case when no match is found. Note that it is coerced to `integer`.

`incomparables`      a vector of values that cannot be matched. Any value in `x` matching a value in this vector is assigned the `nomatch` value. For historical reasons, `FALSE` is equivalent to `NULL`.

## Details

`%in%` is currently defined as

```
"%in%" <- function(x, table) match(x, table, nomatch = 0) > 0
```

Factors, raw vectors and lists are converted to character vectors, and then `x` and `table` are coerced to a common type (the later of the two types in R's ordering, `logical < integer < numeric < complex < character`) before matching. If `incomparables` has positive length it is coerced to the common type.

Matching for lists is potentially very slow and best avoided except in simple cases.

Exactly what matches what is to some extent a matter of definition. For all types, `NA` matches `NA` and no other value. For real and complex values, `NaN` values are regarded as matching any other `NaN` value, but not matching `NA`.

## Value

A vector of the same length as `x`.

`match`: An integer vector giving the position in `table` of the first match if there is a match, otherwise `nomatch`.

If `x[i]` is found to equal `table[j]` then the value returned in the `i`-th position of the return value is `j`, for the smallest possible `j`. If no match is found, the value is `nomatch`.

`%in%`: A logical vector, indicating if a match was located for each element of `x`.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[pmatch](#) and [charmatch](#) for (*partial*) string matching, [match.arg](#), etc for function argument matching. [findInterval](#) similarly returns a vector of positions, but finds numbers within intervals, rather than exact matches.

[is.element](#) for an S-compatible equivalent of `%in%`.

## Examples

```
## The intersection of two sets can be defined via match():
## Simple version: intersect <- function(x, y) y[match(x, y, nomatch = 0)]
intersect # the R function in base, slightly more careful
intersect(1:10, 7:20)

1:10 %in% c(1, 3, 5, 9)
sstr <- c("c", "ab", "B", "bba", "c", "@", "bla", "a", "Ba", "%")
sstr[sstr %in% c(letters, LETTERS)]

"%w/o%" <- function(x, y) x[!x %in% y] #-- x without y
(1:10) %w/o% c(3, 7, 12)
```

---

 match.arg

*Argument Verification Using Partial Matching*


---

## Description

`match.arg` matches `arg` against a table of candidate values as specified by `choices`, where `NULL` means to take the first one.

## Usage

```
match.arg(arg, choices, several.ok = FALSE)
```

## Arguments

`arg` a character vector (of length one unless `several.ok` is `TRUE`) or `NULL`.  
`choices` a character vector of candidate values  
`several.ok` logical specifying if `arg` should be allowed to have more than one element.

## Details

In the one-argument form `match.arg(arg)`, the `choices` are obtained from a default setting for the formal argument `arg` of the function from which `match.arg` was called. (Since default argument matching will set `arg` to `choices`, this is allowed as an exception to the ‘length one unless `several.ok` is `TRUE`’ rule, and returns the first element.)

Matching is done using [pmatch](#), so `arg` may be abbreviated.

## Value

The unabbreviated version of the exact or unique partial match if there is one; otherwise, an error is signalled if `several.ok` is false, as per default. When `several.ok` is true and more than one element of `arg` has a match, all unabbreviated versions of matches are returned.

## See Also

[pmatch](#), [match.fun](#), [match.call](#).

## Examples

```
require(stats)
## Extends the example for 'switch'
center <- function(x, type = c("mean", "median", "trimmed")) {
  type <- match.arg(type)
  switch(type,
         mean = mean(x),
         median = median(x),
         trimmed = mean(x, trim = .1))
}
x <- rcauchy(10)
center(x, "t")      # Works
center(x, "med")    # Works
try(center(x, "m")) # Error
stopifnot(identical(center(x),      center(x, "mean")),
```

```
identical(center(x, NULL), center(x, "mean")) )

## Allowing more than one match:
match.arg(c("gauss", "rect", "ep"),
          c("gaussian", "epanechnikov", "rectangular", "triangular"),
          several.ok = TRUE)
```

---

match.call

*Argument Matching*

---

## Description

`match.call` returns a call in which all of the specified arguments are specified by their full names.

## Usage

```
match.call(definition = NULL, call = sys.call(sys.parent()),
           expand.dots = TRUE)
```

## Arguments

<code>definition</code>	a function, by default the function from which <code>match.call</code> is called. See details.
<code>call</code>	an unevaluated call to the function specified by <code>definition</code> , as generated by <a href="#">call</a> .
<code>expand.dots</code>	logical. Should arguments matching <code>...</code> in the call be included or left as a <code>...</code> argument?

## Details

‘function’ on this help page means an interpreted function (also known as a ‘closure’): `match.call` does not support primitive functions (where argument matching is normally positional).

`match.call` is most commonly used in two circumstances:

- To record the call for later re-use: for example most model-fitting functions record the call as element `call` of the list they return. Here the default `expand.dots = TRUE` is appropriate.
- To pass most of the call to another function, often `model.frame`. Here the common idiom is that `expand.dots = FALSE` is used, and the `...` element of the matched call is removed. An alternative is to explicitly select the arguments to be passed on, as is done in `lm`.

Calling `match.call` outside a function without specifying `definition` is an error.

## Value

An object of class `call`.

## References

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

**See Also**

`sys.call()` is similar, but does *not* expand the argument names; `call`, `pmatch`, `match.arg`, `match.fun`.

**Examples**

```
match.call(get, call("get", "abc", i = FALSE, p = 3))
## -> get(x = "abc", pos = 3, inherits = FALSE)
fun <- function(x, lower = 0, upper = 1) {
  structure((x - lower) / (upper - lower), CALL = match.call())
}
fun(4 * atan(1), u = pi)
```

---

match.fun

*Function Verification for “Function Variables”*

---

**Description**

When called inside functions that take a function as argument, extract the desired function object while avoiding undesired matching to objects of other types.

**Usage**

```
match.fun(FUN, descend = TRUE)
```

**Arguments**

FUN	item to match as function: a function, symbol or character string. See ‘Details’.
descend	logical; control whether to search past non-function objects.

**Details**

`match.fun` is not intended to be used at the top level since it will perform matching in the *parent* of the caller.

If FUN is a function, it is returned. If it is a symbol (for example, enclosed in backquotes) or a character vector of length one, it will be looked up using `get` in the environment of the parent of the caller. If it is of any other mode, it is attempted first to get the argument to the caller as a symbol (using `substitute` twice), and if that fails, an error is declared.

If `descend = TRUE`, `match.fun` will look past non-function objects with the given name; otherwise if FUN points to a non-function object then an error is generated.

This is used in base functions such as `apply`, `lapply`, `outer`, and `sweep`.

**Value**

A function matching FUN or an error is generated.

**Bugs**

The `descend` argument is a bit of misnomer and probably not actually needed by anything. It may go away in the future.

It is impossible to fully foolproof this. If one attaches a list or data frame containing a length-one character vector with the same name as a function, it may be used (although name spaces will help).

**Author(s)**

Peter Dalgaard and Robert Gentleman, based on an earlier version by Jonathan Rougier.

**See Also**

[match.arg](#), [get](#)

**Examples**

```
# Same as get("*"):
match.fun("*")
# Overwrite outer with a vector
outer <- 1:5
## Not run:
match.fun(outer, descend = FALSE) #-> Error: not a function

## End(Not run)
match.fun(outer) # finds it anyway
is.function(match.fun("outer")) # as well
```

---

 MathFun

*Miscellaneous Mathematical Functions*


---

**Description**

These functions compute miscellaneous mathematical functions. The naming follows the standard for computer languages such as C or Fortran.

**Usage**

```
abs(x)
sqrt(x)
```

**Arguments**

`x` a numeric or [complex](#) vector or array.

**Details**

These are [internal generic primitive](#) functions: methods can be defined for them individually or via the [Math](#) group generic. For complex arguments (and the default method), `z`, `abs(z) == Mod(z)` and `sqrt(z) == z^0.5`.

`abs(x)` returns an [integer](#) vector when `x` is `integer` or `logical`.

**S4 methods**

Both are S4 generic and members of the [Math](#) group generic.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.



**See Also**

[Arithmetic](#) for simple, [log](#) for logarithmic, [sin](#) for trigonometric, and [Special](#) for special mathematical functions.

'[plotmath](#)' for the use of `sqrt` in plot annotation.

**Examples**

```
require(stats) # for spline
require(graphics)
xx <- -9:9
plot(xx, sqrt(abs(xx)), col = "red")
lines(spline(xx, sqrt(abs(xx)), n=101), col = "pink")
```

---

matmult

*Matrix Multiplication*


---

**Description**

Multiplies two matrices, if they are conformable. If one argument is a vector, it will be promoted to either a row or column matrix to make the two arguments conformable. If both are vectors it will return the inner product (as a matrix).

**Usage**

```
x %*% y
```

**Arguments**

`x`, `y` numeric or complex matrices or vectors.

**Details**

When a vector is promoted to a matrix, its names are not promoted to row or column names, unlike [as.matrix](#).

This operator is S4 generic but not S3 generic. S4 methods need to be written for a function of two arguments named `x` and `y`.

**Value**

A double or complex matrix product. Use [drop](#) to remove dimensions which have only one level.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[matrix](#), [Arithmetic](#), [diag](#).

**Examples**

```
x <- 1:4
(z <- x %*% x)      # scalar ("inner") product (1 x 1 matrix)
drop(z)            # as scalar

y <- diag(x)
z <- matrix(1:12, ncol = 3, nrow = 4)
y %*% z
y %*% x
x %*% z
```

matrix

*Matrices***Description**

`matrix` creates a matrix from the given set of values.

`as.matrix` attempts to turn its argument into a matrix.

`is.matrix` tests if its argument is a (strict) matrix.

**Usage**

```
matrix(data = NA, nrow = 1, ncol = 1, byrow = FALSE,
        dimnames = NULL)

as.matrix(x, ...)
## S3 method for class 'data.frame':
as.matrix(x, rownames.force = NA, ...)

is.matrix(x)
```

**Arguments**

<code>data</code>	an optional data vector.
<code>nrow</code>	the desired number of rows.
<code>ncol</code>	the desired number of columns.
<code>byrow</code>	logical. If <code>FALSE</code> (the default) the matrix is filled by columns, otherwise the matrix is filled by rows.
<code>dimnames</code>	A <code>dimnames</code> attribute for the matrix: <code>NULL</code> or a list of length 2 giving the row and column names respectively. An empty list is treated as <code>NULL</code> , and a list of length one as row names. The list can be named, and the list names will be used as names for the dimensions.
<code>x</code>	an R object.
<code>...</code>	additional arguments to be passed to or from methods.
<code>rownames.force</code>	logical indicating if the resulting matrix should have character (rather than <code>NULL</code> ) <code>rownames</code> . The default, <code>NA</code> , uses <code>NULL</code> rownames if the data frame has ‘automatic’ row.names or for a zero-row data frame.

## Details

If one of `nrow` or `ncol` is not given, an attempt is made to infer it from the length of `data` and the other parameter. If neither is given, a one-column matrix is returned.

If there are too few elements in `data` to fill the matrix, then the elements in `data` are recycled. If `data` has length zero, NA of an appropriate type is used for atomic vectors (0 for raw vectors) and NULL for lists.

`is.matrix` returns TRUE if `x` is a vector and has a "dim" attribute of length 2) and FALSE otherwise. Note that a `data.frame` is **not** a matrix by this test. The function is generic: you can write methods to handle specific classes of objects, see [InternalMethods](#).

`as.matrix` is a generic function. The method for data frames will return a character matrix if there is any non-(numeric/logical/complex) column, applying `format` to non-character columns. Otherwise, the usual coercion hierarchy (logical < integer < double < complex) will be used, e.g., all-logical data frames will be coerced to a logical matrix, mixed logical-integer will give a integer matrix, etc.

When coercing a vector, it produces a one-column matrix, and promotes the names (if any) of the vector to the rownames of the matrix.

`is.matrix` is a [primitive](#) function.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[data.matrix](#), which attempts to convert to a numeric matrix.

A matrix is the special case of a two-dimensional [array](#).

## Examples

```
is.matrix(as.matrix(1:10))
!is.matrix(warpbreaks) # data.frame, NOT matrix!
warpbreaks[1:10,]
as.matrix(warpbreaks[1:10,]) #using as.matrix.data.frame(.) method

# Example of setting row and column names
mdat <- matrix(c(1,2,3, 11,12,13), nrow = 2, ncol=3, byrow=TRUE,
               dimnames = list(c("row1", "row2"),
                               c("C.1", "C.2", "C.3")))
mdat
```

---

maxCol

*Find Maximum Position in Matrix*

---

## Description

Find the maximum position for each row of a matrix, breaking ties at random.

## Usage

```
max.col(m, ties.method=c("random", "first", "last"))
```

## Arguments

`m` numerical matrix

`ties.method` a character string specifying how ties are handled, "random" by default; can be abbreviated; see 'Details'.

## Details

When `ties.method = "random"`, as per default, ties are broken at random. In this case, the determination of a tie assumes that the entries are probabilities: there is a relative tolerance of  $10^{-5}$ , relative to the largest (in magnitude, omitting infinity) entry in the row.

If `ties.method = "first"`, `max.col` returns the column number of the *first* of several maxima in every row, the same as `unname(apply(m, 1, which.max))`.

Correspondingly, `ties.method = "last"` returns the *last* of possibly several indices.

## Value

index of a maximal value for each row, an integer vector of length `nrow(m)`.

## References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. New York: Springer (4th ed).

## See Also

`which.max` for vectors.

## Examples

```
table(mc <- max.col(swiss)) # mostly "1" and "5", 5 x "2" and once "4"
swiss[unique(print(mr <- max.col(t(swiss))), ), ] # 3 33 45 45 33 6

set.seed(1) # reproducible example:
(mmm <- rbind(x = round(2*stats::runif(12)),
              y = round(5*stats::runif(12)),
              z = round(8*stats::runif(12))))

## Not run:
  [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
x    1    1    1    2    0    2    2    1    1    0    0    0
y    3    2    4    2    4    5    2    4    5    1    3    1
z    2    3    0    3    7    3    4    5    4    1    7    5

## End(Not run)
## column indices of all row maxima :
utils::str(lapply(1:3, function(i) which(mmm[i,] == max(mmm[i,]))))
max.col(mmm) ; max.col(mmm) # "random"
max.col(mmm, "first") # -> 4 6 5
max.col(mmm, "last") # -> 7 9 11
```

---

mean	<i>Arithmetic Mean</i>
------	------------------------

---

### Description

Generic function for the (trimmed) arithmetic mean.

### Usage

```
mean(x, ...)
```

```
## Default S3 method:
mean(x, trim = 0, na.rm = FALSE, ...)
```

### Arguments

<code>x</code>	An R object. Currently there are methods for numeric/logical vectors and <a href="#">date</a> , <a href="#">date-time</a> and <a href="#">time interval</a> objects, and for data frames all of whose columns have a method. Complex vectors are allowed for <code>trim = 0</code> , only.
<code>trim</code>	the fraction (0 to 0.5) of observations to be trimmed from each end of <code>x</code> before the mean is computed. Values of <code>trim</code> outside that range are taken as the nearest endpoint.
<code>na.rm</code>	a logical value indicating whether NA values should be stripped before the computation proceeds.
<code>...</code>	further arguments passed to or from other methods.

### Value

For a data frame, a named vector with the appropriate method being applied column by column.

If `trim` is zero (the default), the arithmetic mean of the values in `x` is computed, as a numeric or complex vector of length one. If `x` is not logical (coerced to numeric), numeric (including integer) or complex, `NA_real_` is returned, with a warning.

If `trim` is non-zero, a symmetrically trimmed mean is computed with a fraction of `trim` observations deleted from each end before the mean is computed.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[weighted.mean](#), [mean.POSIXct](#), [colMeans](#) for row and column means.

### Examples

```
x <- c(0:10, 50)
xm <- mean(x)
c(xm, mean(x, trim = 0.10))

mean(USArrests, trim = 0.2)
```

memCompress

*In-memory Compression and Decompression***Description**

In-memory compression or decompression for raw vectors.

**Usage**

```
memCompress(from, type = c("gzip", "bzip2", "xz", "none"))

memDecompress(from,
               type = c("unknown", "gzip", "bzip2", "xz", "none"),
               asChar = FALSE)
```

**Arguments**

from	A raw vector. For memCompress a character vector will be converted to a raw vector with character strings separated by "\n".
type	character string, the type of compression. May be abbreviated to a single letter, defaults to the first of the alternatives.
asChar	logical: should the result be converted to a character string?

**Details**

type = "none" passes the input through unchanged, but may be useful if type is a variable.

type = "unknown" attempts to detect the type of compression applied (if any): this will always succeed for bzip2 compression, and will succeed for other forms if there is a suitable header. It will auto-detect the 'magic' header ("\x1f\x8b") added to files by the gzip program (and to files written by [gzfile](#)), but memCompress does not add such a header.

bzip2 compression always adds a header ("BZh").

Compressing with type = "xz" is equivalent to compressing a file with xz -9e (including adding the 'magic' header): decompression should cope with the contents of any file compressed with xz version 4.999 and some versions of lzma. There are other versions, in particular 'raw' streams, that are not currently handled.

All the types of compression can expand the input: for "gzip" and "bzip" the maximum expansion is known and so memCompress can always allocate sufficient space. For "xz" it is possible (but extremely unlikely) that compression will fail if the output would have been too large.

**Value**

A raw vector or a character string (if asChar = TRUE).

**See Also**

[connections](#).

[http://en.wikipedia.org/wiki/Data\\_compression](http://en.wikipedia.org/wiki/Data_compression) for background on data compression, <http://zlib.net/>, <http://en.wikipedia.org/wiki/Gzip>, <http://www.bzip.org/>, <http://en.wikipedia.org/wiki/Bzip2>, <http://tukaani.org/xz/> and <http://en.wikipedia.org/wiki/Xz> for references about the particular schemes used.

**Examples**

```

txt <- readLines(file.path(R.home("doc"), "COPYING"))
sum(nchar(txt))
txt.gz <- memCompress(txt, "g")
length(txt.gz)
txt2 <- strsplit(memDecompress(txt.gz, "g", asChar = TRUE), "\n")[[1]]
stopifnot(identical(txt, txt2))
txt.bz2 <- memCompress(txt, "b")
length(txt.bz2)
## can auto-detect bzip2:
txt3 <- strsplit(memDecompress(txt.bz2, asChar = TRUE), "\n")[[1]]
stopifnot(identical(txt, txt3))

## xz compression is only worthwhile for large objects
txt.xz <- memCompress(txt, "x")
length(txt.xz)
txt3 <- strsplit(memDecompress(txt.xz, asChar = TRUE), "\n")[[1]]
stopifnot(identical(txt, txt3))

```

---

Memory

*Memory Available for Data Storage*


---

**Description**

Use command line options to control the memory available for R.

**Usage**

```

R --min-vsize=v1 --max-vsize=vu --min-nsz=nl --max-nsz=nu --max-ppsize=N

mem.limits(nsize = NA, vsize = NA)

```

**Arguments**

v1, vu, vsize	Heap memory in bytes.
nl, nu, nsize	Number of cons cells.
N	Number of nested PROTECT calls..

**Details**

R has a variable-sized workspace. There is much less need to set memory options than prior to R 1.2.0, and most users will never need to set these. They are provided both as a way to control the overall memory usage (which can also be done by operating-system facilities such as `limit` on Unix and by using the command-line option ‘`--max-mem-size`’ on Windows), and since setting larger values of the minima will make R slightly more efficient on large tasks.

To understand the options, one needs to know that R maintains separate areas for fixed and variable sized objects. The first of these is allocated as an array of *cons cells* (Lisp programmers will know what they are, others may think of them as the building blocks of the language itself, parse trees, etc.), and the second are thrown on a *heap* of ‘Vcells’ of 8 bytes each. Effectively, the inputs `v1` and `vu` are rounded up to the next multiple of 8.

Each cons cell occupies 28 bytes on a 32-bit build of R, (usually) 56 bytes on a 64-bit build.

The ‘`--nsize`’ options can be used to specify the number of cons cells and the ‘`--vsize`’ options specify the size of the vector heap in bytes. Both options must be integers or integers followed by G, M, K, or k meaning *Giga* ( $2^{30} = 1073741824$ ) *Mega* ( $2^{20} = 1048576$ ), (computer) *Kilo* ( $2^{10} = 1024$ ), or regular *kilo* (1000).

The ‘`--min-`’ options set the minimal sizes for the number of cons cells and for the vector heap. These values are also the initial values, but thereafter R will grow or shrink the areas depending on usage, but never exceeding the limits set by the ‘`--max-`’ options nor decreasing below the initial values.

The default values are currently minima of 350k cons cells, 6Mb of vector heap and no maxima (other than machine resources). The maxima can be changed during an R session by calling `mem.limits`. (If this is called with the default values, it reports the current settings.)

You can find out the current memory consumption (the heap and cons cells used as numbers and megabytes) by typing `gc()` at the R prompt. Note that following `gcinfo(TRUE)`, automatic garbage collection always prints memory use statistics. Maxima will never be reduced below the current values for triggering garbage collection, and attempts to do so will be silently ignored.

The command-line option ‘`--max-ppsize`’ controls the maximum size of the pointer protection stack. This defaults to 50000, but can be increased to allow deep recursion or large and complicated calculations to be done. *Note* that parts of the garbage collection process goes through the full reserved pointer protection stack and hence becomes slower when the size is increased. Currently the maximum value accepted is 500000.

## Value

`mem.limits()` returns an integer vector giving the current settings of the maxima, possibly NA.

## See Also

*An Introduction to R* for more command-line options

`Memory-limits` for the design limitations.

`gc` for information on the garbage collector and total memory usage, `object.size(a)` for the (approximate) size of R object a. `memory.profile` for profiling the usage of cons cells.

## Examples

```
# Start R with 10MB of heap memory and 500k cons cells, limit to
# 100Mb and 1M cells
## Not run:
## Unix
R --min-vsize=10M --max-vsize=100M --min-nsize=500k --max-nsize=1M

## End(Not run)
```

## Description

R holds objects it is using in virtual memory. This help file documents the current design limitations on large objects: these differ between 32-bit and 64-bit builds of R.



## Details

Currently R runs on 32- and 64-bit operating systems, and most 64-bit OSES (including Linux, Solaris, Windows and Mac OS X) can run either 32- or 64-bit builds of R. The memory limits depends mainly on the build, but for a 32-bit build of R on Windows they also depend on the underlying OS version.

R holds all objects in memory, and there are limits based on the amount of memory that can be used by all objects:

- There may be limits on the size of the heap and the number of cons cells allowed – see [Memory](#) – but these are usually not imposed.
- There is a limit on the (user) address space of a single process such as the R executable. This is system-specific, and can depend on the executable.
- The environment may impose limitations on the resources available to a single process: Windows' versions of R do so directly.

Error messages beginning `cannot allocate vector of size` indicate a failure to obtain memory, either because the size exceeded the address-space limit for a process or, more likely, because the system was unable to provide the memory. Note that on a 32-bit build there may well be enough free memory available, but not a large enough contiguous block of address space into which to map it.

There are also limits on individual objects. On all builds of R, the maximum length (number of elements) of a vector is  $2^{31} - 1 \approx 2 \cdot 10^9$ , as lengths are stored as signed integers. In addition, the storage space cannot exceed the address limit, and if you try to exceed that limit, the error message begins `cannot allocate vector of length`. The number of characters in a character string is in theory only limited by the address space.

## Unix

The address-space limit is system-specific: 32-bit OSES imposes a limit of no more than 4Gb: it is often 3Gb. Running 32-bit executables on a 64-bit OS will have similar limits: 64-bit executables will have an essentially infinite system-specific limit (e.g. 128Tb for Linux on x86\_64 cpus).

See the OS/shell's help on commands such as `limit` or `ulimit` for how to impose limitations on the resources available to a single process. For example a `bash` user could use

```
ulimit -t 600 -m 2000000
```

whereas a `csh` user might use

```
limit cputime 10m
limit memoryuse 2048m
```

to limit a process to 10 minutes of CPU time and (around) 2Gb of memory.

## Windows

The address-space limit is 2Gb under 32-bit Windows unless the OS's default has been changed to allow more (up to 3Gb). See <http://www.microsoft.com/whdc/system/platform/server/PAE/PAEmem.aspx> and [http://msdn.microsoft.com/en-us/library/bb613473\(VS.85\).aspx](http://msdn.microsoft.com/en-us/library/bb613473(VS.85).aspx). Under most 64-bit versions of Windows the limit for a 32-bit build of R is 4Gb: for the oldest ones it is 2Gb. The limit for a 64-bit build of R (imposed by the OS) is 8Tb.

It is not normally possible to allocate as much as 2Gb to a single vector in a 32-bit build of R even on 64-bit Windows because of preallocations by Windows in the middle of the address space.

Under Windows, R imposes limits on the total memory allocation available to a single session as the OS provides no way to do so: see [memory.size](#) and [memory.limit](#).

### See Also

[object.size](#) (a) for the (approximate) size of R object a.

---

memory.profile	<i>Profile the Usage of Cons Cells</i>
----------------	--

---

### Description

Lists the usage of the cons cells by SEXPREC type.

### Usage

```
memory.profile()
```

### Details

The current types and their uses are listed in the include file 'Rinternals.h'.

### Value

A vector of counts, named by the types. See [typeof](#) for an explanation of types.

### See Also

[gc](#) for the overall usage of cons cells. [Rprofmem](#) and [tracemem](#) allow memory profiling of specific code or objects, but need to be enabled at compile time.

### Examples

```
memory.profile()
```

---

merge	<i>Merge Two Data Frames</i>
-------	------------------------------

---

### Description

Merge two data frames by common columns or row names, or do other versions of database *join* operations.

**Usage**

```
merge(x, y, ...)

## Default S3 method:
merge(x, y, ...)

## S3 method for class 'data.frame':
merge(x, y, by = intersect(names(x), names(y)),
      by.x = by, by.y = by, all = FALSE, all.x = all, all.y = all,
      sort = TRUE, suffixes = c(".x", ".y"), incomparables = NULL, ...)
```

**Arguments**

`x`, `y` data frames, or objects to be coerced to one.

`by`, `by.x`, `by.y` specifications of the common columns. See ‘Details’.

`all` logical; `all = L` is shorthand for `all.x = L` and `all.y = L`.

`all.x` logical; if `TRUE`, then extra rows will be added to the output, one for each row in `x` that has no matching row in `y`. These rows will have NAs in those columns that are usually filled with values from `y`. The default is `FALSE`, so that only rows with data from both `x` and `y` are included in the output.

`all.y` logical; analogous to `all.x` above.

`sort` logical. Should the results be sorted on the `by` columns?

`suffixes` character(2) specifying the suffixes to be used for making non-`by` names () unique.

`incomparables` values which cannot be matched. See [match](#).

`...` arguments to be passed to or from methods.

**Details**

By default the data frames are merged on the columns with names they both have, but separate specifications of the columns can be given by `by.x` and `by.y`. Columns can be specified by name, number or by a logical vector: the name `"row.names"` or the number 0 specifies the row names. The rows in the two data frames that match on the specified columns are extracted, and joined together. If there is more than one match, all possible matches contribute one row each. For the precise meaning of ‘match’, see [match](#).

If `by` or both `by.x` and `by.y` are of length 0 (a length zero vector or `NULL`), the result, `r`, is the *Cartesian product* of `x` and `y`, i.e.,  $\text{dim}(r) = c(\text{nrow}(x) * \text{nrow}(y), \text{ncol}(x) + \text{ncol}(y))$ .

If `all.x` is true, all the non matching cases of `x` are appended to the result as well, with NA filled in the corresponding columns of `y`; analogously for `all.y`.

If the remaining columns in the data frames have any common names, these have `suffixes` (`".x"` and `".y"` by default) appended to make the names of the result unique.

The complexity of the algorithm used is proportional to the length of the answer.

In SQL database terminology, the default value of `all = FALSE` gives a *natural join*, a special case of an *inner join*. Specifying `all.x = TRUE` gives a *left (outer) join*, `all.y = TRUE` a *right (outer) join*, and both (`all=TRUE`) a *(full) outer join*. DBMSes do not match `NULL` records, equivalent to `incomparables = NA` in R.

**Value**

A data frame. The rows are by default lexicographically sorted on the common columns, but for `sort = FALSE` are in an unspecified order. The columns are the common columns followed by the remaining columns in `x` and then those in `y`. If the matching involved row names, an extra character column called `Row.names` is added at the left, and in all cases the result has ‘automatic’ row names.

**See Also**

[data.frame](#), [by](#), [cbind](#)

**Examples**

```
## use character columns of names to get sensible sort order
authors <- data.frame(
  surname = I(c("Tukey", "Venables", "Tierney", "Ripley", "McNeil")),
  nationality = c("US", "Australia", "US", "UK", "Australia"),
  deceased = c("yes", rep("no", 4)))
books <- data.frame(
  name = I(c("Tukey", "Venables", "Tierney",
            "Ripley", "Ripley", "McNeil", "R Core")),
  title = c("Exploratory Data Analysis",
            "Modern Applied Statistics ...",
            "LISP-STAT",
            "Spatial Statistics", "Stochastic Simulation",
            "Interactive Data Analysis",
            "An Introduction to R"),
  other.author = c(NA, "Ripley", NA, NA, NA, NA,
                  "Venables & Smith"))

(m1 <- merge(authors, books, by.x = "surname", by.y = "name"))
(m2 <- merge(books, authors, by.x = "name", by.y = "surname"))
stopifnot(as.character(m1[,1]) == as.character(m2[,1]),
          all.equal(m1[, -1], m2[, -1][ names(m1)[-1] ]),
          dim(merge(m1, m2, by = integer(0))) == c(36, 10))

## "R core" is missing from authors and appears only here :
merge(authors, books, by.x = "surname", by.y = "name", all = TRUE)

## example of using 'incomparables'
x <- data.frame(k1=c(NA,NA,3,4,5), k2=c(1,NA,NA,4,5), data=1:5)
y <- data.frame(k1=c(NA,2,NA,4,5), k2=c(NA,NA,3,4,5), data=1:5)
merge(x, y, by=c("k1","k2")) # NA's match
merge(x, y, by=c("k1","k2"), incomparables=NA)
merge(x, y, by="k1") # NA's match, so 6 rows
merge(x, y, by="k2", incomparables=NA) # 2 rows
```

---

message

*Diagnostic Messages*

---

**Description**

Generate a diagnostic message from its arguments.

## Usage

```

message(..., domain = NULL, appendLF = TRUE)
suppressMessages(expr)

packageStartupMessage(..., domain = NULL, appendLF = TRUE)
suppressPackageStartupMessages(expr)

.makeMessage(..., domain = NULL, appendLF = FALSE)

```

## Arguments

<code>...</code>	zero or more objects which can be coerced to character (and which are pasted together with no separator) or (for <code>message</code> only) a single condition object.
<code>domain</code>	see <a href="#">gettext</a> . If NA, messages will not be translated.
<code>appendLF</code>	logical: should messages given as a character string have a newline appended?
<code>expr</code>	expression to evaluate.

## Details

`message` is used for generating ‘simple’ diagnostic messages which are neither warnings nor errors, but nevertheless represented as conditions. Unlike warnings and errors, a final newline is regarded as part of the message, and is optional. The default handler sends the message to the `stderr()` connection.

If a condition object is supplied to `message` it should be the only argument, and further arguments will be ignored, with a warning.

While the message is being processed, a `muffleMessage` restart is available.

`suppressMessages` evaluates its expression in a context that ignores all ‘simple’ diagnostic messages.

`packageStartupMessage` is a variant whose messages can be suppressed separately by `suppressPackageStartupMessages`. (They are still messages, so can be suppressed by `suppressMessages`.)

`.makeMessage` is a utility used by `message`, `warning` and `stop` to generate a text message from the `...` arguments by possible translation (see [gettext](#)) and concatenation (with no separator).

## See Also

[warning](#) and [stop](#) for generating warnings and errors; [conditions](#) for condition handling and recovery.

[gettext](#) for the mechanisms for the automated translation of text.

## Examples

```

message("ABC", "DEF")
suppressMessages(message("ABC"))

testit <- function() {
  message("testing package startup messages")
  packageStartupMessage("initializing ...", appendLF = FALSE)
  Sys.sleep(1)
  packageStartupMessage(" done")
}

```

```
}  
  
testit()  
suppressPackageStartupMessages(testit())  
suppressMessages(testit())
```

---

missing

*Does a Formal Argument have a Value?*

---

## Description

`missing` can be used to test whether a value was specified as an argument to a function.

## Usage

```
missing(x)
```

## Arguments

`x` a formal argument.

## Details

`missing(x)` is only reliable if `x` has not been altered since entering the function: in particular it will *always* be false after `x <- match.arg(x)`.

The example shows how a plotting function can be written to work with either a pair of vectors giving `x` and `y` coordinates of points to be plotted or a single vector giving `y` values to be plotted against their indices.

Currently `missing` can only be used in the immediate body of the function that defines the argument, not in the body of a nested function or a `local` call. This may change in the future.

This is a ‘special’ [primitive](#) function: it must not evaluate its argument.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

## See Also

[substitute](#) for argument expression; [NA](#) for missing values in data.

## Examples

```
myplot <- function(x,y) {  
  if(missing(y)) {  
    y <- x  
    x <- 1:length(y)  
  }  
  plot(x,y)  
}
```

mode

*The (Storage) Mode of an Object***Description**

Get or set the type or storage mode of an object.

**Usage**

```
mode(x)
mode(x) <- value
storage.mode(x)
storage.mode(x) <- value
```

**Arguments**

<code>x</code>	any R object.
<code>value</code>	a character string giving the desired mode or ‘storage mode’ (type) of the object.

**Details**

Both `mode` and `storage.mode` return a character string giving the (storage) mode of the object — often the same — both relying on the output of `typeof(x)`, see the example below.

`mode(x) <- "newmode"` changes the mode of object `x` to `newmode`. This is only supported if there is an appropriate `as.newmode` function, for example "logical", "integer", "double", "complex", "raw", "character", "list", "expression", "name", "symbol" and "function". Attributes are preserved (but see below).

`storage.mode(x) <- "newmode"` is a more efficient primitive version of `mode<-`, which works for "newmode" which is one of the internal types (see `typeof`), but not for "single". Attributes are preserved.

As storage mode "single" is only a pseudo-mode in R, it will not be reported by `mode` or `storage.mode`: use `attr(object, "Csingle")` to examine this. However, `mode<-` can be used to set the mode to "single", which sets the real mode to "double" and the "Csingle" attribute to TRUE. Setting any other mode will remove this attribute.

Note (in the examples below) that some `calls` have mode " (" which is S compatible.

**Mode names**

Modes have the same set of names as types (see `typeof`) except that

- types "integer" and "double" are returned as "numeric".
- types "special" and "builtin" are returned as "function".
- type "symbol" is called mode "name".
- type "language" is returned as " (" or "call".

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[typeof](#) for the R-internal ‘mode’, [attributes](#).

**Examples**

```
require(stats)

sapply(options(),mode)

cex3 <- c("NULL", "1", "1:1", "1i", "list(1)", "data.frame(x=1)",
  "pairlist(pi)", "c", "lm", "formals(lm)[[1]]", "formals(lm)[[2]]",
  "y~x", "expression(1)[[1]]", "(y~x)[[1]]",
  "expression(x <- pi)[[1]][[1]]")
lex3 <- sapply(cex3, function(x) eval(parse(text=x)))
mex3 <- t(sapply(lex3,
  function(x) c(typeof(x), storage.mode(x), mode(x))))
dimnames(mex3) <- list(cex3, c("typeof(.)", "storage.mode(.)", "mode(.)))
mex3

## This also makes a local copy of 'pi':
storage.mode(pi) <- "complex"
storage.mode(pi)
rm(pi)
```

---

NA

*Not Available / “Missing” Values*


---

**Description**

NA is a logical constant of length 1 which contains a missing value indicator. NA can be freely coerced to any other vector type except raw. There are also constants `NA_integer_`, `NA_real_`, `NA_complex_` and `NA_character_` of the other atomic vector types which support missing values: all of these are [reserved](#) words in the R language.

The generic function `is.na` indicates which elements are missing.

The generic function `is.na<-` sets elements to NA.

**Usage**

```
NA
is.na(x)
## S3 method for class 'data.frame':
is.na(x)

is.na(x) <- value
```

**Arguments**

`x` an R object to be tested: the default method handles atomic vectors, lists and pairlists.

`value` a suitable index vector for use with `x`.



## Details

The NA of character type is distinct from the string "NA". Programmers who need to specify an explicit string NA should use `NA_character_` rather than "NA", or set elements to NA using `is.na<-`.

`is.na(x)` works elementwise when `x` is a `list`. It is generic: you can write methods to handle specific classes of objects, see [InternalMethods](#). A complex value is regarded as NA if either its real or imaginary part is NA or NaN.

Function `is.na<-` may provide a safer way to set missingness. It behaves differently for factors, for example.

## Value

The default method for `is.na` applied to an atomic vector returns a logical vector of the same length as its argument `x`, containing TRUE for those elements marked NA or, for numeric or complex vectors, NaN (!) and FALSE otherwise. `dim`, `dimnames` and `names` attributes are preserved.

The default method also works for lists and pairlists: the result for an element is false unless that element is a length-one atomic vector and the single element of that vector is regarded as NA or NaN.

The method `is.na.data.frame` returns a logical matrix with the same dimensions as the data frame, and with `dimnames` taken from the row and column names of the data frame.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

## See Also

NaN, `is.nan`, etc., and the utility function `complete.cases`.

`na.action`, `na.omit`, `na.fail` on how methods can be tuned to deal with missing values.

## Examples

```
is.na(c(1, NA))           #> FALSE TRUE
is.na(paste(c(1, NA)))   #> FALSE FALSE

(xx <- c(0:4))
is.na(xx) <- c(2, 4)
xx                       #> 0 NA 2 NA 4
```

---

name

*Names and Symbols*

---

## Description

A ‘name’ (also known as a ‘symbol’) is a way to refer to R objects by name (rather than the value of the object, if any, bound to that name).

`as.name` and `as.symbol` are identical: they attempt to coerce the argument to a name.

`is.symbol` and the identical `is.name` return TRUE or FALSE depending on whether the argument is a name or not.

## Usage

```
as.symbol(x)
is.symbol(x)

as.name(x)
is.name(x)
```

## Arguments

`x` object to be coerced or tested.

## Details

`as.name` first coerces its argument internally to a character vector (so methods for `as.character` are not used). It then takes the first element and provided it is not "", returns a symbol of that name (and if the element is `NA_character_`, the name is `'NA'`).

`as.name` is implemented as `as.vector(x, "symbol")`, and hence will dispatch methods for the generic function `as.vector`.

`is.name` and `is.symbol` are [primitive](#) functions.

## Value

For `as.name` and `as.symbol`, an R object of type "symbol" (see [typeof](#)).

For `is.name` and `is.symbol`, a length-one logical vector with value TRUE or FALSE.

## Note

The term 'symbol' is from the LISP background of R, whereas 'name' has been the standard S term for this.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[call](#), [is.language](#). For the internal object mode, [typeof](#).

[plotmath](#) for another use of 'symbol'.

## Examples

```
an <- as.name("arrg")
is.name(an) # TRUE
mode(an)   # name
typeof(an) # symbol
```

names

*The Names of an Object***Description**

Functions to get or set the names of an object.

**Usage**

```
names(x)
names(x) <- value
```

**Arguments**

`x` an R object.  
`value` a character vector of up to the same length as `x`, or `NULL`.

**Details**

`names` is a generic accessor function, and `names<-` is a generic replacement function. The default methods get and set the "names" attribute of a vector (including a list) or pairlist.

If `value` is shorter than `x`, it is extended by character `NA`s to the length of `x`.

It is possible to update just part of the names attribute via the general rules: see the examples. This works because the expression there is evaluated as `z <- "names<-"(z, "[<-"(names(z), 3, "c2"))`.

The name "" is special: it is used to indicate that there is no name associated with an element of a (atomic or generic) vector. Subscripting by "" will match nothing (not even elements which have no name).

A name can be character `NA`, but such a name will never be matched and is likely to lead to confusion.

Both are [primitive](#) functions.

**Value**

For `names`, `NULL` or a character vector of the same length as `x`. (`NULL` is given if the object has no names, including for objects of types which cannot have names.)

For `names<-`, the updated object. (Note that the value of `names(x) <- value` is that of the assignment, `value`, not the return value from the left-hand side.)

**Note**

For vectors, the names are one of the [attributes](#) with restrictions on the possible values. For pairlists, the names are the tags and converted to and from a character vector.

For a one-dimensional array the `names` attribute really is `dimnames[[1]]`.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## Examples

```
# print the names attribute of the islands data set
names(islands)

# remove the names attribute
names(islands) <- NULL
islands
rm(islands) # remove the copy made

z <- list(a=1, b="c", c=1:3)
names(z)
# change just the name of the third element.
names(z)[3] <- "c2"
z

z <- 1:3
names(z)
## assign just one name
names(z)[2] <- "b"
z
```

---

nargs

*The Number of Arguments to a Function*

---

## Description

When used inside a function body, `nargs` returns the number of arguments supplied to that function, *including* positional arguments left blank.

## Usage

```
nargs()
```

## Details

The count includes empty (missing) arguments, so that `foo(x, , z)` will be considered to have three arguments (see ‘Examples’). This can occur in rather indirect ways, so for example `x[]` might dispatch a call to ``[.some_method`(x, )` which is considered to have two arguments.

This is a [primitive](#) function.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[args](#), [formals](#) and [sys.call](#).

**Examples**

```
tst <- function(a, b = 3, ...) {nargs()}
tst() # 0
tst(clicketyclack) # 1 (even non-existing)
tst(c1, a2, rr3) # 3

foo <- function(x, y, z, w) {
  cat("call was", deparse(match.call()), "\n")
  nargs()
}
foo() # 0
foo(, , 3) # 3
foo(z=3) # 1, even though this is the same call

nargs()# not really meaningful
```

---

nchar

---

*Count the Number of Characters (or Bytes or Width)*


---

**Description**

nchar takes a character vector as an argument and returns a vector whose elements contain the sizes of the corresponding elements of x.

nzchar is a fast way to find out if elements of a character vector are non-empty strings.

**Usage**

```
nchar(x, type = "chars", allowNA = FALSE)
```

```
nzchar(x)
```

**Arguments**

x	character vector, or a vector to be coerced to a character vector.
type	character string: partial matching to one of c("bytes", "chars", "width"). See 'Details'.
allowNA	logical: show NA be returned for invalid multibyte strings (rather than throwing an error)?

**Details**

The 'size' of a character string can be measured in one of three ways

**bytes** The number of bytes needed to store the string (plus in C a final terminator which is not counted).

**chars** The number of human-readable characters.

**width** The number of columns cat will use to print the string in a monospaced font. The same as chars if this cannot be calculated.

These will often be the same, and almost always will be in single-byte locales. There will be differences between the first two with multibyte character sequences, e.g. in UTF-8 locales.

The internal equivalent of the default method of `as.character` is performed on `x` (so there is no method dispatch). If you want to operate on non-vector objects passing them through `deparse` first will be required.

### Value

For `nchar`, an integer vector giving the sizes of each element, currently always 2 for missing values (for NA).

If `allowNA = TRUE` and an element is invalid in a multi-byte character set such as UTF-8, its number of characters and the width will be NA. Otherwise the number of characters will be non-negative, so `!is.na(nchar(x, "chars", TRUE))` is a test of validity.

Names, dims and dimnames are copied from the input.

For `nzchar`, a logical vector of the same length as `x`, true if and only if the element has non-zero length.

### Note

This does **not** by default give the number of characters that will be used to `print()` the string. Use `encodeString` to find the characters used to print the string. Where character strings have been marked as UTF-8, the number of characters and widths will be computed in UTF-8, even though printing may use escapes such as `<U+2642>` in a non-UTF-8 locale.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

`strwidth` giving width of strings for plotting; `paste`, `substr`, `strsplit`

### Examples

```
x <- c("asfef", "qwerty", "yuiop[", "b", "stuff.blah.yech")
nchar(x)
# 5 6 6 1 15

nchar(deparse(mean))
# 18 17
```

---

nlevels

*The Number of Levels of a Factor*


---

### Description

Return the number of levels which its argument has.

### Usage

```
nlevels(x)
```

**Arguments**

`x` an object, usually a factor.

**Details**

This is usually applied to a factor, but other objects can have levels.

The actual factor levels (if they exist) can be obtained with the `levels` function.

**Value**

The length of `levels(x)`, which is zero if `x` has no levels.

**See Also**

`levels`, `factor`.

**Examples**

```
nlevels(gl(3, 7)) # = 3
```

---

noquote

*Class for “no quote” Printing of Character Strings*

---

**Description**

Print character strings without quotes.

**Usage**

```
noquote(obj)

## S3 method for class 'noquote':
print(x, ...)

## S3 method for class 'noquote':
c(..., recursive = FALSE)
```

**Arguments**

`obj` any R object, typically a vector of `character` strings.  
`x` an object of class "noquote".  
`...` further options passed to next methods, such as `print`.  
`recursive` for compatibility with the generic `c` function.

**Details**

`noquote` returns its argument as an object of class "noquote". There is a method for `c()` and subscript method (`"[.noquote"`) which ensures that the class is not lost by subsetting. The `print` method (`print.noquote`) prints character strings *without* quotes (`"..."`).

These functions exist both as utilities and as an example of using (S3) `class` and object orientation.

**Author(s)**

Martin Maechler <maechler@stat.math.ethz.ch>

**See Also**

[methods](#), [class](#), [print](#).

**Examples**

```
letters
nql <- noquote(letters)
nql
nql[1:4] <- "oh"
nql[1:12]

cmp.logical <- function(log.v)
{
  ## Purpose: compact printing of logicals
  log.v <- as.logical(log.v)
  noquote(if(length(log.v)==0) "()" else c(".", "|")[1+log.v])
}
cmp.logical(stats::runif(20) > 0.8)
```

---

norm

*Compute the Norm of a Matrix*

---

**Description**

Computes a matrix norm of  $x$  using Lapack. The norm can be the one norm, the infinity norm, the Frobenius norm, or the maximum modulus among elements of a matrix, as determined by the value of `type`.

**Usage**

```
norm(x, type = c("O", "I", "F", "M"))
```

**Arguments**

<code>x</code>	numeric matrix; note that packages such as <b>Matrix</b> define more <code>norm()</code> methods.
<code>type</code>	character string, specifying the <i>type</i> of matrix norm to be computed. A character indicating the type of norm desired. <b>"O"</b> , <b>"o"</b> or <b>"1"</b> specifies the <b>one</b> norm, (maximum absolute column sum); <b>"I"</b> or <b>"i"</b> specifies the <b>infinity</b> norm (maximum absolute row sum); <b>"F"</b> or <b>"f"</b> specifies the <b>Frobenius</b> norm (the Euclidean norm of $x$ treated as if it were a vector); and <b>"M"</b> or <b>"m"</b> specifies the <b>maximum modulus</b> of all the elements in $x$ . The default is "O". Only the first character of <code>type[1]</code> is used.



**Details**

The **base** method of `norm()` calls the Lapack function `dlange`.

Note that the 1-, Inf- and "M" norm is faster to calculate than the Frobenius one.

**Value**

The matrix norm, a non-negative number.

**References**

Anderson, E., et al. (1994). *LAPACK User's Guide*, 2nd edition, SIAM, Philadelphia.

**See Also**

[rcond](#) for the (reciprocal) condition number.

**Examples**

```
(x1 <- cbind(1,1:10))
norm(x1)
norm(x1, "I")
norm(x1, "M")
stopifnot(all.equal(norm(x1, "F"),
                    sqrt(sum(x1^2))))

hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, "+") }
h9 <- hilbert(9)
## all 4 types of norm:
(nTyp <- eval(formals(base::norm)$type))
sapply(nTyp, norm, x=h9)
```

---

NotYet

*Not Yet Implemented Functions and Unused Arguments*

---

**Description**

In order to pinpoint missing functionality, the R core team uses these functions for missing R functions and not yet used arguments of existing R functions (which are typically there for compatibility purposes).

You are very welcome to contribute your code ...

**Usage**

```
.NotYetImplemented()
.NotYetUsed(arg, error = TRUE)
```

**Arguments**

`arg` an argument of a function that is not yet used.  
`error` a logical. If TRUE, an error is signalled; if FALSE; only a warning is given.

**See Also**

the contrary, [Deprecated](#) and [Defunct](#) for outdated code.

**Examples**

```
require(graphics)
require(stats)
plot.mlm          # to see how the "NotYetImplemented"
                  # reference is made automagically
try(plot.mlm())

barplot(1:5, inside = TRUE) # 'inside' is not yet used
```

---

nrow

*The Number of Rows/Columns of an Array*


---

**Description**

`nrow` and `ncol` return the number of rows or columns present in `x`. `NCOL` and `NROW` do the same treating a vector as 1-column matrix.

**Usage**

```
nrow(x)
ncol(x)
NCOL(x)
NROW(x)
```

**Arguments**

`x` a vector, array or data frame

**Value**

an [integer](#) of length 1 or `NULL`.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole (`ncol` and `nrow`.)

**See Also**

[dim](#) which returns *all* dimensions; [array](#), [matrix](#).

**Examples**

```
ma <- matrix(1:12, 3, 4)
nrow(ma) # 3
ncol(ma) # 4

ncol(array(1:24, dim = 2:4)) # 3, the second dimension
NCOL(1:12) # 1
NROW(1:12) # 12
```

---

`ns-dblcolon`*Double Colon and Triple Colon Operators*

---

## Description

Accessing exported and internal variables in a name space, or variables in an attached package.

## Usage

```
pkg::name
pkg:::name
```

## Arguments

<code>pkg</code>	package name: symbol or literal character string.
<code>name</code>	variable name: symbol or literal character string.

## Details

For a package with a name space, `pkg::name` returns the value of the exported variable `name` in name space `pkg`, whereas `pkg:::name` returns the value of the internal variable `name`. The name space will be loaded if it was not loaded before the call, but the package will not be attached to the search path.

If the package `pkg` does not have a name space but is on the search path then `pkg::name` returns the value of `name` in the package environment. Thus `pkg::name` has the same effect for attached packages whether or not they have a name space.

Specifying a variable that does not exist is an error, as is specifying a package that does not exist or does not have a name space and is not on the search path.

Note that it is typically a design mistake to use `:::` in your code since the corresponding object has probably been kept internal for a good reason. Consider contacting the package maintainer if you feel the need to access the object for anything but mere inspection.

## See Also

[get](#) to access an object masked by another of the same name.

## Examples

```
base::log
base::"+"

## Beware -- use ':::' at your own risk! (see "Details")
stats:::coef.default
```

---

 ns-hooks

*Hooks for Name Space events*


---

## Description

Packages with name spaces can supply functions to be called when loaded, attached or unloaded.

## Usage

```
.onLoad(libname, pkgname)
.onAttach(libname, pkgname)
.onUnload(libpath)
```

## Arguments

libname	a character string giving the library directory where the package defining the namespace was found.
pkgname	a character string giving the name of the package.
libpath	a character string giving the complete path to the package.

## Details

These functions apply only to packages with name spaces.

After loading, `loadNamespace` looks for a hook function named `.onLoad` and runs it before sealing the namespace and processing exports.

If a name space is unloaded (via `unloadNamespace`), a hook function `.onUnload` is run before final unloading.

Note that the code in `.onLoad` and `.onUnload` is run without the package being on the search path, but (unless circumvented) lexical scope will make objects in the namespace and its imports visible. (Do not use the double colon operator in `.onLoad` as exports have not been processed at the point it is run.)

When the package is attached (via `library`), the hook function `.onAttach` is looked for and if found is called after the exported functions are attached and before the package environment is sealed. This is less likely to be useful than `.onLoad`, which should be seen as the analogue of `.First.lib` (which is only used for packages without a name space).

`.onLoad`, `.onUnload` and `.onAttach` are looked for as internal variables in the name space and should not be exported.

If a function `.Last.lib` is visible in the package, it will be called when the package is detached: this does need to be exported.

Anything needed for the functioning of the name space should be handled at load/unload times by the `.onLoad` and `.onUnload` hooks. For example, DLLs can be loaded (unless done by a `useDynLib` directive in the 'NAMESPACE' file) and initialized in `.onLoad` and unloaded in `.onUnload`. Use `.onAttach` only for actions that are needed only when the package becomes visible to the user, for example a start-up message.

## See Also

`setHook` shows how users can set hooks on the same events.

ns-load

*Loading and Unloading Name Spaces***Description**

Functions to load and unload namespaces.

**Usage**

```
attachNamespace(ns, pos = 2, dataPath = NULL, depends = NULL)
loadNamespace(package, lib.loc = NULL,
              keep.source = getOption("keep.source.pkgs"),
              partial = FALSE, declarativeOnly = FALSE)
loadedNamespaces()
unloadNamespace(ns)
```

**Arguments**

ns	string or namespace object.
pos	integer specifying position to attach.
dataPath	path to directory containing a database of datasets to be lazy-loaded into the attached environment.
depends	NULL or a character vector of dependencies to be recorded in object <code>.Depends</code> in the package.
package	string naming the package/name space to load.
lib.loc	character vector specifying library search path.
keep.source	logical specifying whether to retain source. This applies only to the specified name space, and not to other name spaces which might be loaded to satisfy imports. For more details see this argument to <a href="#">library</a> .
partial	logical; if true, stop just after loading code.
declarativeOnly	logical; disables <code>.Import</code> , etc, if true.

**Details**

The functions `loadNamespace` and `attachNamespace` are usually called implicitly when `library` is used to load a name space and any imports needed. However it may be useful to call these functions directly at times.

`loadNamespace` loads the specified name space and registers it in an internal data base. A request to load a name space when one of that name is already loaded has no effect. The arguments have the same meaning as the corresponding arguments to [library](#), whose help page explains the details of how a particular installed package comes to be chosen. After loading, `loadNamespace` looks for a hook function named `.onLoad` as an internal variable in the name space (it should not be exported). This function is called with the same arguments as `.First.lib`. Partial loading is used to support installation with the `--save` and `--lazy` options.

`loadNamespace` does not attach the name space it loads to the search path. `attachNamespace` can be used to attach a frame containing the exported values of a

name space to the search path (but this is almost always done *via library*). The hook function `.onAttach` is run after the name space exports are attached.

`loadedNamespaces` returns a character vector of the names of the loaded name spaces.

`unloadNamespace` can be used to attempt to force a name space to be unloaded. If the namespace is attached, it is first `detached`, thereby running a `.Last.lib` function in the namespace if one is exported. Then an error is signaled if the name space is imported by other loaded name spaces, and the namespace is not unloaded. If defined, a hook function `.onUnload` is run before removing the name space from the internal registry.

See the comments in the help for `detach` about some issues with unloading and reloading namespaces.

### Value

`attachNamespace` returns invisibly the environment it adds to the search path.

`loadNamespace` returns the namespace environment, either one already loaded or the one the function causes to be loaded.

`loadedNamespaces` returns a character vector.

`unloadNamespace` returns `NULL`, invisibly.

### Author(s)

Luke Tierney

---

ns-topenv

*Top Level Environment*

---

### Description

Finding the top level environment.

### Usage

```
topenv(envir = parent.frame(),
       matchThisEnv = getOption("topLevelEnvironment"))
```

### Arguments

`envir` environment.

`matchThisEnv` return this environment, if it matches before any other criterion is satisfied. The default, the option `'topLevelEnvironment'`, is set by `sys.source`, which treats a specific environment as the top level environment. Supplying the argument as `NULL` means it will never match.

### Details

`topenv` returns the first top level environment found when searching `envir` and its parent environments. An environment is considered top level if it is the internal environment of a name space, a package environment in the search path, or `.GlobalEnv`.

## Examples

```
topenv(.GlobalEnv)
topenv(new.env())
```

---

NULL

*The Null Object*

---

## Description

NULL represents the null object in R: it is a [reserved](#) word. NULL is often returned by expressions and functions whose value is undefined: it is also used as the empty [pairlist](#).

`as.null` ignores its argument and returns the value NULL.

`is.null` returns TRUE if its argument is NULL and FALSE otherwise.

## Usage

```
NULL
as.null(x, ...)
is.null(x)
```

## Arguments

<code>x</code>	an object to be tested or coerced.
<code>...</code>	ignored.

## Note

`is.null` is a [primitive](#) function.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## Examples

```
is.null(list())      # FALSE (on purpose!)
is.null(integer(0)) # F
is.null(logical(0)) # F
as.null(list(a=1,b='c'))
```

---

 numeric

*Numeric Vectors*


---

### Description

Creates or coerces objects of type "numeric". `is.numeric` is a more general test of an object being interpretable as numbers.

### Usage

```
numeric(length = 0)
as.numeric(x, ...)
is.numeric(x)
```

### Arguments

<code>length</code>	desired length.
<code>x</code>	object to be coerced or tested.
<code>...</code>	further arguments passed to or from other methods.

### Details

`numeric` is identical to `double` (and `real`). It creates a double-precision vector of the specified `length` with each element equal to 0.

`as.numeric` is a generic function, but S3 methods must be written for `as.double`. It is identical to `as.double` (and `as.real`).

`is.numeric` is an **internal generic** primitive function: you can write methods to handle specific classes of objects, see [InternalMethods](#). It is **not** the same as `is.double`. Factors are handled by the default method, and there are methods for classes "Date", "POSIXt" and "difftime" (all of which return false). Methods for `is.numeric` should only return true if the base type of the class is `double` or `integer` *and* values can reasonably be regarded as numeric (e.g. arithmetic on them makes sense, and comparison should be done via the base type).

### Value

for `numeric` and `as.numeric` see [double](#).

The default method for `is.numeric` returns TRUE if its argument is of mode "numeric" (type "double" or type "integer") and not a factor, and FALSE otherwise. That is, `is.integer(x) || is.double(x), or (mode(x) == "numeric") && !is.factor(x)`.

### S4 methods

`as.numeric` and `is.numeric` are internally S4 generic and so methods can be set for them *via* `setMethod`.

To ensure that `as.numeric`, `as.double` and `as.real` remain identical, S4 methods can only be set for `as.numeric`.



**Note on names**

It is a historical anomaly that R has three names for its floating-point vectors, `double`, `numeric` and `real`.

`double` is the name of the `type`. `numeric` is the name of the `mode` and also of the implicit `class`. As an S4 formal class, use `"numeric"`.

`real` is deprecated and should not be used in new code.

The potential confusion is that R has used `mode "numeric"` to mean ‘double or integer’, which conflicts with the S4 usage. Thus `is.numeric` tests the mode, not the class, but `as.numeric` (which is identical to `as.double`) coerces to the class.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`double`, `integer`, `storage.mode`.

**Examples**

```
as.numeric(c("-.1", " 2.7 ", "B")) # (-0.1, 2.7, NA) + warning
as.numeric(factor(5:10))
```

---

NumericConstants    *Numeric Constants*

---

**Description**

How R parses numeric constants.

**Details**

R parses numeric constants in its input in a very similar way to C99 floating-point constants.

`Inf` and `NaN` are numeric constants (with `typeof(.)` `"double"`). These are recognized ignoring case, as is `infinity` as an alternative to `Inf`. `NA_real_` and `NA_integer_` are constants of types `"double"` and `"integer"` representing missing values. All other numeric constants start with a digit or period and are either a decimal or hexadecimal constant optionally followed by `L`.

Hexadecimal constants start with `0x` or `0X` followed by a nonempty sequence from `0-9 a-f A-F` which is interpreted as a hexadecimal number, optionally followed by a binary exponent. A binary exponent consists of an `P` or `p` followed by an optional plus or minus sign followed by a non-empty sequence of (decimal) digits, and indicates multiplication by a power of two. Thus `0x123p456` is  $291 \times 2^{456}$ .

Decimal constants consist of a nonempty sequence of digits possibly containing a period (the decimal point), optionally followed by a decimal exponent. A decimal exponent consists of an `E` or `e` followed by an optional plus or minus sign followed by a non-empty sequence of digits, and indicates multiplication by a power of ten.

Values which are too large or too small to be representable will overflow to `Inf` or underflow to `0.0`.

A numeric constant immediately followed by `i` is regarded as an imaginary [complex](#) number.

An numeric constant immediately followed by `L` is regarded as an [integer](#) number when possible (and with a warning if it contains a `.`).

Only the ASCII digits 0–9 are recognized as digits, even in languages which have other representations of digits. The ‘decimal separator’ is always a period and never a comma.

Note that a leading plus or minus is not regarded by the parser as part of a numeric constant but as a unary operator applied to the constant.

### Note

When a string is parsed to input a numeric constant, the number may or may not be representable exactly in the C double type used. If not one of the nearest representable numbers will be returned.

Since R 2.7.0 R’s own C code has been used to parse constants, so the effect can be expected to be the same on all platforms implementing full IEC 600559 arithmetic (the most likely area of difference being the handling of numbers less than `.Machine$double.xmin`). The same code is used by [scan](#).

### See Also

[Syntax](#).

[Quotes](#) for the parsing of character constants,

### Examples

```
2.1
typeof(2)
sqrt(1i) # remember elementary math?
utils::str(0xA0)
identical(1L, as.integer(1))

## You can combine the "0x" prefix with the "L" suffix :
identical(0xFL, as.integer(15))
```

---

numeric\_version      *Numeric Versions*

---

### Description

A simple S3 class for representing numeric versions including package versions, and associated methods.

### Usage

```
numeric_version(x, strict = TRUE)
package_version(x, strict = TRUE)
R_system_version(x, strict = TRUE)
getRversion()
```

**Arguments**

x	a character vector with suitable numeric version strings (see ‘Details’); for <code>package_version</code> , alternatively an R version object as obtained by <code>R.version</code> .
strict	a logical indicating whether invalid numeric versions should results in an error (default) or not.

**Details**

Numeric versions are sequences of one or more non-negative integers, usually (e.g., in package ‘DESCRIPTION’ files) represented as character strings with the elements of the sequence concatenated and separated by single ‘.’ or ‘-’ characters. R package versions consist of at least two such integers, an R system version of exactly three (major, minor and patchlevel).

Functions `numeric_version`, `package_version` and `R_system_version` create a representation from such strings (if suitable) which allows for coercion and testing, combination, comparison, summaries (min/max), inclusion in data frames, subscripting, and printing. The classes can hold a vector of such representations.

`getRversion` returns the version of the running R as an R system version object.

The `[]` operator extracts or replaces a single version. To access the integers of a version use two indices: see the examples.

**See Also**

[compareVersion](#)

**Examples**

```
x <- package_version(c("1.2-4", "1.2-3", "2.1"))
x < "1.4-2.3"
c(min(x), max(x))
x[2, 2]
x$major
x$minor

if(getRversion() <= "2.5.0") { ## work around missing feature
  cat("Your version of R, ", as.character(getRversion()),
      ", is outdated.\n",
      "Now trying to work around that ... \n", sep = "")
}

x[[c(1,3)]] # '4' as a numeric vector, same as x[1, 3]
x[1, 3]     # 4 as an integer
x[[2, 3]] <- 0 # zero the patchlevel
x[[c(2,3)]] <- 0 # same
x
x[[3]] <- "2.2.3"; x
```

---

`octmode`*Display Numbers in Octal*

---

## Description

Convert or print integers in octal format, with as many digits as are needed to display the largest, using leading zeroes as necessary.

## Usage

```
as.octmode(x)

## S3 method for class 'octmode':
as.character(x, ...)

## S3 method for class 'octmode':
format(x, width = NULL, ...)

## S3 method for class 'octmode':
print(x, ...)
```

## Arguments

<code>x</code>	An object, for the methods inheriting from class "octmode".
<code>width</code>	NULL or a positive integer specifying the minimum field width to be used, with padding by leading zeroes.
<code>...</code>	further arguments passed to or from other methods.

## Details

Class "octmode" consists of integer vectors with that class attribute, used merely to ensure that they are printed in octal notation, specifically for Unix-like file permissions such as 755. Subsetting (`[]`) works too.

If `width = NULL` (the default), the output is padded with leading zeroes to the smallest width needed for all the non-missing elements.

`as.octmode` can convert integers (of [type](#) "integer" or "double") and character vectors whose elements contain only digits 0–7 (or are NA) to class "octmode".

## See Also

These are auxiliary functions for [file.info](#).

[hexmode](#), [sprintf](#) for other options in converting integers to octal, [strtoi](#) to convert octal strings to integers.

## Examples

```
(on <- as.octmode(c(16,32, 127:129))) # "020" "040" "177" "200" "201"
unclass(on[3:4]) # subsetting
```

---

`on.exit`*Function Exit Code*

---

### Description

`on.exit` records the expression given as its argument as needing to be executed when the current function exits (either naturally or as the result of an error). This is useful for resetting graphical parameters or performing other cleanup actions.

If no expression is provided, i.e., the call is `on.exit()`, then the current `on.exit` code is removed.

### Usage

```
on.exit(expr = NULL, add = FALSE)
```

### Arguments

<code>expr</code>	an expression to be executed.
<code>add</code>	if TRUE, add <code>expr</code> to be executed after any previously set expressions; otherwise (the default) <code>expr</code> will overwrite any previously set expressions.

### Details

Where `expr` was evaluated changed in R 2.8.0, and the following applies only to that and later versions.

The `expr` argument passed to `on.exit` is recorded without evaluation. If it is not subsequently removed/replaced by another `on.exit` call in the same function, it is evaluated in the evaluation frame of the function when it exits (including during standard error handling). Thus any functions or variables in the expression will be looked for in the function and its environment at the time of exit: to capture the current value in `expr` use `substitute` or similar.

This is a ‘special’ [primitive](#) function: it only evaluates the argument `add`.

### Value

Invisible NULL.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[sys.on.exit](#) which returns the expression stored for use by `on.exit()` in the function in which `sys.on.exit()` is evaluated.

**Examples**

```
require(graphics)

opar <- par(mai = c(1,1,1,1))
on.exit(par(opar))
```

Ops.Date

*Operators on the Date Class***Description**

Operators for the "Date" class.

There is an `Ops` method and specific methods for `+` and `-` for the `Date` class.

**Usage**

```
date + x
x + date
date - x
date1 lop date2
```

**Arguments**

<code>date</code>	date objects
<code>date1, date2</code>	date objects or character vectors. (Character vectors are converted by <code>as.Date</code> .)
<code>x</code>	a numeric vector (in days) <i>or</i> an object of class "difftime", rounded to the nearest whole day.
<code>lop</code>	One of <code>==</code> , <code>!=</code> , <code>&lt;</code> , <code>&lt;=</code> , <code>&gt;</code> or <code>&gt;=</code> .

**Details**

`x` does not need to be integer if specified as a numeric vector, but see the comments about fractional days in the help for `Dates`.

**Examples**

```
(z <- Sys.Date())
z + 10
z < c("2009-06-01", "2010-01-01", "2015-01-01")
```

options

*Options Settings***Description**

Allow the user to set and examine a variety of global *options* which affect the way in which R computes and displays its results.

**Usage**

```
options(...)  
getOption(x, default = NULL)  
.Options
```

**Arguments**

...	any options can be defined, using <code>name = value</code> or by passing a list of such tagged values. However, only the ones below are used in base R. Further, <code>options('name') == options()['name']</code> , see the example.
x	a character string holding an option name.
default	if the specified option is not set in the options list, this value is returned. This facilitates retrieving an option and checking whether it is set and setting it separately if not.

**Details**

Invoking `options()` with no arguments returns a list with the current values of the options. Note that not all options listed below are set initially. To access the value of a single option, one should use `getOption("width")`, e.g., rather than `options("width")` which is a *list* of length one.

`.Options` also always contains the `options()` list (as a pairlist, unsorted), for S compatibility. Assigning to it will make a local copy and not change the original.

**Value**

For `getOption`, the current value set for option `x`, or `NULL` if the option is unset.

For `options()`, a list of all set options sorted by name. For `options(name)`, a list of length one containing the set value, or `NULL` if it is unset. For uses setting one or more options, a list with the previous values of the options changed (returned invisibly).

**Options used in base R**

`add.smooth`: typically logical, defaulting to `TRUE`. Could also be set to an integer for specifying how many (simulated) smooths should be added. This is currently only used by `plot.lm`.

`checkPackageLicense`: logical, not set by default. If true, `library` asks a user to accept any non-standard license at first use.

`check.bounds`: logical, defaulting to `FALSE`. If true, a **warning** is produced whenever a vector (atomic or `list`) is extended, by something like `x <- 1:3; x[5] <- 6`.

- continue:** a non-empty string setting the prompt used for lines which continue over one line.
- defaultPackages:** the packages that are attached by default when R starts up. Initially set from value of the environment variable `R_DEFAULT_PACKAGES`, or if that is unset to `c("datasets", "utils", "grDevices", "graphics", "stats", "methods")`. (Set `R_DEFAULT_PACKAGES` to `NULL` or a comma-separated list of package names.) A call to `options` should be in your `‘.Rprofile’` file to ensure that the change takes effect before the base package is initialized (see [Startup](#)).
- deparse.max.lines:** controls the number of lines used when deparsing in [traceback](#), [browser](#), and upon entry to a function whose debugging flag is set. Initially unset, and only used if set to a positive integer.
- digits:** controls the number of digits to print when printing numeric values. It is a suggestion only. Valid values are 1...22 with default 7. See the warning in [print.default](#) about values greater than 15.
- digits.secs:** controls the maximum number of digits to print when formatting time values in seconds. Valid values are 0..6 with default 0. See [strftime](#).
- download.file.method:** Method to be used for `download.file`. Currently download methods "internal", "wget" and "lynx" are available. There is no default for this option, when `method = "auto"` is chosen: see [download.file](#).
- echo:** logical. Only used in non-interactive mode, when it controls whether input is echoed. Command-line option `‘--slave’` sets this to `FALSE`, but otherwise it starts the session as `TRUE`.
- encoding:** The name of an encoding, default `"native.enc"`). See [connections](#).
- error:** either a function or an expression governing the handling of non-catastrophic errors such as those generated by [stop](#) as well as by signals and internally detected errors. If the option is a function, a call to that function, with no arguments, is generated as the expression. The default value is `NULL`: see [stop](#) for the behaviour in that case. The functions [dump.frames](#) and [recover](#) provide alternatives that allow post-mortem debugging. Note that these need to be specified as e.g. `options(error=utils::recover)` in startup files such as `‘.Rprofile’`.
- expressions:** sets a limit on the number of nested expressions that will be evaluated. Valid values are 25...500000 with default 5000. If you increase it, you may also want to start R with a larger protection stack; see `‘--max-ppsize’` in [Memory](#). Note too that you may cause a segfault from overflow of the C stack, and on OSes where it is possible you may want to increase that.
- keep.source:** When `TRUE`, the source code for functions (newly defined or loaded) is stored in their "source" attribute (see [attr](#)) allowing comments to be kept in the right places. The default is `interactive()`, i.e., `TRUE` for interactive use.
- keep.source.pkgs:** As for `keep.source`, for functions in packages loaded by [library](#) or [require](#). Defaults to `FALSE` unless the environment variable `R_KEEP_PKG_SOURCE` is set to `yes`.  
Note this does not apply to packages using lazy-loading or saved images. Whether they have kept source is determined when they are installed (and is almost certainly false).
- mailer:** default mailer used by [bug.report\(\)](#). Can be "none".
- max.contour.segments:** positive integer, defaulting to 250000 and usually not set. A limit on the number of segments in a single contour line in [contour](#) or [contourLines](#).
- max.print:** integer, defaulting to 99999. [print](#) or [show](#) methods can make use of this option, to limit the amount of information that is printed, to something in the order of (and typically slightly less than) `max.print` entries.



- OutDec:** character string containing a single-byte character. The character to be used as the decimal point in output conversions, that is in printing, plotting and `as.character` but not deparsing.
- pager:** the command used for displaying text files by `file.show`. Defaults to `'R_HOME/bin/pager'`, which selects a pager via the `\link{PAGER}` environment variable (and that usually defaults to `less`). Can be a character string or an R function, in which case it needs to accept the same first four arguments as `file.show`.
- papersize:** the default paper format used by `postscript`; set by environment variable `R_PAPERSIZE` when R is started: if that is unset or invalid it defaults to a value derived from the locale category `LC_PAPER`, or if that is unavailable to a default set when R was built.
- pdfviewer:** default PDF viewer. The default is set from the environment variable `R_PDFVIEWER`, the default value of which is set when R is configured.
- printcmd:** the command used by `postscript` for printing; set by environment variable `R_PRINTCMD` when R is started. This should be a command that expects either input to be piped to `'stdin'` or to be given a single filename argument. Usually set to `"lpr"` on a Unix-alike.
- prompt:** a non-empty string to be used for R's prompt; should usually end in a blank (`" "`).
- rl\_word\_breaks:** Used for the readline-based terminal interface. Default value `"\t\n\"\\' '><=%;, |&\\{ () \\}"`. This is the set of characters use to break the input line up into tokens for object- and file-name completion. Those who do not use spaces around operators may prefer `"\t\n\"\\' '><=+-*%;, |&\\{ () \\}"` which was the default in R 2.5.0. (The default in pre-2.5.0 versions of R was `"\t\n\"\\' '@$><=; |&\\{ (".)`
- save.defaults, save.image.defaults:** see `save`.
- scipen:** integer. A penalty to be applied when deciding to print numeric values in fixed or exponential notation. Positive values bias towards fixed and negative towards scientific notation: fixed notation will be preferred unless it is more than `scipen` digits wider.
- showWarnCalls, showErrorCalls:** a logical. Should warning and error messages show a summary of the call stack? By default error calls are shown in non-interactive sessions.
- showNCalls:** a integer. Controls how long the sequence of calls must be (in bytes) before ellipses are used. Defaults to 40 and should be at least 30 and no more than 500.
- show.error.messages:** a logical. Should error messages be printed? Intended for use with `try` or a user-installed error handler.
- stringsAsFactors:** The default setting for arguments of `data.frame` and `read.table`.
- texi2dvi:** used by function `texi2dvi` in package `tools`. Set at startup from the environment variable `R_TEXI2DVICMD`.
- timeout:** integer. The timeout for some Internet operations, in seconds. Default 60 seconds. See `download.file` and `connections`.
- topLevelEnvironment:** see `topenv` and `sys.source`.
- useFancyQuotes:** logical: controls the use of directional quotes in `sQuote`, `dQuote` and in rendering text help (see `Rd2txt`).
- verbose:** logical. Should R report extra information on progress? Set to `TRUE` by the command-line option `'--verbose'`.

**warn:** sets the handling of warning messages. If `warn` is negative all warnings are ignored. If `warn` is zero (the default) warnings are stored until the top-level function returns. If fewer than 10 warnings were signalled they will be printed otherwise a message saying how many (max 50) were signalled. An object called `last.warning` is created and can be printed through the function `warnings`. If `warn` is one, warnings are printed as they occur. If `warn` is two or larger all warnings are turned into errors.

**warnPartialMatchArgs:** logical. If true, warns if partial matching is used in argument matching.

**warnPartialMatchAttr:** logical. If true, warns if partial matching is used in extracting attributes via `attr`.

**warnPartialMatchDollar:** logical. If true, warns if partial matching is used for extraction by `$`.

**warning.expression:** an R code expression to be called if a warning is generated, replacing the standard message. If non-null it is called irrespective of the value of option `warn`.

**warning.length:** sets the truncation limit for error and warning messages. A non-negative integer, with allowed values 100...8170, default 1000.

**width:** controls the maximum number of columns on a line used in printing vectors, matrices and arrays, and when filling by `cat`.

Columns are normally the same as characters except in CJK languages.

You may want to change this if you re-size the window that R is running in. Valid values are 10...10000 with default normally 80. (The limits on valid values are in file 'Print.h' and can be changed by re-compiling R.) Some R consoles automatically change the value when they are resized.

See the examples on [Startup](#) for one way to set this automatically from the terminal width when R is started.

The 'factory-fresh' default settings of some of these options are

<code>add.smooth</code>	TRUE
<code>check.bounds</code>	FALSE
<code>continue</code>	" + "
<code>digits</code>	7
<code>echo</code>	TRUE
<code>encoding</code>	"native.enc"
<code>error</code>	NULL
<code>expressions</code>	5000
<code>keep.source</code>	<code>interactive()</code>
<code>keep.source.pkgs</code>	FALSE
<code>max.print</code>	99999
<code>OutDec</code>	"."
<code>prompt</code>	"> "
<code>scipen</code>	0
<code>show.error.messages</code>	TRUE
<code>timeout</code>	60
<code>verbose</code>	FALSE
<code>warn</code>	0
<code>warnings.length</code>	1000
<code>width</code>	80

Others are set from environment variables or are platform-dependent.

### Options set in package `grDevices`

These will be set when package `grDevices` (or its name space) is loaded if not already set.

`device`: a character string giving the name of a function, or the function object itself, which when called creates a new graphics device of the default type for that session. The value of this option defaults to the normal screen device (e.g., `X11`, `windows` or `quartz`) for an interactive session, and `pdf` in batch use or if a screen is not available. If set to the name of a device, the device is looked for first from the global environment (that is down the usual search path) and then in the `grDevices` namespace.

The default values in interactive and non-interactive sessions are configurable via environment variables `R_INTERACTIVE_DEVICE` and `R_DEFAULT_DEVICE` respectively.

`locatorBell`: logical. Should selection in `locator` and `identify` be confirmed by a bell? Default `TRUE`. Honoured at least on `X11` and `windows` devices.

`device.ask.default`: logical. The default for `devAskNewPage("ask")` when a device is opened.

`bitmapType`: character. The default type for the bitmap devices such as `png`. Defaults to `"cairo"` on systems where that is available, or to `"quartz"` on Mac OS X where that is available.

### Options set in package `stats`

These will be set when package `stats` (or its name space) is loaded if not already set.

`contrasts`: the default `contrasts` used in model fitting such as with `aoV` or `lm`. A character vector of length two, the first giving the function to be used with unordered factors and the second the function to be used with ordered factors. By default the elements are named `c("unordered", "ordered")`, but the names are unused.

`na.action`: the name of a function for treating missing values (`NA`'s) for certain situations.

`show.coef.Pvalues`: logical, affecting whether P values are printed in summary tables of coefficients. See `printCoefmat`.

`show.signif.stars`: logical, should stars be printed on summary tables of coefficients? See `printCoefmat`.

`ts.eps`: the relative tolerance for certain time series (`ts`) computations. Default `1e-05`.

`ts.S.compat`: logical. Used to select S compatibility for plotting time-series spectra. See the description of argument `log` in `plot.spec`.

### Options set in package `utils`

These will be set when package `utils` (or its name space) is loaded if not already set.

`BioC_mirror`: The URL of a Bioconductor mirror for use by `setRepositories`, e.g. the default `"http://www.bioconductor.org"` or the European mirror `"http://bioconductor.statistik.tu-dortmund.de"`. Can be set by `chooseBioCmirror`.

`browser`: default HTML browser used by `help.start()` and `browseURL` on UNIX, or a non-default browser on Windows. Alternatively, an R function that is called with a URL as its argument.

`de.cellwidth`: integer: the cell widths (number of characters) to be used in the data editor `dataentry`. If this is unset (the default), 0, negative or `NA`, variable cell widths are used.

`demo.ask`: default for the `ask` argument of `demo`.

- `editor`: a non-empty string, or a function that is called with a file path as argument. Sets the default text editor, e.g., for `edit`. Set from the environment variable `EDITOR` on UNIX, or if unset `VISUAL` or `vi`.
- `example.ask`: default for the `ask` argument of `example`.
- `help_text_width`: The target pager width when formatting text help. Usually unset, when the default is 80 columns.
- `help.try.all.packages`: default for an argument of `help`.
- `help_type`: default for an argument of `help`.
- `HTTPUserAgent`: string used as the user agent in HTTP requests. If `NULL`, HTTP requests will be made without a user agent header. The default is `R (<version> <platform> <arch> <os>)`
- `internet.info`: The minimum level of information to be printed on URL downloads etc. Default is 2, for failure causes. Set to 1 or 0 to get more information.
- `menu.graphics`: Logical: should graphical menus be used if available?. Defaults to `TRUE`. Currently applies to `select.list`, `chooseCRANmirror`, `setRepositories` and to select from multiple (text) help files in `help`.
- `pkgType`: The default type of packages to be downloaded and installed – see `install.packages`. Possible values are "source" (the default except under the CRAN Mac OS X build) and "mac.binary". The latter can have a suffix if supported by a special build, such as "mac.binary.leopard" to access the "leopard" tree of repositories instead of the default "universal".
- `repos`: URLs of the repositories for use by `update.packages`. Defaults to `c(CRAN="@CRAN@")`, a value that causes some utilities to prompt for a CRAN mirror. To avoid this do set the CRAN mirror, by something like `local({r <- getOption("repos"); r["CRAN"] <- "http://my.local.cran"; options(repos=r)})`.  
Note that you can add more repositories (Bioconductor and Omegahat, notably) using `setRepositories()`.
- `SweaveHooks`, `SweaveSyntax`: see `Sweave`.
- `unzip`: a character string, the path of the command used for unzipping help files, or "internal". Defaults to the value of `R_UNZIPCMD`, which is set in 'etc/Renviron' if an `unzip` command was found during configuration.

### Options used on Unix only

These will be "" if no suitable path is known.

`dvipscmd`: character string giving command to be used in off-line printing of help pages.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### Examples

```
op <- options(); utils::str(op) # op() may contain functions.

getOption("width") == options()$width # the latter needs more memory
options(digits = 15)
```

```

pi

# set the editor, and save previous value
old.o <- options(editor = "nedit")
old.o

options(check.bounds = TRUE, warn = 1)
x <- NULL; x[4] <- "yes" # gives a warning

options(digits=5)
print(1e5)
options(scipen=3); print(1e5)

options(op)      # reset (all) initial options
options("digits")

## Not run: ## set contrast handling to be like S
options(contrasts = c("contr.helmert", "contr.poly"))

## End(Not run)

## Not run: ## on error, terminate the R session with error status 66
options(error = quote(q("no", status=66, runLast=FALSE)))
stop("test it")

## End(Not run)

## Not run: ## Set error actions for debugging:
## enter browser on error, see ?recover:
options(error = recover)
## allows to call debugger() afterwards, see ?debugger:
options(error = dump.frames)
## A possible setting for non-interactive sessions
options(error = quote({dump.frames(to.file=TRUE); q()}))

## End(Not run)

# Compare the two ways to get an option and use it
# accounting for the possibility it might not be set.
if(as.logical(getOption("performCleanup", TRUE)))
  cat("do cleanup\n")

## Not run:
# a clumsier way of expressing the above w/o the default.
tmp <- getOption("performCleanup")
if(is.null(tmp))
  tmp <- TRUE
if(tmp)
  cat("do cleanup\n")

## End(Not run)

```

## Description

`order` returns a permutation which rearranges its first argument into ascending or descending order, breaking ties by further arguments. `sort.list` is the same, using only one argument. See the examples for how to use these functions to sort data frames, etc.

## Usage

```
order(..., na.last = TRUE, decreasing = FALSE)
```

```
sort.list(x, partial = NULL, na.last = TRUE, decreasing = FALSE,
         method = c("shell", "quick", "radix"))
```

## Arguments

<code>...</code>	a sequence of numeric, complex, character or logical vectors, all of the same length, or a classed R object.
<code>x</code>	a vector.
<code>partial</code>	vector of indices for partial sorting. (Non-NULL values are not implemented.)
<code>decreasing</code>	logical. Should the sort order be increasing or decreasing?
<code>na.last</code>	for controlling the treatment of NAs. If <code>TRUE</code> , missing values in the data are put last; if <code>FALSE</code> , they are put first; if <code>NA</code> , they are removed.
<code>method</code>	the method to be used: partial matches are allowed.

## Details

In the case of ties in the first vector, values in the second are used to break the ties. If the values are still tied, values in the later arguments are used to break the tie (see the first example). The sort used is *stable* (except for `method = "quick"`), so any unresolved ties will be left in their original ordering.

Complex values are sorted first by the real part, then the imaginary part.

The sort order for character vectors will depend on the collating sequence of the locale in use: see [Comparison](#).

The default method for `sort.list` is a good compromise. Method `"quick"` is only supported for numeric `x` with `na.last=NA`, and is not stable, but will be faster for long vectors. Method `"radix"` is only implemented for integer `x` with a range of less than 100,000. For such `x` it is very fast (and stable), and hence is ideal for sorting factors.

`partial` is supplied for compatibility with other implementations of S, but no other values are accepted and ordering is always complete.

For a classed R object, the sort order is taken from `xtfrm`: as its help page notes, this can be slow unless a suitable method has been defined or `is.numeric(x)` is true. For factors, this sorts on the internal codes, which is particularly appropriate for ordered factors.

## Note

`sort.list` can get called by mistake as a method for `sort` with a list argument, and gives a suitable error message for list `x`.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[sort](#), [rank](#), [xtfrm](#).

**Examples**

```
require(stats)

(ii <- order(x <- c(1,1,3:1,1:4,3), y <- c(9,9:1), z <-c(2,1:9)))
## 6 5 2 1 7 4 10 8 3 9
rbind(x,y,z)[,ii] # shows the reordering (ties via 2nd & 3rd arg)

## Suppose we wanted descending order on y.
## A simple solution for numeric 'y' is
rbind(x,y,z)[, order(x, -y, z)]
## More generally we can make use of xtfrm
cy <- as.character(y)
rbind(x,y,z)[, order(x, -xtfrm(cy), z)]

## Sorting data frames:
dd <- transform(data.frame(x,y,z),
                 z = factor(z, labels=LETTERS[9:1]))
## Either as above {for factor 'z' : using internal coding}:
dd[ order(x, -y, z) ,]
## or along 1st column, ties along 2nd, ... *arbitrary* no.{columns}:
dd[ do.call(order, dd) ,]

set.seed(1)# reproducible example:
d4 <- data.frame(x = round( rnorm(100)), y = round(10*runif(100)),
                 z = round( 8*rnorm(100)), u = round(50*runif(100)))
(d4s <- d4[ do.call(order, d4) ,])
(i <- which(diff(d4s[,3]) == 0))
# in 2 places, needed 3 cols to break ties:
d4s[ rbind(i,i+1), ]

## rearrange matched vectors so that the first is in ascending order
x <- c(5:1, 6:8, 12:9)
y <- (x - 5)^2
o <- order(x)
rbind(x[o], y[o])

## tests of na.last
a <- c(4, 3, 2, NA, 1)
b <- c(4, NA, 2, 7, 1)
z <- cbind(a, b)
(o <- order(a, b)); z[o, ]
(o <- order(a, b, na.last = FALSE)); z[o, ]
(o <- order(a, b, na.last = NA)); z[o, ]

## Not run:
## speed examples for long vectors:
x <- factor(sample(letters, 1e6, replace=TRUE))
system.time(o <- sort.list(x)) ## 1.2 secs
stopifnot(!is.unsorted(x[o]))
system.time(o <- sort.list(x, method="quick", na.last=NA)) # 0.15 sec
stopifnot(!is.unsorted(x[o]))
system.time(o <- sort.list(x, method="radix")) # 0.02 sec
```

```

stopifnot(!is.unsorted(x[o]))
xx <- sample(1:26, 1e7, replace=TRUE)
system.time(o <- sort.list(xx, method="radix")) # 0.2 sec
xx <- sample(1:100000, 1e7, replace=TRUE)
system.time(o <- sort.list(xx, method="radix")) # 0.8 sec
system.time(o <- sort.list(xx, method="quick", na.last=NA)) # 1.4 sec

## End(Not run)

```

---

outer

*Outer Product of Arrays*


---

### Description

The outer product of the arrays  $X$  and  $Y$  is the array  $A$  with dimension  $c(\dim(X), \dim(Y))$  where element  $A[c(\text{arrayindex.x}, \text{arrayindex.y})] = \text{FUN}(X[\text{arrayindex.x}], Y[\text{arrayindex.y}], \dots)$ .

### Usage

```

outer(X, Y, FUN="*", ...)
X %o% Y

```

### Arguments

$X, Y$	First and second arguments for function <code>FUN</code> . Typically a vector or array.
<code>FUN</code>	a function to use on the outer products, found <i>via</i> <code>match.fun</code> (except for the special case <code>"*"</code> ).
<code>...</code>	optional arguments to be passed to <code>FUN</code> .

### Details

$X$  and  $Y$  must be suitable arguments for `FUN`. Each will be extended by `rep` to length the products of the lengths of  $X$  and  $Y$  before `FUN` is called.

`FUN` is called with these two extended vectors as arguments. Therefore, it must be a vectorized function (or the name of one), expecting at least two arguments.

Where they exist, the `[dim]names` of  $X$  and  $Y$  will be copied to the answer, and a dimension assigned which is the concatenation of the dimensions of  $X$  and  $Y$  (or lengths if dimensions do not exist).

`FUN = "*" is handled internally as a special case, via as.vector(X) %*% t(as.vector(Y)), and is intended only for numeric vectors and arrays.`

`%o%` is binary operator providing a wrapper for `outer(x, y, "*")`.

### Author(s)

Jonathan Rougier

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.



**See Also**

`%*%` for usual (*inner*) matrix vector multiplication; `kronecker` which is based on `outer`; `Vectorize` for vectorizing a non-vectorized function.

**Examples**

```
x <- 1:9; names(x) <- x
# Multiplication & Power Tables
x %o% x
y <- 2:8; names(y) <- paste(y, ":", sep="")
outer(y, x, "^")

outer(month.abb, 1999:2003, FUN = "paste")

## three way multiplication table:
x %o% x %o% y[1:3]
```

---

 Paren

*Parentheses and Braces*


---

**Description**

Open parenthesis, (, and open brace, {, are `.Primitive` functions in R.

Effectively, ( is semantically equivalent to the identity function(x) x, whereas { is slightly more interesting, see examples.

**Usage**

```
( ... )
```

```
{ ... }
```

**Value**

For (, the result of evaluating the argument. This has visibility set, so will auto-print if used at top-level.

For {, the result of the last expression evaluated. This has the visibility of the last evaluation.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`if`, `return`, etc for other objects used in the R language itself.

`Syntax` for operator precedence.

**Examples**

```
f <- get("(")
e <- expression(3 + 2 * 4)
identical(f(e), e)

do <- get("{")
do(x <- 3, y <- 2*x-3, 6-x-y); x; y

## note the differences
(2+3)
{2+3; 4+5}
(invisible(2+3))
{invisible(2+3)}
```

---

 parse

*Parse Expressions*


---

**Description**

`parse` returns the parsed but unevaluated expressions in a list.

**Usage**

```
parse(file = "", n = NULL, text = NULL, prompt = "?", srcfile,
      encoding = "unknown")
```

**Arguments**

<code>file</code>	a connection, or a character string giving the name of a file or a URL to read the expressions from. If <code>file</code> is "" and <code>text</code> is missing or <code>NULL</code> then input is taken from the console.
<code>n</code>	integer (or coerced to integer). The maximum number of expressions to parse. If <code>n</code> is <code>NULL</code> or negative or <code>NA</code> the input is parsed in its entirety.
<code>text</code>	character vector. The text to parse. Elements are treated as if they were lines of a file. Other R objects will be coerced to character if possible.
<code>prompt</code>	the prompt to print when parsing from the keyboard. <code>NULL</code> means to use R's prompt, <code>getOption("prompt")</code> .
<code>srcfile</code>	<code>NULL</code> , or a <code>srcfile</code> object. See the 'Details' section.
<code>encoding</code>	encoding to be assumed for input strings. If the value is "latin1" or "UTF-8" it is used to mark character strings as known to be in Latin-1 or UTF-8: it is not used to re-encode the input. To do the latter, specify the encoding as part of the connection <code>con</code> or via <code>options(encoding=)</code> : see the example under <a href="#">file</a> .

**Details**

If `text` has length greater than zero (after coercion) it is used in preference to `file`.

All versions of R accept input from a connection with end of line marked by LF (as used on Unix), CRLF (as used on DOS/Windows) or CR (as used on classic Mac OS). The final line can be incomplete, that is missing the final EOL marker.

See [source](#) for the limits on the size of functions that can be parsed (by default).

When input is taken from the console, `n = NULL` is equivalent to `n = 1`, and `n < 0` will read until an EOF character is read. (The EOF character is Ctrl-Z for the Windows front-ends.) The line-length limit is 4095 bytes when reading from the console (which may impose a lower limit: see ‘An Introduction to R’).

The default for `srcfile` is set as follows. If `options("keep.source")` is `FALSE`, `srcfile` defaults to `NULL`. Otherwise, if `text` is used, `srcfile` will be set to a [srcfilecopy](#) containing the text. If a character string is used for `file`, a [srcfile](#) object referring to that file will be used.

### Value

An object of type `"expression"`, with up to `n` elements if specified as a non-negative integer.

When `srcfile` is non-`NULL`, a `"srcref"` attribute will be attached to the result containing a list of [srcref](#) records corresponding to each element, and a `"srcfile"` attribute will be attached containing a copy of `srcfile`.

A syntax error (including an incomplete expression) will throw an error.

Character strings in the result will have a declared encoding if `encoding` is `"latin1"` or `"UTF-8"`, or if `text` is supplied with every element of known encoding in a Latin-1 or UTF-8 locale.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[scan](#), [source](#), [eval](#), [deparse](#).

### Examples

```
cat("x <- c(1,4)\n x ^ 3 -10 ; outer(1:7,5:9)\n", file="xyz.Rdmped")
# parse 3 statements from the file "xyz.Rdmped"
parse(file = "xyz.Rdmped", n = 3)
unlink("xyz.Rdmped")
```

---

paste

*Concatenate Strings*

---

### Description

Concatenate vectors after converting to character.

### Usage

```
paste(..., sep = " ", collapse = NULL)
```

## Arguments

...	one or more R objects, to be converted to character vectors.
sep	a character string to separate the terms. Not <a href="#">NA_character_</a> .
collapse	an optional character string to separate the results. Not <a href="#">NA_character_</a> .

## Details

`paste` converts its arguments (via [as.character](#)) to character strings, and concatenates them (separating them by the string given by `sep`). If the arguments are vectors, they are concatenated term-by-term to give a character vector result. Vector arguments are recycled as needed, with zero-length arguments being recycled to `" "`.

Note that `paste()` coerces [NA\\_character\\_](#), the character missing value, to `"NA"` which may seem undesirable, e.g., when pasting two character vectors, or very desirable, e.g. in `paste("the value of p is ", p)`.

If a value is specified for `collapse`, the values in the result are then concatenated into a single string, with the elements being separated by the value of `collapse`.

## Value

A character vector of the concatenated values. This will be of length zero if all the objects are, unless `collapse` is non-NULL in which case it is a single empty string.

If any input into an element of the result is in UTF-8, that element will be in UTF-8, otherwise in the current encoding in which case the encoding of an element of the element is declared if the current locale is either Latin-1 or UTF-8, at least one of the corresponding inputs (including separators) had a declared encoding and all inputs were either ASCII or declared.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

String manipulation with [as.character](#), [substr](#), [nchar](#), [strsplit](#); further, [cat](#) which concatenates and writes to a file, and [sprintf](#) for C like string construction.

[‘plotmath’](#) for the use of `paste` in plot annotation.

## Examples

```
paste(1:12) # same as as.character(1:12)
paste("A", 1:6, sep = "")
paste("Today is", date())
```

---

`path.expand`                      *Expand File Paths*

---

### Description

Expand a path name, for example by replacing a leading tilde by the user's home directory (if defined on that platform).

### Usage

```
path.expand(path)
```

### Arguments

`path`                      character vector containing one or more path names.

### Details

On *some* Unix builds of R, a leading `~user` will expand to the home directory of `user`, but not on Unix versions without `readline` installed, nor if R is invoked with `'--no-readline'`.

In an interactive session `capabilities("cledit")` will report if `readline` is available.

### See Also

[basename](#)

### Examples

```
path.expand("~/foo")
```

---

`pmatch`                              *Partial String Matching*

---

### Description

`pmatch` seeks matches for the elements of its first argument among those of its second.

### Usage

```
pmatch(x, table, nomatch = NA_integer_, duplicates.ok = FALSE)
```

### Arguments

`x`                              the values to be matched: converted to a character vector by [as.character](#).

`table`                        the values to be matched against: converted to a character vector.

`nomatch`                      the value to be returned at non-matching or multiply partially matching positions. Note that it is coerced to `integer`.

`duplicates.ok`                should elements be in `table` be used more than once?

## Details

The behaviour differs by the value of `duplicates.ok`. Consider first the case if this is true. First exact matches are considered, and the positions of the first exact matches are recorded. Then unique partial matches are considered, and if found recorded. (A partial match occurs if the whole of the element of `x` matches the beginning of the element of `table`.) Finally, all remaining elements of `x` are regarded as unmatched. In addition, an empty string can match nothing, not even an exact match to an empty string. This is the appropriate behaviour for partial matching of character indices, for example.

If `duplicates.ok` is `FALSE`, values of `table` once matched are excluded from the search for subsequent matches. This behaviour is equivalent to the R algorithm for argument matching, except for the consideration of empty strings (which in argument matching are matched after exact and partial matching to any remaining arguments).

`charmatch` is similar to `pmatch` with `duplicates.ok` true, the differences being that it differentiates between no match and an ambiguous partial match, it does match empty strings, and it does not allow multiple exact matches.

NA values are treated as if they were the string constant "NA".

## Value

An integer vector (possibly including NA if `nomatch = NA`) of the same length as `x`, giving the indices of the elements in `table` which matched, or `nomatch`.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

## See Also

`match`, `charmatch` and `match.arg`, `match.fun`, `match.call`, for function argument matching etc., `grep` etc for more general (regexp) matching of strings.

## Examples

```
pmatch("", "") # returns NA
pmatch("m", c("mean", "median", "mode")) # returns NA
pmatch("med", c("mean", "median", "mode")) # returns 2

pmatch(c("", "ab", "ab"), c("abc", "ab"), dup=FALSE)
pmatch(c("", "ab", "ab"), c("abc", "ab"), dup=TRUE)
## compare
charmatch(c("", "ab", "ab"), c("abc", "ab"))
```

---

`polyroot`*Find Zeros of a Real or Complex Polynomial*

---

**Description**

Find zeros of a real or complex polynomial.

**Usage**

```
polyroot(z)
```

**Arguments**

`z` the vector of polynomial coefficients in increasing order.

**Details**

A polynomial of degree  $n - 1$ ,

$$p(x) = z_1 + z_2x + \dots + z_nx^{n-1}$$

is given by its coefficient vector `z[1:n]`. `polyroot` returns the  $n - 1$  complex zeros of  $p(x)$  using the Jenkins-Traub algorithm.

If the coefficient vector `z` has zeroes for the highest powers, these are discarded.

There is no maximum degree, but numerical stability may be an issue for all but low-degree polynomials.

**Value**

A complex vector of length  $n - 1$ , where  $n$  is the position of the largest non-zero element of `z`.

**References**

Jenkins and Traub (1972) TOMS Algorithm 419. *Comm. ACM*, **15**, 97–99.

**See Also**

[uniroot](#) for numerical root finding of arbitrary functions; [complex](#) and the `zero` example in the demos directory.

**Examples**

```
polyroot(c(1, 2, 1))
round(polyroot(choose(8, 0:8)), 11) # guess what!
for (n1 in 1:4) print(polyroot(1:n1), digits = 4)
polyroot(c(1, 2, 1, 0, 0)) # same as the first
```

---

pos.to.env	<i>Convert Positions in the Search Path to Environments</i>
------------	---

---

**Description**

Returns the environment at a specified position in the search path.

**Usage**

```
pos.to.env(x)
```

**Arguments**

`x` an integer between 1 and `length(search())`, the length of the search path.

**Details**

Several R functions for manipulating objects in environments (such as `get` and `ls`) allow specifying environments via corresponding positions in the search path. `pos.to.env` is a convenience function for programmers which converts these positions to corresponding environments; users will typically have no need for it. It is [primitive](#).

**Examples**

```
pos.to.env(1) # R_GlobalEnv
# the next returns the base environment
pos.to.env(length(search()))
```

---

pretty	<i>Pretty Breakpoints</i>
--------	---------------------------

---

**Description**

Compute a sequence of about `n+1` equally spaced ‘round’ values which cover the range of the values in `x`. The values are chosen so that they are 1, 2 or 5 times a power of 10.

**Usage**

```
pretty(x, n = 5, min.n = n %/% 3, shrink.sml = 0.75,
       high.u.bias = 1.5, u5.bias = .5 + 1.5*high.u.bias,
       eps.correct = 0)
```

**Arguments**

`x` an object coercible to numeric by `as.numeric`.

`n` integer giving the *desired* number of intervals. Non-integer values are rounded down.

`min.n` nonnegative integer giving the *minimal* number of intervals. If `min.n == 0`, `pretty(.)` may return a single value.



<code>shrink.sml</code>	positive numeric by which a default scale is shrunk in the case when <code>range(x)</code> is very small (usually 0).
<code>high.u.bias</code>	non-negative numeric, typically $> 1$ . The interval unit is determined as $\{1,2,5,10\}$ times <code>b</code> , a power of 10. Larger <code>high.u.bias</code> values favor larger units.
<code>u5.bias</code>	non-negative numeric multiplier favoring factor 5 over 2. Default and ‘optimal’: <code>u5.bias = .5 + 1.5*high.u.bias</code> .
<code>eps.correct</code>	integer code, one of $\{0,1,2\}$ . If non-0, an <i>epsilon correction</i> is made at the boundaries such that the result boundaries will be outside <code>range(x)</code> ; in the <i>small</i> case, the correction is only done if <code>eps.correct</code> $\geq 2$ .

### Details

`pretty` ignores non-finite values in `x`.

Let  $d \leftarrow \max(x) - \min(x) \geq 0$ . If  $d$  is not (very close) to 0, we let  $c \leftarrow d/n$ , otherwise more or less  $c \leftarrow \max(\text{abs}(\text{range}(x))) * \text{shrink.sml} / \text{min.n}$ . Then, the 10 base  $b$  is  $10^{\lfloor \log_{10}(c) \rfloor}$  such that  $b \leq c < 10b$ .

Now determine the basic *unit*  $u$  as one of  $\{1,2,5,10\}b$ , depending on  $c/b \in [1,10)$  and the two ‘*bias*’ coefficients,  $h = \text{high.u.bias}$  and  $f = \text{u5.bias}$ .

.....

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[axTicks](#) for the computation of `pretty` axis tick locations in plots, particularly on the log scale.

### Examples

```
pretty(1:15)      # 0  2  4  6  8 10 12 14 16
pretty(1:15, h=2) # 0  5 10 15
pretty(1:15, n=4) # 0  5 10 15
pretty(1:15 * 2)  # 0  5 10 15 20 25 30
pretty(1:20)     # 0  5 10 15 20
pretty(1:20, n=2) # 0 10 20
pretty(1:20, n=10) # 0  2  4 ... 20

for(k in 5:11) {
  cat("k=", k, ": "); print(diff(range(pretty(100 + c(0, pi*10^-k)))))}

##-- more bizarre, when min(x) == max(x):
pretty(pi)

add.names <- function(v) { names(v) <- paste(v); v }
utils::str(lapply(add.names(-10:20), pretty))
utils::str(lapply(add.names(0:20), pretty, min.n = 0))
sapply(  add.names(0:20), pretty, min.n = 4)

pretty(1.234e100)
pretty(1001.1001)
```

```
pretty(1001.1001, shrink = .2)
for(k in -7:3)
  cat("shrink=", formatC(2^k, width=9), ":",
      formatC(pretty(1001.1001, shrink.sml = 2^k), width=6), "\n")
```

---

Primitive

*Look Up a Primitive Function*

---

## Description

`.Primitive` looks up by name a ‘primitive’ (internally implemented) function.

## Usage

```
.Primitive(name)
```

## Arguments

name                    name of the R function.

## Details

The advantage of `.Primitive` over `.Internal` functions is the potential efficiency of argument passing, and that positional matching can be used where desirable, e.g. in `switch`. For more details, see the ‘R Internals Manual’.

All primitive functions are in the base name space.

This function is almost never used: ``name`` or, more carefully, `get(name, envir=baseenv())` work equally well and do not depend on knowing which functions are primitive (which does change as R evolves).

## See Also

[.Internal](#).

## Examples

```
mysqrt <- .Primitive("sqrt")
c
.Internal # this one *must* be primitive!
`if` # need backticks
```

print

*Print Values***Description**

`print` prints its argument and returns it *invisibly* (via `invisible(x)`). It is a generic function which means that new printing methods can be easily added for new `classes`.

**Usage**

```
print(x, ...)

## S3 method for class 'factor':
print(x, quote = FALSE, max.levels = NULL,
      width = getOption("width"), ...)

## S3 method for class 'table':
print(x, digits = getOption("digits"), quote = FALSE,
      na.print = "", zero.print = "0", justify = "none", ...)

## S3 method for class 'function':
print(x, useSource = TRUE, ...)
```

**Arguments**

<code>x</code>	an object used to select a method.
<code>...</code>	further arguments passed to or from other methods.
<code>quote</code>	logical, indicating whether or not strings should be printed with surrounding quotes.
<code>max.levels</code>	integer, indicating how many levels should be printed for a factor; if 0, no extra "Levels" line will be printed. The default, <code>NULL</code> , entails choosing <code>max.levels</code> such that the levels print on one line of width <code>width</code> .
<code>width</code>	only used when <code>max.levels</code> is <code>NULL</code> , see above.
<code>digits</code>	minimal number of <i>significant</i> digits, see <code>print.default</code> .
<code>na.print</code>	character string (or <code>NULL</code> ) indicating <code>NA</code> values in printed output, see <code>print.default</code> .
<code>zero.print</code>	character specifying how zeros (0) should be printed; for sparse tables, using <code>"."</code> can produce stronger results.
<code>justify</code>	character indicating if strings should left- or right-justified or left alone, passed to <code>format</code> .
<code>useSource</code>	logical indicating if a "source" attribute should be used for printing when present, e.g., if <code>options(keep.source=TRUE)</code> has been in use.

**Details**

The default method, `print.default` has its own help page. Use `methods("print")` to get all the methods for the `print` generic.

`print.factor` allows some customization and is used for printing `ordered` factors as well.

print.table for printing tables allows other customization.

See `noquote` as an example of a class whose main purpose is a specific print method.

## References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

## See Also

The default method `print.default`, and help for the methods above; further `options`, `noquote`.

For more customizable (but cumbersome) printing, see `cat`, `format` or also `write`.

## Examples

```
require(stats)

ts(1:20)##-- print is the "Default function" --> print.ts(.) is called
for(i in 1:3) print(1:i)

## Printing of factors
attenu$station ## 117 levels -> 'max.levels' depending on width

## ordered factors: levels "11 < 12 < .."
esoph$agegp[1:12]
esoph$alcgp[1:12]

## Printing of sparse (contingency) tables
set.seed(521)
t1 <- round(abs(rt(200, df=1.8)))
t2 <- round(abs(rt(200, df=1.4)))
table(t1,t2) # simple
print(table(t1,t2), zero.print = ".")# nicer to read
```

---

print.data.frame     *Printing Data Frames*

---

## Description

Print a data frame.

## Usage

```
## S3 method for class 'data.frame':
print(x, ..., digits = NULL,
      quote = FALSE, right = TRUE, row.names = TRUE)
```

**Arguments**

x	object of class <code>data.frame</code> .
...	optional arguments to <code>print</code> or <code>plot</code> methods.
digits	the minimum number of significant digits to be used: see <code>print.default</code> .
quote	logical, indicating whether or not entries should be printed with surrounding quotes.
right	logical, indicating whether or not strings should be right-aligned. The default is right-alignment.
row.names	logical (or character vector), indicating whether (or what) row names should be printed.

**Details**

This calls `format` which formats the data frame column-by-column, then converts to a character matrix and dispatches to the `print` method for matrices.

When `quote = TRUE` only the entries are quoted not the row names nor the column names.

**See Also**

`data.frame`.

**Examples**

```
(dd <- data.frame(x=1:8, f=gl(2,4), ch=I(letters[1:8])))
# print() with defaults
print(dd, quote = TRUE, row.names = FALSE)
# suppresses row.names and quotes all entries
```

---

print.default	<i>Default Printing</i>
---------------	-------------------------

---

**Description**

`print.default` is the *default* method of the generic `print` function which prints its argument.

**Usage**

```
## Default S3 method:
print(x, digits = NULL, quote = TRUE,
      na.print = NULL, print.gap = NULL, right = FALSE,
      max = NULL, useSource = TRUE, ...)
```

**Arguments**

x	the object to be printed.
digits	a non-null value for <code>digits</code> specifies the minimum number of significant digits to be printed in values. The default, <code>NULL</code> , uses <code>getOption(digits)</code> . (For the interpretation for complex numbers see <code>signif</code> .) Non-integer values will be rounded down, and only values greater than or equal to 1 and no greater than 22 are accepted.

quote	logical, indicating whether or not strings ( <a href="#">characters</a> ) should be printed with surrounding quotes.
na.print	a character string which is used to indicate <a href="#">NA</a> values in printed output, or NULL (see 'Details').
print.gap	a non-negative integer $\leq 1024$ , or NULL (meaning 1), giving the spacing between adjacent columns in printed vectors, matrices and arrays.
right	logical, indicating whether or not strings should be right aligned. The default is left alignment.
max	a non-null value for max specifies the approximate maximum number of entries to be printed. The default, NULL, uses <code>getOption(max.print)</code> ; see that help page for more details.
useSource	logical, indicating whether to use source references or copies rather than deparsing language objects. The default is to use the original source if it is available.
...	further arguments to be passed to or from other methods. They are ignored in this function.

### Details

The default for printing NAs is to print NA (without quotes) unless this is a character NA *and* quote = FALSE, when '<NA>' is printed.

The same number of decimal places is used throughout a vector. This means that digits specifies the minimum number of significant digits to be used, and that at least one entry will be encoded with that minimum number. However, if all the encoded elements then have trailing zeroes, the number of decimal places is reduced until at least one element has a non-zero final digit. Decimal points are only included if at least one decimal place is selected.

Attributes are printed respecting their class(es), using the values of digits to print.default, but using the default values (for the methods called) of the other arguments.

When the **methods** package is attached, print will call `show` for R objects with formal classes if called with no optional arguments.

### Warning

Using too large a value of digits may lead to representation errors in the calculation of the number of significant digits and the decimal representation: these are likely for digits  $\geq 16$ , and these possible errors are taken into account in assessing the number of significant digits to be printed in that case.

Whereas earlier versions of R might have printed further digits for digits  $\geq 16$  on some platforms, they were not necessarily reliable.

### Single-byte locales

If a non-printable character is encountered during output, it is represented as one of the ANSI escape sequences ('\a', '\b', '\f', '\n', '\r', '\t', '\v', '\\') and '\0': see [Quotes](#), or failing that as a 3-digit octal code: for example the UK currency pound sign in the C locale (if implemented correctly) is printed as '\243'. Which characters are non-printable depends on the locale. (Because some versions of Windows get this wrong, all bytes with the upper bit set are regarded as printable on Windows in a single-byte locale.)

### Unicode and other multi-byte locales

In all locales, the characters in the ASCII range ('0x00' to '0x7f') are printed in the same way, as-is if printable, otherwise via ANSI escape sequences or 3-digit octal escapes as described for single-byte locales.

Multi-byte non-printing characters are printed as an escape sequence of the form '\uxxxx' or '\Uxxxxxxxx' (in hexadecimal). This is the internal code for the wide-character representation of the character. If this is not known to be the Unicode point, a warning is issued. The only known exceptions are certain Japanese ISO2022 locales on commercial Unixes, which use a concatenation of the bytes: it is unlikely that R compiles on such a system.

It is possible to have a character string in a character vector that is not valid in the current locale. If a byte is encountered that is not part of a valid character it is printed in hex in the form '\xab' and this is repeated until the start of a valid character. (This will rapidly recover from minor errors in UTF-8.)

### See Also

The generic `print, options`. The "noquote" class and print method.  
`encodeString`, which encodes a character vector the way it would be printed.

### Examples

```
pi
print(pi, digits = 16)
LETTERS[1:16]
print(LETTERS, quote = FALSE)

M <- cbind(I = 1, matrix(1:10000, ncol = 10,
                        dimnames = list(NULL, LETTERS[1:10])))
utils::head(M) # makes more sense than
print(M, max = 1000) # prints 90 rows and a message about omitting 910
```

---

prmatrix

*Print Matrices, Old-style*

---

### Description

An earlier method for printing matrices, provided for S compatibility.

### Usage

```
prmatrix(x, rowlab =, collab =,
         quote = TRUE, right = FALSE, na.print = NULL, ...)
```

### Arguments

`x` numeric or character matrix.  
`rowlab, collab` (optional) character vectors giving row or column names respectively. By default, these are taken from `dimnames(x)`.  
`quote` logical; if TRUE and `x` is of mode "character", *quotes* (") are used.

right	if TRUE and <code>x</code> is of mode "character", the output columns are <i>right-justified</i> .
na.print	how NAs are printed. If this is non-null, its value is used to represent NA.
...	arguments for <code>print</code> methods.

### Details

`prmatrix` is an earlier form of `print.matrix`, and is very similar to the S function of the same name.

### Value

Invisibly returns its argument, `x`.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[print.default](#), and other `print` methods.

### Examples

```
prmatrix(m6 <- diag(6), rowlab = rep("",6), collab =rep("",6))

chm <- matrix(scan(system.file("help", "AnIndex", package = "splines"),
                        what = ""), , 2, byrow = TRUE)
chm # uses print.matrix()
prmatrix(chm, collab = paste("Column",1:3), right=TRUE, quote=FALSE)
```

---

proc.time

*Running Time of R*

---

### Description

`proc.time` determines how much real and CPU time (in seconds) the currently running R process has already taken.

### Usage

```
proc.time()
```

### Details

`proc.time` returns five elements for backwards compatibility, but its `print` method prints a named vector of length 3. The first two entries are the total user and system CPU times of the current R process and any child processes on which it has waited, and the third entry is the 'real' elapsed time since the process was started.



**Value**

An object of class "proc\_time" which is a numeric vector of length 5, containing the user, system, and total elapsed times for the currently running R process, and the cumulative sum of user and system times of any child processes spawned by it on which it has waited. (The `print` method combines the child times with those of the main process.)

The definition of 'user' and 'system' times is from your OS. Typically it is something like

*The 'user time' is the CPU time charged for the execution of user instructions of the calling process. The 'system time' is the CPU time charged for execution by the system on behalf of the calling process.*

The resolution of the times will be system-specific and on Unix-alikes times are rounded to the nearest 1ms. On modern systems they will be that accurate, but on older systems they might be accurate to 1/100 or 1/60 sec, and are typically available to 10ms on Windows.

This is a [primitive](#) function.

**Note**

It is possible to compile R without support for `proc.time`, when the function will throw an error.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[system.time](#) for timing a valid R expression, [gc.time](#) for how much of the time was spent in garbage collection.

**Examples**

```
## Not run:
## a way to time an R expression: system.time is preferred
ptm <- proc.time()
for (i in 1:50) mad(stats::runif(500))
proc.time() - ptm

## End(Not run)
```

---

prod

*Product of Vector Elements*

---

**Description**

`prod` returns the product of all the values present in its arguments.

**Usage**

```
prod(..., na.rm = FALSE)
```

**Arguments**

`...` numeric or complex or logical vectors.  
`na.rm` logical. Should missing values be removed?

**Details**

If `na.rm` is `FALSE` an NA value in any of the arguments will cause a value of NA to be returned, otherwise NA values are ignored.

This is a generic function: methods can be defined for it directly or via the [Summary](#) group generic. For this to work properly, the arguments `...` should be unnamed, and dispatch is on the first argument.

Logical true values are regarded as one, false values as zero. For historical reasons, `NULL` is accepted and treated as if it were `numeric(0)`.

**Value**

The product, a numeric (of type "double") or complex vector of length one. **NB:** the product of an empty set is one, by definition.

**S4 methods**

This is part of the S4 [Summary](#) group generic. Methods for it must use the signature `x, ..., na.rm`.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[sum](#), [cumprod](#), [cumsum](#).  
 ‘[plotmath](#)’ for the use of `prod` in plot annotation.

**Examples**

```
print(prod(1:7)) == print(gamma(8))
```

---

 prop.table

*Express Table Entries as Fraction of Marginal Table*


---

**Description**

This is really `sweep(x, margin, margin.table(x, margin), "/")` for newbies, except that if `margin` has length zero, then one gets `x/sum(x)`.

**Usage**

```
prop.table(x, margin=NULL)
```

**Arguments**

<code>x</code>	table
<code>margin</code>	index, or vector of indices to generate margin for

**Value**

Table like `x` expressed relative to `margin`

**Author(s)**

Peter Dalgaard

**See Also**

[margin.table](#)

**Examples**

```
m <- matrix(1:4, 2)
m
prop.table(m, 1)
```

---

pushBack

*Push Text Back on to a Connection*

---

**Description**

Functions to push back text lines onto a connection, and to enquire how many lines are currently pushed back.

**Usage**

```
pushBack(data, connection, newLine = TRUE)
pushBackLength(connection)
```

**Arguments**

<code>data</code>	a character vector.
<code>connection</code>	A connection.
<code>newLine</code>	logical. If true, a newline is appended to each string pushed back.

**Details**

Several character strings can be pushed back on one or more occasions. The occasions form a stack, so the first line to be retrieved will be the first string from the last call to `pushBack`. Lines which are pushed back are read prior to the normal input from the connection, by the normal text-reading functions such as [readLines](#) and [scan](#).

Pushback is only allowed for readable connections in text mode.

Not all uses of connections respect pushbacks, in particular the input connection is still wired directly, so for example parsing commands from the console and `scan("")` ignore pushbacks on [stdin](#).

When character strings with a marked encoding (see [Encoding](#)) are pushed back they are converted to the current encoding. This may involve representing characters as ‘<U+xxxx>’ if they cannot be converted.

### Value

`pushBack` returns nothing.

`pushBackLength` returns number of lines currently pushed back.

### See Also

[connections](#), [readLines](#).

### Examples

```
zz <- textConnection(LETTERS)
readLines(zz, 2)
pushBack(c("aa", "bb"), zz)
pushBackLength(zz)
readLines(zz, 1)
pushBackLength(zz)
readLines(zz, 1)
readLines(zz, 1)
close(zz)
```

### Description

`qr` computes the QR decomposition of a matrix. It provides an interface to the techniques used in the LINPACK routine DQRDC or the LAPACK routines DGEQP3 and (for complex matrices) ZGEQP3.

### Usage

```
qr(x, ...)
## Default S3 method:
qr(x, tol = 1e-07 , LAPACK = FALSE, ...)

qr.coef(qr, y)
qr.qy(qr, y)
qr.qty(qr, y)
qr.resid(qr, y)
qr.fitted(qr, y, k = qr$rank)
qr.solve(a, b, tol = 1e-7)
## S3 method for class 'qr':
solve(a, b, ...)

is.qr(x)
as.qr(x)
```

**Arguments**

<code>x</code>	a matrix whose QR decomposition is to be computed.
<code>tol</code>	the tolerance for detecting linear dependencies in the columns of <code>x</code> . Only used if LAPACK is false and <code>x</code> is real.
<code>qr</code>	a QR decomposition of the type computed by <code>qr</code> .
<code>y, b</code>	a vector or matrix of right-hand sides of equations.
<code>a</code>	a QR decomposition or ( <code>qr.solve</code> only) a rectangular matrix.
<code>k</code>	effective rank.
LAPACK	logical. For real <code>x</code> , if true use LAPACK otherwise use LINPACK.
...	further arguments passed to or from other methods

**Details**

The QR decomposition plays an important role in many statistical techniques. In particular it can be used to solve the equation  $Ax = b$  for given matrix  $A$ , and vector  $b$ . It is useful for computing regression coefficients and in applying the Newton-Raphson algorithm.

The functions `qr.coef`, `qr.resid`, and `qr.fitted` return the coefficients, residuals and fitted values obtained when fitting `y` to the matrix with QR decomposition `qr`. (If pivoting is used, some of the coefficients will be NA.) `qr.qy` and `qr.qty` return  $Q \%*\% y$  and  $t(Q) \%*\% y$ , where  $Q$  is the (complete)  $Q$  matrix.

All the above functions keep `dimnames` (and `names`) of `x` and `y` if there are.

`solve.qr` is the method for `solve` for `qr` objects. `qr.solve` solves systems of equations via the QR decomposition: if `a` is a QR decomposition it is the same as `solve.qr`, but if `a` is a rectangular matrix the QR decomposition is computed first. Either will handle over- and under-determined systems, providing a least-squares fit if appropriate.

`is.qr` returns TRUE if `x` is a `list` with components named `qr`, `rank` and `qraux` and FALSE otherwise.

It is not possible to coerce objects to mode "qr". Objects either are QR decompositions or they are not.

**Value**

The QR decomposition of the matrix as computed by LINPACK or LAPACK. The components in the returned value correspond directly to the values returned by DQRDC/DGEQP3/ZGEQP3.

<code>qr</code>	a matrix with the same dimensions as <code>x</code> . The upper triangle contains the $R$ of the decomposition and the lower triangle contains information on the $Q$ of the decomposition (stored in compact form). Note that the storage used by DQRDC and DGEQP3 differs.
<code>qraux</code>	a vector of length <code>ncol(x)</code> which contains additional information on $Q$ .
<code>rank</code>	the rank of <code>x</code> as computed by the decomposition: always full rank in the LAPACK case.
<code>pivot</code>	information on the pivoting strategy used during the decomposition.

Non-complex QR objects computed by LAPACK have the attribute "useLAPACK" with value TRUE.

**Note**

To compute the determinant of a matrix (do you *really* need it?), the QR decomposition is much more efficient than using Eigen values (`eigen`). See `det`.

Using LAPACK (including in the complex case) uses column pivoting and does not attempt to detect rank-deficient matrices.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Dongarra, J. J., Bunch, J. R., Moler, C. B. and Stewart, G. W. (1978) *LINPACK Users Guide*. Philadelphia: SIAM Publications.

Anderson. E. and ten others (1999) *LAPACK Users' Guide*. Third Edition. SIAM.  
Available on-line at [http://www.netlib.org/lapack/lug/lapack\\_lug.html](http://www.netlib.org/lapack/lug/lapack_lug.html).

**See Also**

`qr.Q`, `qr.R`, `qr.X` for reconstruction of the matrices. `lm.fit`, `lsfit`, `eigen`, `svd`.

`det` (using `qr`) to compute the determinant of a matrix.

**Examples**

```

hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, "+") }
h9 <- hilbert(9); h9
qr(h9)$rank          #--> only 7
qrh9 <- qr(h9, tol = 1e-10)
qrh9$rank           #--> 9
##-- Solve linear equation system H %**% x = y :
y <- 1:9/10
x <- qr.solve(h9, y, tol = 1e-10) # or equivalently :
x <- qr.coef(qrh9, y) #-- is == but much better than
                        #-- solve(h9) %**% y
h9 %**% x             # = y

## overdetermined system
A <- matrix(runif(12), 4)
b <- 1:4
qr.solve(A, b) # or solve(qr(A), b)
solve(qr(A, LAPACK=TRUE), b)
# this is a least-squares solution, cf. lm(b ~ 0 + A)

## underdetermined system
A <- matrix(runif(12), 3)
b <- 1:3
qr.solve(A, b)
solve(qr(A, LAPACK=TRUE), b)
# solutions will have one zero, not necessarily the same one

```

**Description**

Returns the original matrix from which the object was constructed or the components of the decomposition.

**Usage**

```
qr.X(qr, complete = FALSE, ncol =)
qr.Q(qr, complete = FALSE, Dvec =)
qr.R(qr, complete = FALSE)
```

**Arguments**

<code>qr</code>	object representing a QR decomposition. This will typically have come from a previous call to <code>qr</code> or <code>lsfit</code> .
<code>complete</code>	logical expression of length 1. Indicates whether an arbitrary orthogonal completion of the $Q$ or $X$ matrices is to be made, or whether the $R$ matrix is to be completed by binding zero-value rows beneath the square upper triangle.
<code>ncol</code>	integer in the range $1:nrow(qr\$qr)$ . The number of columns to be in the reconstructed $X$ . The default when <code>complete</code> is <code>FALSE</code> is the first $\min(ncol(X), nrow(X))$ columns of the original $X$ from which the <code>qr</code> object was constructed. The default when <code>complete</code> is <code>TRUE</code> is a square matrix with the original $X$ in the first $ncol(X)$ columns and an arbitrary orthogonal completion (unitary completion in the complex case) in the remaining columns.
<code>Dvec</code>	vector (not matrix) of diagonal values. Each column of the returned $Q$ will be multiplied by the corresponding diagonal value. Defaults to all 1s.

**Value**

`qr.X` returns  $X$ , the original matrix from which the `qr` object was constructed, provided  $ncol(X) \leq nrow(X)$ . If `complete` is `TRUE` or the argument `ncol` is greater than  $ncol(X)$ , additional columns from an arbitrary orthogonal (unitary) completion of  $X$  are returned.

`qr.Q` returns part or all of  $Q$ , the order- $nrow(X)$  orthogonal (unitary) transformation represented by `qr`. If `complete` is `TRUE`,  $Q$  has  $nrow(X)$  columns. If `complete` is `FALSE`,  $Q$  has  $ncol(X)$  columns. When `Dvec` is specified, each column of  $Q$  is multiplied by the corresponding value in `Dvec`.

`qr.R` returns  $R$ . The number of rows of  $R$  is either  $nrow(X)$  or  $ncol(X)$  (and may depend on whether `complete` is `TRUE` or `FALSE`).

**See Also**

`qr`, `qr.qy`.

**Examples**

```
p <- ncol(x <- LifeCycleSavings[,-1]) # not the 'sr'
qrstr <- qr(x) # dim(x) == c(n,p)
qrstr $ rank # = 4 = p
Q <- qr.Q(qrstr) # dim(Q) == dim(x)
R <- qr.R(qrstr) # dim(R) == ncol(x)
X <- qr.X(qrstr) # X == x
range(X - as.matrix(x)) # ~ < 6e-12
## X == Q %*% R if there has been no pivoting, as here.
Q %*% R
```

quit

*Terminate an R Session***Description**

The function `quit` or its alias `q` terminate the current R session.

**Usage**

```
quit(save = "default", status = 0, runLast = TRUE)
q(save = "default", status = 0, runLast = TRUE)
.Last <- function(x) { ..... }
```

**Arguments**

<code>save</code>	a character string indicating whether the environment (workspace) should be saved, one of "no", "yes", "ask" or "default".
<code>status</code>	the (numerical) error status to be returned to the operating system, where relevant. Conventionally 0 indicates successful completion.
<code>runLast</code>	should <code>.Last()</code> be executed?

**Details**

`save` must be one of "no", "yes", "ask" or "default". In the first case the workspace is not saved, in the second it is saved and in the third the user is prompted and can also decide *not* to quit. The default is to ask in interactive use but may be overridden by command-line arguments (which must be supplied in non-interactive use).

Immediately *before* terminating, the function `.Last()` is executed if it exists and `runLast` is true. If in interactive use there are errors in the `.Last` function, control will be returned to the command prompt, so do test the function thoroughly. There is a system analogue, `.Last.sys()`, which is run after `.Last()` if `runLast` is true.

Exactly what happens at termination of an R session depends on the platform and GUI interface in use. A typical sequence is to run `.Last()` and `.Last.sys()` (unless `runLast` is false), to save the workspace if requested (and in most cases also to save the session history: see [savehistory](#)), then run any finalizers (see [reg.finalizer](#)) that have been set to be run on exit, close all open graphics devices, remove the session temporary directory and print any remaining warnings (e.g. from `.Last()` and device closure).

Some error statuses are used by R itself. The default error handler for non-interactive use effectively calls `q("no", 1, FALSE)` and returns error code 1. Error status 2 is used for R 'suicide', that is



a catastrophic failure, and other small numbers are used by specific ports for initialization failures. It is recommended that users choose statuses of 10 or more.

Valid values of `status` are system-dependent, but `0:255` are normally valid. (Many OSes will report the last byte of the value, that is report the number modulo 256. But not all.)

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

`.First` for setting things on startup.

## Examples

```
## Not run: ## Unix-flavour example
.Last <- function() {
  cat("Now sending PostScript graphics to the printer:\n")
  system("lpr Rplots.ps")
  cat("bye bye...\n")
}
quit("yes")
## End(Not run)
```

---

Quotes

*Quotes*

---

## Description

Descriptions of the various uses of quoting in R.

## Details

Three types of quotes are part of the syntax of R: single and double quotation marks and the backtick (or back quote, ‘`’). In addition, backslash is used for escaping the following character inside character constants.

## Character constants

Single and double quotes delimit character constants. They can be used interchangeably but double quotes are preferred (and character constants are printed using double quotes), so single quotes are normally only used to delimit character constants containing double quotes.

Backslash is used to start an escape sequence inside character constants. Escaping a character not in the following table is an error (since R 2.11.0; earlier versions accepted them with a warning).

Single quotes need to be escaped by backslash in single-quoted strings, and double quotes in double-quoted strings.

<code>‘\n’</code>	newline
<code>‘\r’</code>	carriage return
<code>‘\t’</code>	tab
<code>‘\b’</code>	backspace

<code>'\a'</code>	alert (bell)
<code>'\f'</code>	form feed
<code>'\v'</code>	vertical tab
<code>'\\'</code>	backslash <code>'\'</code>
<code>'\''</code>	ASCII apostrophe <code>''</code>
<code>'\"'</code>	ASCII quotation mark <code>''</code>
<code>'\nnn'</code>	character with given octal code (1, 2 or 3 digits)
<code>'\xnn'</code>	character with given hex code (1 or 2 hex digits)
<code>'\unnnn'</code>	Unicode character with given code (1–4 hex digits)
<code>'\Unnnnnnnn'</code>	Unicode character with given code (1–8 hex digits)

Alternative forms for the last two are `'\u{nnnn}'` and `'\U{nnnnnnnn}'`. All except the Unicode escape sequences are also supported when reading character strings by `scan` and `read.table` if `allowEscapes = TRUE`. Unicode escapes can be used to enter Unicode characters not in the current locale (which will be stored internally in UTF-8).

It is not advisable to use both octal/hex and Unicode escapes in a single string: the results can be unintended and this will be disallowed in future versions of R.

These forms will also be used by `print.default` when outputting non-printable characters (including backslash).

Embedded nuls are not allowed in character strings, so using escapes (such as `'\0'`) for a nul will result in the string being truncated at that point (usually with a warning).

## Names and Identifiers

Identifiers consist of a sequence of letters, digits, the period (`.`) and the underscore. They must not start with a digit nor underscore, nor with a period followed by a digit. `Reserved` words are not valid identifiers.

The definition of a *letter* depends on the current locale, but only ASCII digits are considered to be digits.

Such identifiers are also known as *syntactic names* and may be used directly in R code. Almost always, other names can be used provided they are quoted. The preferred quote is the backtick (```), and `deparse` will normally use it, but under many circumstances single or double quotes can be used (as a character constant will often be converted to a name). One place where backticks may be essential is to delimit variable names in formulae: see [formula](#).

## See Also

[Syntax](#) for other aspects of the syntax.

[sQuote](#) for quoting English text.

[shQuote](#) for quoting OS commands.

The *R Language Definition* manual.

---

R.Version	<i>Version Information</i>
-----------	----------------------------

---

**Description**

`R.Version()` provides detailed information about the version of R running.

`R.version` is a variable (a [list](#)) holding this information (and `version` is a copy of it for S compatibility).

**Usage**

```
R.Version()
R.version
R.version.string
version
```

**Value**

`R.Version` returns a list with character-string components

<code>platform</code>	the platform for which R was built. A triplet of the form CPU-VENDOR-OS, as determined by the configure script. E.g. "i586-unknown-linux" or "i386-pc-mingw32".
<code>arch</code>	the architecture (CPU) R was built on/for.
<code>os</code>	the underlying operating system
<code>system</code>	CPU and OS, separated by a comma.
<code>status</code>	the status of the version (e.g., "Alpha")
<code>major</code>	the major version number
<code>minor</code>	the minor version number, including the patchlevel
<code>year</code>	the year the version was released
<code>month</code>	the month the version was released
<code>day</code>	the day the version was released
<code>svn rev</code>	the Subversion revision number, which should be either "unknown" or a single number. (A range of numbers or a number with 'M' or 'S' appended indicates inconsistencies in the sources used to build this version of R.)
<code>language</code>	always "R".
<code>version.string</code>	a <a href="#">character</a> string concatenating some of the info above, useful for plotting, etc.

`R.version` and `version` are lists of class "simple.list" which has a `print` method.

**Note**

Do *not* use `R.version$os` to test the platform the code is running on: use `.Platform$OS.type` instead. Slightly different versions of the OS may report different values of `R.version$os`, as may different versions of R.

`R.version.string` is a copy of `R.version$version.string` for simplicity and backwards compatibility.

**See Also**

`sessionInfo` which provides additional information; `getRversion` typically used inside R code, `.Platform`.

**Examples**

```
require(graphics)

R.version$os # to check how lucky you are ...
plot(0) # any plot
mtext(R.version.string, side=1,line=4,adj=1) # a useful bottom-right note
```

---

Random

*Random Number Generation*


---

**Description**

`.Random.seed` is an integer vector, containing the random number generator (RNG) **state** for random number generation in R. It can be saved and restored, but should not be altered by the user.

`RNGkind` is a more friendly interface to query or set the kind of RNG in use.

`RNGversion` can be used to set the random generators as they were in an earlier R version (for reproducibility).

`set.seed` is the recommended way to specify seeds.

**Usage**

```
.Random.seed <- c(rng.kind, n1, n2, ...)
save.seed <- .Random.seed

RNGkind(kind = NULL, normal.kind = NULL)
RNGversion(vstr)
set.seed(seed, kind = NULL, normal.kind = NULL)
```

**Arguments**

<code>kind</code>	character or NULL. If <code>kind</code> is a character string, set R's RNG to the kind desired. Use "default" to return to the R default. See 'Details' for the interpretation of NULL.
<code>normal.kind</code>	character string or NULL. If it is a character string, set the method of Normal generation. Use "default" to return to the R default. NULL makes no change.
<code>seed</code>	a single value, interpreted as an integer.
<code>vstr</code>	a character string containing a version number, e.g., "1.6.2"
<code>rng.kind</code>	integer code in 0:k for the above kind.
<code>n1, n2, ...</code>	integers. See the details for how many are required (which depends on <code>rng.kind</code> ).

## Details

The currently available RNG kinds are given below. `kind` is partially matched to this list. The default is "Mersenne-Twister".

"Wichmann-Hill" The seed, `.Random.seed[-1] == r[1:3]` is an integer vector of length 3, where each `r[i]` is in  $1:(p[i] - 1)$ , where `p` is the length 3 vector of primes, `p = (30269, 30307, 30323)`. The Wichmann-Hill generator has a cycle length of  $6.9536 \times 10^{12}$  ( $= \text{prod}(p-1) / 4$ , see *Applied Statistics* (1984) **33**, 123 which corrects the original article).

"Marsaglia-Multicarry": A *multiply-with-carry* RNG is used, as recommended by George Marsaglia in his post to the mailing list 'sci.stat.math'. It has a period of more than  $2^{60}$  and has passed all tests (according to Marsaglia). The seed is two integers (all values allowed).

"Super-Duper": Marsaglia's famous Super-Duper from the 70's. This is the original version which does *not* pass the MTUPLE test of the Diehard battery. It has a period of  $\approx 4.6 \times 10^{18}$  for most initial seeds. The seed is two integers (all values allowed for the first seed: the second must be odd).

We use the implementation by Reeds et al. (1982-84).

The two seeds are the Tausworthe and congruence long integers, respectively. A one-to-one mapping to S's `.Random.seed[1:12]` is possible but we will not publish one, not least as this generator is **not** exactly the same as that in recent versions of S-PLUS.

"Mersenne-Twister": From Matsumoto and Nishimura (1998). A twisted GFSR with period  $2^{19937} - 1$  and equidistribution in 623 consecutive dimensions (over the whole period). The 'seed' is a 624-dimensional set of 32-bit integers plus a current position in that set.

"Knuth-TAOCP-2002": A 32-bit integer GFSR using lagged Fibonacci sequences with subtraction. That is, the recurrence used is

$$X_j = (X_{j-100} - X_{j-37}) \bmod 2^{30}$$

and the 'seed' is the set of the 100 last numbers (actually recorded as 101 numbers, the last being a cyclic shift of the buffer). The period is around  $2^{129}$ .

"Knuth-TAOCP": An earlier version from Knuth (1997).

The 2002 version was not backwards compatible with the earlier version: the initialization of the GFSR from the seed was altered. R did not allow you to choose consecutive seeds, the reported 'weakness', and already scrambled the seeds.

Initialization of this generator is done in interpreted R code and so takes a short but noticeable time.

"user-supplied": Use a user-supplied generator. See [Random.user](#) for details.

`normal.kind` can be "Kinderman-Ramage", "Buggy Kinderman-Ramage" (not for `set.seed`), "Ahrens-Dieter", "Box-Muller", "Inversion" (the default), or "user-supplied". (For inversion, see the reference in [qnorm](#).) The Kinderman-Ramage generator used in versions prior to 1.7.1 (now called "Buggy" had several approximation errors and should only be used for reproduction of older results. The "Box-Muller" generator is stateful as pairs of normals are generated and returned sequentially. The state is reset whenever it is selected (even if it is the current normal generator) and when `kind` is changed.

`set.seed` uses its single integer argument to set as many seeds as are required. It is intended as a simple way to get quite different seeds by specifying small integer arguments, and also as a way to get valid seed sets for the more complicated methods (especially "Mersenne-Twister" and "Knuth-TAOCP").

The use of `kind=NULL` or `normal.kind=NULL` in `RNGkind` or `set.seed` selects the currently-used generator (including that used in the previous session if the workspace has been restored): if no generator has been used it selects "default".

**Value**

`.Random.seed` is an `integer` vector whose first element *codes* the kind of RNG and normal generator. The lowest two decimal digits are in  $0:(k-1)$  where  $k$  is the number of available RNGs. The hundreds represent the type of normal generator (starting at 0).

In the underlying C, `.Random.seed[-1]` is unsigned; therefore in R `.Random.seed[-1]` can be negative, due to the representation of an unsigned integer by a signed integer.

`RNGkind` returns a two-element character vector of the RNG and normal kinds selected *before* the call, invisibly if either argument is not NULL. A type starts a session as the default, and is selected either by a call to `RNGkind` or by setting `.Random.seed` in the workspace.

`RNGversion` returns the same information as `RNGkind` about the defaults in a specific R version.

`set.seed` returns NULL, invisibly.

**Note**

Initially, there is no seed; a new one is created from the current time when one is required. Hence, different sessions started at (sufficiently) different times will give different simulation results, by default. However, the seed might be restored from a previous session if a previously saved workspace is restored.

`.Random.seed` saves the seed set for the uniform random-number generator, at least for the system generators. It does not necessarily save the state of other generators, and in particular does not save the state of the Box–Muller normal generator. If you want to reproduce work later, call `set.seed` (preferably with explicit values for `kind` and `normal.kind`) rather than `set.Random.seed`.

The object `.Random.seed` is only looked for in the user's workspace.

Do not rely on randomness of low-order bits from RNGs. Most of the supplied uniform generators return 32-bit integer values that are converted to doubles, so they take at most  $2^{32}$  distinct values and long runs will return duplicated values (Wichmann-Hill is the exception, and all give at least 30 varying bits.)

**Author(s)**

of `RNGkind`: Martin Maechler. Current implementation, B. D. Ripley

**References**

- Ahrens, J. H. and Dieter, U. (1973) Extensions of Forsythe's method for random sampling from the normal distribution. *Mathematics of Computation* **27**, 927-937.
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Marsaglia, G. (1997) *A random number generator for C*. Discussion paper, posting on Usenet newsgroup `sci.stat.math` on September 29, 1997.

Marsaglia, G. and Zaman, A. (1994) Some portable very-long-period random number generators. *Computers in Physics*, **8**, 117–121.

Matsumoto, M. and Nishimura, T. (1998) Mersenne Twister: A 623-dimensionally equidistributed uniform pseudo-random number generator, *ACM Transactions on Modeling and Computer Simulation*, **8**, 3–30.

Source code at <http://www.math.keio.ac.jp/~matumoto/emt.html>.

Reeds, J., Hubert, S. and Abrahams, M. (1982–4) C implementation of SuperDuper, University of California at Berkeley. (Personal communication from Jim Reeds to Ross Ihaka.)

Wichmann, B. A. and Hill, I. D. (1982) *Algorithm AS 183: An Efficient and Portable Pseudo-random Number Generator*, *Applied Statistics*, **31**, 188–190; Remarks: **34**, 198 and **35**, 89.

## See Also

[runif](#), [rnorm](#), ...

## Examples

```
require(stats)

## the default random seed is 626 integers, so only print a few
runif(1); .Random.seed[1:6]; runif(1); .Random.seed[1:6]
## If there is no seed, a "random" new one is created:
rm(.Random.seed); runif(1); .Random.seed[1:6]

ok <- RNGkind()
RNGkind("Wich")# (partial string matching on 'kind')

## This shows how 'runif(.)' works for Wichmann-Hill,
## using only R functions:

p.WH <- c(30269, 30307, 30323)
a.WH <- c( 171,  172,  170)
next.WHseed <- function(i.seed = .Random.seed[-1])
  { (a.WH * i.seed) %% p.WH }
my.runif1 <- function(i.seed = .Random.seed)
  { ns <- next.WHseed(i.seed[-1]); sum(ns / p.WH) %% 1 }
rs <- .Random.seed
(WHs <- next.WHseed(rs[-1]))
u <- runif(1)
stopifnot(
  next.WHseed(rs[-1]) == .Random.seed[-1],
  all.equal(u, my.runif1(rs))
)

## ----
.Random.seed
RNGkind("Super")#matches "Super-Duper"
RNGkind()
.Random.seed # new, corresponding to Super-Duper

## Reset:
RNGkind(ok[1])
```

```
## ----
sum(duplicated(runif(1e6))) # around 110 for default generator
## and we would expect about almost sure duplicates beyond about
qbirthday(1-1e-6, classes=2e9) # 235,000
```

---

Random.user

*User-supplied Random Number Generation*


---

## Description

Function `RNGkind` allows user-coded uniform and normal random number generators to be supplied. The details are given here.

## Details

A user-specified uniform RNG is called from entry points in dynamically-loaded compiled code. The user must supply the entry point `user_unif_rand`, which takes no arguments and returns a *pointer to a double*. The example below will show the general pattern.

Optionally, the user can supply the entry point `user_unif_init`, which is called with an `unsigned int` argument when `RNGkind` (or `set.seed`) is called, and is intended to be used to initialize the user's RNG code. The argument is intended to be used to set the 'seeds'; it is the seed argument to `set.seed` or an essentially random seed if `RNGkind` is called.

If only these functions are supplied, no information about the generator's state is recorded in `.Random.seed`. Optionally, functions `user_unif_nseed` and `user_unif_seedloc` can be supplied which are called with no arguments and should return pointers to the number of seeds and to an integer (specifically, 'Int32') array of seeds. Calls to `GetRNGstate` and `PutRNGstate` will then copy this array to and from `.Random.seed`.

A user-specified normal RNG is specified by a single entry point `user_norm_rand`, which takes no arguments and returns a *pointer to a double*.

## Warning

As with all compiled code, mis-specifying these functions can crash R. Do include the '`R_ext/Random.h`' header file for type checking.

## Examples

```
## Not run:
## Marsaglia's congruential PRNG
#include <R_ext/Random.h>

static Int32 seed;
static double res;
static int nseed = 1;

double * user_unif_rand()
{
    seed = 69069 * seed + 1;
    res = seed * 2.32830643653869e-10;
    return &res;
}
```



```

void user_unif_init(Int32 seed_in) { seed = seed_in; }
int * user_unif_nseed() { return &nseed; }
int * user_unif_seedloc() { return (int *) &seed; }

/* ratio-of-uniforms for normal */
#include <math.h>
static double x;

double * user_norm_rand()
{
  double u, v, z;
  do {
    u = unif_rand();
    v = 0.857764 * (2. * unif_rand() - 1);
    x = v/u; z = 0.25 * x * x;
    if (z < 1. - u) break;
    if (z > 0.259/u + 0.35) continue;
  } while (z > -log(u));
  return &x;
}

## Use under Unix:
R CMD SHLIB urand.c
R
> dyn.load("urand.so")
> RNGkind("user")
> runif(10)
> .Random.seed
> RNGkind(, "user")
> rnorm(10)
> RNGkind()
[1] "user-supplied" "user-supplied"

## End(Not run)

```

---

range

*Range of Values*


---

### Description

range returns a vector containing the minimum and maximum of all the given arguments.

### Usage

```
range(..., na.rm = FALSE)
```

```
## Default S3 method:
```

```
range(..., na.rm = FALSE, finite = FALSE)
```

### Arguments

... any [numeric](#) or character objects.

na.rm logical, indicating if [NA](#)'s should be omitted.

finite logical, indicating if all non-finite elements should be omitted.

**Details**

`range` is a generic function: methods can be defined for it directly or via the [Summary](#) group generic. For this to work properly, the arguments `...` should be unnamed, and dispatch is on the first argument.

If `na.rm` is `FALSE`, `NA` and `NaN` values in any of the arguments will cause `NA` values to be returned, otherwise `NA` values are ignored.

If `finite` is `TRUE`, the minimum and maximum of all finite values is computed, i.e., `finite=TRUE` *includes* `na.rm=TRUE`.

A special situation occurs when there is no (after omission of `NA`s) nonempty argument left, see [min](#).

**S4 methods**

This is part of the S4 [Summary](#) group generic. Methods for it must use the signature `x, ..., na.rm`.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[min](#), [max](#).

The [extendrange](#) () utility in package **grDevices**.

**Examples**

```
(r.x <- range(stats::rnorm(100)))
diff(r.x) # the SAMPLE range

x <- c(NA, 1:3, -1:1/0); x
range(x)
range(x, na.rm = TRUE)
range(x, finite = TRUE)
```

---

rank

*Sample Ranks*


---

**Description**

Returns the sample ranks of the values in a vector. Ties (i.e., equal values) and missing values can be handled in several ways.

**Usage**

```
rank(x, na.last = TRUE,
     ties.method = c("average", "first", "random", "max", "min"))
```

## Arguments

<code>x</code>	a numeric, complex, character or logical vector.
<code>na.last</code>	for controlling the treatment of NAs. If <code>TRUE</code> , missing values in the data are put last; if <code>FALSE</code> , they are put first; if <code>NA</code> , they are removed; if <code>"keep"</code> they are kept with rank <code>NA</code> .
<code>ties.method</code>	a character string specifying how ties are treated, see ‘Details’; can be abbreviated.

## Details

If all components are different (and no NAs), the ranks are well defined, with values in `seq_len(x)`. With some values equal (called ‘ties’), the argument `ties.method` determines the result at the corresponding indices. The `"first"` method results in a permutation with increasing values at each index set of ties. The `"random"` method puts these in random order whereas the default, `"average"`, replaces them by their mean, and `"max"` and `"min"` replaces them by their maximum and minimum respectively, the latter being the typical sports ranking.

NA values are never considered to be equal: for `na.last = TRUE` and `na.last = FALSE` they are given distinct ranks in the order in which they occur in `x`.

**NB:** `rank` is not itself generic but `xtfrm` is, and `rank(xtfrm(x), ...)` will have the desired result if there is a `xtfrm` method. Otherwise, `rank` will make use of `==`, `>` and `is.na` methods for classed objects, possibly rather slowly.

## Value

A numeric vector of the same length as `x` with names copied from `x` (unless `na.last = NA`, when missing values are removed). The vector is of integer type unless `ties.method = "average"` when it is of double type (whether or not there are any ties).

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[order](#) and [sort](#).

## Examples

```
(r1 <- rank(x1 <- c(3, 1, 4, 15, 92)))
x2 <- c(3, 1, 4, 1, 5, 9, 2, 6, 5, 3, 5)
names(x2) <- letters[1:11]
(r2 <- rank(x2)) # ties are averaged

## rank() is "idempotent": rank(rank(x)) == rank(x) :
stopifnot(rank(r1) == r1, rank(r2) == r2)

## ranks without averaging
rank(x2, ties.method= "first") # first occurrence wins
rank(x2, ties.method= "random") # ties broken at random
rank(x2, ties.method= "random") # and again

## keep ties ties, no average
```

```
(rma <- rank(x2, ties.method= "max")) # as used classically
(rmi <- rank(x2, ties.method= "min")) # as in Sports
stopifnot(rma + rmi == round(r2 + r2))
```

---

rapply *Recursively Apply a Function to a List*

---

## Description

rapply is a recursive version of [lapply](#).

## Usage

```
rapply(object, f, classes = "ANY", deflt = NULL,
       how = c("unlist", "replace", "list"), ...)
```

## Arguments

object	A list.
f	A function of a single argument.
classes	A character vector of <a href="#">class</a> names, or "ANY" to match any class.
deflt	The default result (not used if how = "replace").
how	A character string matching the three possibilities given: see 'Details'.
...	additional arguments passed to the call to f.

## Details

This function has two basic modes. If how = "replace", each element of the list which is not itself a list and has a class included in classes is replaced by the result of applying f to the element.

If the mode is how = "list" or how = "unlist", the list is copied, all non-list elements which have a class included in classes are replaced by the result of applying f to the element and all others are replaced by deflt. Finally, if how = "unlist", `unlist(recursive = TRUE)` is called on the result.

The semantics differ in detail from [lapply](#): in particular the arguments are evaluated before calling the C code.

## Value

If how = "unlist", a vector, otherwise a list of similar structure to object.

## References

Chambers, J. A. (1998) *Programming with Data*. Springer.  
(rapply is only described briefly there.)

## See Also

[lapply](#), [dendrapply](#).

## Examples

```
X <- list(list(a=pi, b=list(c=1:1)), d="a test")
rapply(X, function(x) x, how="replace")
rapply(X, sqrt, classes="numeric", how="replace")
rapply(X, nchar, classes="character",
       deflt = as.integer(NA), how="list")
rapply(X, nchar, classes="character",
       deflt = as.integer(NA), how="unlist")
rapply(X, nchar, classes="character", how="unlist")
rapply(X, log, classes="numeric", how="replace", base=2)
```

---

raw

*Raw Vectors*

---

## Description

Creates or tests for objects of type "raw".

## Usage

```
raw(length = 0)
as.raw(x)
is.raw(x)
```

## Arguments

length	desired length.
x	object to be coerced.

## Details

The raw type is intended to hold raw bytes. It is possible to extract subsequences of bytes, and to replace elements (but only by elements of a raw vector). The relational operators (see [Comparison](#)) work, as do the logical operators (see [Logic](#)) with a bitwise interpretation.

A raw vector is printed with each byte separately represented as a pair of hex digits. If you want to see a character representation (with escape sequences for non-printing characters) use [rawToChar](#).

Coercion to raw treats the input values as representing a small (decimal) integers, so the input is first coerced to integer, and then values which are outside the range [0 . . . 255] or are NA are set to 0 (the nul byte).

`as.raw` and `is.raw` are [primitive](#) functions.

## Value

`raw` creates a raw vector of the specified length. Each element of the vector is equal to 0. Raw vectors are used to store fixed-length sequences of bytes.

`as.raw` attempts to coerce its argument to be of raw type. The (elementwise) answer will be 0 unless the coercion succeeds (or if the original value successfully coerces to 0).

`is.raw` returns true if and only if `typeof(x) == "raw"`.

**See Also**

[charToRaw](#), [rawShift](#), etc.

**Examples**

```
xx <- raw(2)
xx[1] <- as.raw(40)      # NB, not just 40.
xx[2] <- charToRaw("A")
xx

x <- "A test string"
(y <- charToRaw(x))
is.vector(y) # TRUE
rawToChar(y)
is.raw(x)
is.raw(y)

isASCII <- function(txt) all(charToRaw(txt) <= as.raw(127))
isASCII(x) # true
isASCII("\x9c25.63") # false (in Latin-1, this is an amount in UK pounds)
```

---

rawConnection      *Raw Connections*

---

**Description**

Input and output raw connections.

**Usage**

```
rawConnection(object, open = "r")

rawConnectionValue(con)
```

**Arguments**

object	character or raw vector. A description of the connection. For an input this is an R raw vector object, and for an output connection the name for the connection.
open	character. Any of the standard connection open modes.
con	An output raw connection.

**Details**

An input raw connection is opened and the raw vector is copied at the time the connection object is created, and `close` destroys the copy.

An output raw connection is opened and creates an R raw vector internally. The raw vector can be retrieved *via* `rawConnectionValue`.

If a connection is open for both input and output the initial raw vector supplied is copied when the connections is open

**Value**

For `rawConnection`, a connection object of class `"rawConnection"` which inherits from class `"connection"`.

For `rawConnectionValue`, a raw vector.

**Note**

As output raw connections keep the internal raw vector up to date call-by-call, they are relatively expensive to use (although over-allocation is used), and it may be better to use an anonymous `file()` connection to collect output.

On (rare) platforms where `vsnprintf` does not return the needed length of output there is a 100,000 character limit on the length of line for output connections: longer lines will be truncated with a warning.

**See Also**

[connections](#), [showConnections](#).

**Examples**

```
zz <- rawConnection(raw(0), "r+") # start with empty raw vector
writeBin(LETTERS, zz)
seek(zz, 0)
readLines(zz) # raw vector has embedded nuls
seek(zz, 0)
writeBin(letters[1:3], zz)
rawConnectionValue(zz)
close(zz)
```

---

rawConversion

*Convert to or from Raw Vectors*

---

**Description**

Conversion and manipulation of objects of type `"raw"`.

**Usage**

```
charToRaw(x)
rawToChar(x, multiple = FALSE)

rawShift(x, n)

rawToBits(x)
intToBits(x)
packBits(x, type = c("raw", "integer"))
```

**Arguments**

<code>x</code>	object to be converted or shifted.
<code>multiple</code>	logical: should the conversion be to a single character string or multiple individual characters?
<code>n</code>	the number of bits to shift. Positive numbers shift right and negative numbers shift left: allowed values are <code>-8 ... 8</code> .
<code>type</code>	the result type.

**Details**

`packBits` accepts raw, integer or logical inputs, the last two without any NAs.

Note that ‘bytes’ are not necessarily the same as characters, e.g. in UTF-8 locales.

**Value**

`charToRaw` converts a length-one character string to raw bytes. It does so without taking into account any declared encoding (see [Encoding](#)).

`rawToChar` converts raw bytes either to a single character string or a character vector of single bytes (with `" "` for 0). (Note that a single character string could contain embedded nuls; only trailing nuls are allowed and will be removed.) In either case it is possible to create a result which is invalid in a multibyte locale, e.g. one using UTF-8.

`rawShift(x, n)` shift the bits in `x` by `n` positions to the right, see the argument `n`, above.

`rawToBits` returns a raw vector of 8 times the length of a raw vector with entries 0 or 1. `intToBits` returns a raw vector of 32 times the length of an integer vector with entries 0 or 1. (Non-integral numeric values are truncated to integers.) In both cases the unpacking is least-significant bit first.

`packBits` packs its input (using only the lowest bit for raw or integer vectors) least-significant bit first to a raw or integer vector.

**Examples**

```
x <- "A test string"
(y <- charToRaw(x))
is.vector(y) # TRUE

rawToChar(y)
rawToChar(y, multiple = TRUE)
(xx <- c(y, charToRaw("&"), charToRaw("more")))
rawToChar(xx)

rawShift(y, 1)
rawShift(y, -2)

rawToBits(y)

showBits <- function(r) stats::symnum(as.logical(rawToBits(r)))

z <- as.raw(5)
z ; showBits(z)
showBits(rawShift(z, 1)) # shift to right
showBits(rawShift(z, 2))
showBits(z)
```



```
showBits(rawShift(z, -1)) # shift to left
showBits(rawShift(z, -2)) # ..
showBits(rawShift(z, -3)) # shifted off entirely
```

---

RdUtils

*Utilities for Processing Rd Files*


---

## Description

Utilities for converting files in R documentation (Rd) format to other formats or create indices from them, and for converting documentation in other formats to Rd format.

## Usage

```
R CMD Rdconv [options] file
R CMD Rd2dvi [options] files
R CMD Rd2pdf [options] files
R CMD Sd2Rd [options] file
```

## Arguments

<code>file</code>	the path to a file to be processed.
<code>files</code>	a list of file names specifying the R documentation sources to use, by either giving the paths to the files, or the path to a directory with the sources of a package.
<code>options</code>	further options to control the processing, or for obtaining information about usage and version of the utility.

## Details

R CMD `Rdconv` converts Rd format to plain text, HTML or LaTeX formats: it can also extract the examples.

R CMD `Rd2dvi` is the user-level program for producing DVI/PDF output from Rd sources. It will make use of the environment variables `R_PAPERSIZE` (set by R CMD, with a default set when R was installed) and `xdvi` (the DVI previewer, default `xdvi`), and `R_PDFVIEWER` (the PDF previewer). (Valid values for `R_PAPERSIZE` are `a4`, `letter`, `legal` and `executive`.) `Rd2pdf` is shorthand for `Rd2dvi --pdf`.

R CMD `Sd2Rd` converts S (version 3 or 4) documentation formats to Rd format: it is no longer much used and the results may need hand-tuning. (It requires Perl.)

Use R CMD `foo --help` to obtain usage information on utility `foo`.

## See Also

The chapter “Processing Rd format” in the “Writing R Extensions” manual.

readBin

*Transfer Binary Data To and From Connections***Description**

Read binary data from a connection, or write binary data to a connection.

**Usage**

```
readBin(con, what, n = 1L, size = NA_integer_, signed = TRUE,
        endian = .Platform$endian)
```

```
writeBin(object, con, size = NA_integer_,
         endian = .Platform$endian, useBytes = FALSE)
```

**Arguments**

con	A connection object or a character string naming a file or a raw vector.
what	Either an object whose mode will give the mode of the vector to be read, or a character vector of length one describing the mode: one of "numeric", "double", "integer", "int", "logical", "complex", "character", "raw".
n	integer. The (maximal) number of records to be read. You can use an over-estimate here, but not too large as storage is reserved for n items.
size	integer. The number of bytes per element in the byte stream. The default, NA_integer_, uses the natural size. Size changing is not supported for raw and complex vectors.
signed	logical. Only used for integers of sizes 1 and 2, when it determines if the quantity on file should be regarded as a signed or unsigned integer.
endian	The endian-ness ("big" or "little" of the target system for the file. Using "swap" will force swapping endian-ness.
object	An R object to be written to the connection.
useBytes	See <a href="#">writeLines</a> .

**Details**

If `con` is a character string, the functions call [file](#) to obtain an file connection which is opened for the duration of the function call.

If the connection is open it is read/written from its current position. If it is not open, it is opened for the duration of the call in an appropriate mode (binary read or write) and then closed again. An open connection must be in binary mode.

If `readBin` is called with `con` a raw vector, the data in the vector is used as input. If `writeBin` is called with `con` a raw vector, it is just an indication that a raw vector should be returned.

If `size` is specified and not the natural size of the object, each element of the vector is coerced to an appropriate type before being written or as it is read. Possible sizes are 1, 2, 4 and possibly 8 for integer or logical vectors, and 4, 8 and possibly 12/16 for numeric vectors. (Note that coercion occurs as signed types except if `signed = FALSE` when reading integers of sizes 1 and

2.) Changing sizes is unlikely to preserve NAs, and the extended precision sizes are unlikely to be portable across platforms.

`readBin` and `writeBin` read and write C-style zero-terminated character strings. Input strings are limited to 10000 characters. `readChar` and `writeChar` can be used to read and write fixed-length strings. No check is made that the string is valid in the current locale.

Handling R's missing and special (`Inf`, `-Inf` and `NaN`) values is discussed in the *R Data Import/Export* manual.

### Value

For `readBin`, a vector of appropriate mode and length the number of items read (which might be less than `n`).

For `writeBin`, a raw vector (if `con` is a raw vector) or invisibly `NULL`.

### Note

Integer read/writes of size 8 will be available if either C type `long` is of size 8 bytes or C type `long long` exists and is of size 8 bytes.

Real read/writes of size `sizeof(long double)` (usually 12 or 16 bytes) will be available only if that type is available and different from `double`.

If `readBin(what = character())` is used incorrectly on a file which does not contain C-style character strings, warnings (usually many) are given. From a file or connection, the input will be broken into pieces of length 10000 with any final part being discarded.

### See Also

The *R Data Import/Export* manual.

`readChar` to read/write fixed-length strings.

[connections](#), [readLines](#), [writeLines](#).

[.Machine](#) for the sizes of `long`, `long long` and `long double`.

### Examples

```
zz <- file("testbin", "wb")
writeBin(1:10, zz)
writeBin(pi, zz, endian="swap")
writeBin(pi, zz, size=4)
writeBin(pi^2, zz, size=4, endian="swap")
writeBin(pi+3i, zz)
writeBin("A test of a connection", zz)
z <- paste("A very long string", 1:100, collapse=" + ")
writeBin(z, zz)
if(.Machine$sizeof.long == 8 || .Machine$sizeof.longlong == 8)
  writeBin(as.integer(5^(1:10)), zz, size = 8)
if((s <- .Machine$sizeof.longdouble) > 8)
  writeBin((pi/3)^(1:10), zz, size = s)
close(zz)

zz <- file("testbin", "rb")
readBin(zz, integer(), 4)
readBin(zz, integer(), 6)
readBin(zz, numeric(), 1, endian="swap")
```

```

readBin(zz, numeric(), size=4)
readBin(zz, numeric(), size=4, endian="swap")
readBin(zz, complex(), 1)
readBin(zz, character(), 1)
z2 <- readBin(zz, character(), 1)
if(.Machine$sizeof.long == 8 || .Machine$sizeof.longlong == 8)
  readBin(zz, integer(), 10, size = 8)
if((s <- .Machine$sizeof.longdouble) > 8)
  readBin(zz, numeric(), 10, size = s)
close(zz)
unlink("testbin")
stopifnot(z2 == z)

## signed vs unsigned ints
zz <- file("testbin", "wb")
x <- as.integer(seq(0, 255, 32))
writeBin(x, zz, size=1)
writeBin(x, zz, size=1)
x <- as.integer(seq(0, 60000, 10000))
writeBin(x, zz, size=2)
writeBin(x, zz, size=2)
close(zz)
zz <- file("testbin", "rb")
readBin(zz, integer(), 8, size=1)
readBin(zz, integer(), 8, size=1, signed=FALSE)
readBin(zz, integer(), 7, size=2)
readBin(zz, integer(), 7, size=2, signed=FALSE)
close(zz)
unlink("testbin")

## use of raw
z <- writeBin(pi^{1:5}, raw(), size = 4)
readBin(z, numeric(), 5, size = 4)
z <- writeBin(c("a", "test", "of", "character"), raw())
readBin(z, character(), 4)

```

---

readChar

*Transfer Character Strings To and From Connections*


---

## Description

Transfer character strings to and from connections, without assuming they are null-terminated on the connection.

## Usage

```
readChar(con, nchars, useBytes = FALSE)
```

```
writeChar(object, con, nchars = nchar(object, type="chars"),
          eos = "", useBytes = FALSE)
```

**Arguments**

<code>con</code>	A connection object, or a character string naming a file, or a raw vector.
<code>nchars</code>	integer, giving the lengths in characters of (unterminated) character strings to be read or written. Must be $\geq 0$ and not missing.
<code>useBytes</code>	logical: For <code>readChar</code> , should <code>nchars</code> be regarded as a number of bytes not characters in a multi-byte locale? For <code>writeChar</code> , see <a href="#">writeLines</a> .
<code>object</code>	A character vector to be written to the connection, at least as long as <code>nchars</code> .
<code>eos</code>	'end of string': character string . The terminator to be written after each string, followed by an ASCII <code>nul</code> ; use <code>NULL</code> for no terminator at all.

**Details**

These functions complement [readBin](#) and [writeBin](#) which read and write C-style zero-terminated character strings. They are for strings of known length, and can optionally write an end-of-string mark. They are intended only for character strings valid in the current locale.

If `con` is a character string, the functions call [file](#) to obtain an file connection which is opened for the duration of the function call.

If the connection is open it is read/written from its current position. If it is not open, it is opened for the duration of the call in an appropriate mode (binary read or write) and then closed again. An open connection must be in binary mode.

If `readChar` is called with `con` a raw vector, the data in the vector is used as input. If `writeChar` is called with `con` a raw vector, it is just an indication that a raw vector should be returned.

Character strings containing ASCII `nul`(s) will be read correctly by `readChar` but truncated at the first `nul` with a warning.

If the character length requested for `readChar` is longer than the data available on the connection, what is available is returned. For `writeChar` if too many characters are requested the output is zero-padded, with a warning.

Missing strings are written as `NA`.

**Value**

For `readChar`, a character vector of length the number of items read (which might be less than `length(nchars)`).

For `writeChar`, a raw vector (if `con` is a raw vector) or invisibly `NULL`.

**Note**

Earlier versions of R allowed embedded `nul` bytes within character strings, but not R  $\geq$  2.8.0. `readChar` was commonly used to read fixed-size zero-padded byte fields for which `readBin` was unsuitable. `readChar` can still be used for such fields if there are no embedded `nuls`: otherwise `readBin(what="raw")` provides an alternative.

`nchars` will be interpreted in bytes not characters in a non-UTF-8 multi-byte locale, with a warning.

There is little validity checking of UTF-8 reads.

**See Also**

The *R Data Import/Export* manual.

[connections](#), [readLines](#), [writeLines](#), [readBin](#)

## Examples

```
## test fixed-length strings
zz <- file("testchar", "wb")
x <- c("a", "this will be truncated", "abc")
nc <- c(3, 10, 3)
writeChar(x, zz, nc, eos=NULL)
writeChar(x, zz, eos="\r\n")
close(zz)

zz <- file("testchar", "rb")
readChar(zz, nc)
readChar(zz, nchar(x)+3) # need to read the terminator explicitly
close(zz)
unlink("testchar")
```

---

readline

*Read a Line from the Terminal*

---

## Description

`readline` reads a line from the terminal (in interactive use).

## Usage

```
readline(prompt = "")
```

## Arguments

`prompt` the string printed when prompting the user for input. Should usually end with a space " ".

## Details

The prompt string will be truncated to a maximum allowed length, normally 256 chars (but can be changed in the source code).

This can only be used in an [interactive](#) session.

## Value

A character vector of length one. Both leading and trailing spaces and tabs are stripped from the result.

In non-[interactive](#) use the result is as if the response was RETURN and the value is "".

## See Also

[readLines](#) for reading text lines from connections, including files.

**Examples**

```

fun <- function() {
  ANSWER <- readline("Are you a satisfied R user? ")
  ## a better version would check the answer less cursorily, and
  ## perhaps re-prompt
  if (substr(ANSWER, 1, 1) == "n")
    cat("This is impossible. YOU LIED!\n")
  else
    cat("I knew it.\n")
}
if(interactive()) fun()

```

readLines

*Read Text Lines from a Connection***Description**

Read some or all text lines from a connection.

**Usage**

```

readLines(con = stdin(), n = -1L, ok = TRUE, warn = TRUE,
          encoding = "unknown")

```

**Arguments**

con	a connection object or a character string.
n	integer. The (maximal) number of lines to read. Negative values indicate that one should read up to the end of input on the connection.
ok	logical. Is it OK to reach the end of the connection before $n > 0$ lines are read? If not, an error will be generated.
warn	logical. Warn if a text file is missing a final EOL.
encoding	encoding to be assumed for input strings. It is used to mark character strings as known to be in Latin-1 or UTF-8: it is not used to re-encode the input. To do the latter, specify the encoding as part of the connection <code>con</code> or via <code>options(encoding=)</code> : see the example under <a href="#">file</a> .

**Details**

If the `con` is a character string, the function calls [file](#) to obtain a file connection which is opened for the duration of the function call. As from R 2.10.0 this can be a compressed file.

If the connection is open it is read from its current position. If it is not open, it is opened in "rt" mode for the duration of the call and then closed again.

If the final line is incomplete (no final EOL marker) the behaviour depends on whether the connection is blocking or not. For a non-blocking text-mode connection the incomplete line is pushed back, silently. For all other connections the line will be accepted, with a warning.

Whatever mode the connection is opened in, any of LF, CRLF or CR will be accepted as the EOL marker for a line.

**Value**

A character vector of length the number of lines read.

The elements of the result have a declared encoding if encoding is "latin1" or "UTF-8",

**Note**

The default connection, `stdin`, may be different from `con = "stdin"`: see [file](#).

**See Also**

[connections](#), [writeLines](#), [readBin](#), [scan](#)

**Examples**

```
cat("TITLE extra line", "2 3 5 7", "", "11 13 17", file="ex.data",
    sep="\n")
readLines("ex.data", n=-1)
unlink("ex.data") # tidy up

## difference in blocking
cat("123\nabc", file = "test1")
readLines("test1") # line with a warning

con <- file("test1", "r", blocking = FALSE)
readLines(con) # empty
cat(" def\n", file = "test1", append = TRUE)
readLines(con) # gets both
close(con)

unlink("test1") # tidy up
```

---

real

*Real Vectors*

---

**Description**

These functions are the same as their [double](#) equivalents and are provided for backwards compatibility only.

**Usage**

```
real(length = 0)
as.real(x, ...)
is.real(x)
```

**Arguments**

<code>length</code>	desired length.
<code>x</code>	object to be coerced or tested.
<code>...</code>	further arguments passed to or from other methods.



**Details**

`as.real` is a generic function, but S3 methods must be written for `as.double`.

---

 Recall

*Recursive Calling*


---

**Description**

`Recall` is used as a placeholder for the name of the function in which it is called. It allows the definition of recursive functions which still work after being renamed, see example below.

**Usage**

```
Recall(...)
```

**Arguments**

... all the arguments to be passed.

**Note**

`Recall` will not work correctly when passed as a function argument, e.g. to the `apply` family of functions.

**See Also**

`do.call` and `call`.

`local` for another way to write anonymous recursive functions.

**Examples**

```
## A trivial (but inefficient!) example:
fib <- function(n)
  if(n<=2) { if(n>=0) 1 else 0 } else Recall(n-1) + Recall(n-2)
fibonacci <- fib; rm(fib)
## renaming wouldn't work without Recall
fibonacci(10) # 55
```

---

 reg.finalizer

*Finalization of Objects*


---

**Description**

Registers an R function to be called upon garbage collection of object or (optionally) at the end of an R session.

**Usage**

```
reg.finalizer(e, f, onexit = FALSE)
```

**Arguments**

<code>e</code>	Object to finalize. Must be environment or external pointer.
<code>f</code>	Function to call on finalization. Must accept a single argument, which will be the object to finalize.
<code>onexit</code>	logical: should the finalizer be run if the object is still uncollected at the end of the R session?

**Value**

NULL.

**Note**

The purpose of this function is mainly to allow objects that refer to external items (a temporary file, say) to perform cleanup actions when they are no longer referenced from within R. This only makes sense for objects that are never copied on assignment, hence the restriction to environments and external pointers.

**See Also**

[gc](#) and [Memory](#) for garbage collection and memory management.

**Examples**

```
f <- function(e) print("cleaning...")
g <- function(x){ e <- environment(); reg.finalizer(e,f) }
g()
invisible(gc()) # trigger cleanup
```

---

regex

*Regular Expressions as used in R*

---

**Description**

This help page documents the regular expression patterns supported by [grep](#) and related functions `grepl`, `regexpr`, `gregexpr`, `sub` and `gsub`, as well as by [strsplit](#).

**Details**

A ‘regular expression’ is a pattern that describes a set of strings. Two types of regular expressions are used in R, *extended* regular expressions (the default) and *Perl-like* regular expressions used by `perl = TRUE`. There is also `fixed = TRUE` which can be considered to use a *literal* regular expression.

Other functions which use regular expressions (often via the use of `grep`) include `apropos`, `browseEnv`, `help.search`, `list.files` and `ls`. These will all use *extended* regular expressions.

Patterns are described here as they would be printed by `cat`: (*do remember that backslashes need to be doubled when entering R character strings, e.g. from the keyboard*).

## Extended Regular Expressions

This section covers the regular expressions allowed in the default mode of `grep`, `regexpr`, `gregexpr`, `sub`, `gsub` and `strsplit`. They use an implementation of the POSIX 1003.2 standard: that allows some scope for interpretation and the interpretations here are those used as from R 2.10.0.

Regular expressions are constructed analogously to arithmetic expressions, by using various operators to combine smaller expressions. The whole expression matches zero or more characters (read ‘character’ as ‘byte’ if `useBytes = TRUE`).

The fundamental building blocks are the regular expressions that match a single character. Most characters, including all letters and digits, are regular expressions that match themselves. Any metacharacter with special meaning may be quoted by preceding it with a backslash. The metacharacters in EREs are ‘. \ | ( ) [ { ^ \$ \* + ?’, but note that whether these have a special meaning depends on the context.

Escaping non-metacharacters with a backslash is implementation-dependent. The current implementation interprets ‘\a’ as ‘BEL’, ‘\e’ as ‘ESC’, ‘\f’ as ‘FF’, ‘\n’ as ‘LF’, ‘\r’ as ‘CR’ and ‘\t’ as ‘TAB’. (Note that these will be interpreted by R’s parser in literal character strings.)

A *character class* is a list of characters enclosed between ‘[’ and ‘]’ which matches any single character in that list; unless the first character of the list is the caret ‘^’, when it matches any character *not* in the list. For example, the regular expression ‘[0123456789]’ matches any single digit, and ‘[^abc]’ matches anything except the characters ‘a’, ‘b’ or ‘c’. A range of characters may be specified by giving the first and last characters, separated by a hyphen. (Because their interpretation is locale- and implementation-dependent, they are best avoided.) The only portable way to specify all ASCII letters is to list them all as the character class ‘[ABCDEFGHIJKLMNOPQRSTUVWXYZabcdefghijklmnopqrstuvwxyz]’. (The current implementation uses numerical order of the encoding; prior to R 2.10.0 locale-specific collation was used, and might be again.)

Certain named classes of characters are predefined. Their interpretation depends on the *locale* (see [locales](#)); the interpretation below is that of the POSIX locale.

```
‘[:alnum:]’ Alphanumeric characters: ‘[:alpha:]’ and ‘[:digit:]’.
‘[:alpha:]’ Alphabetic characters: ‘[:lower:]’ and ‘[:upper:]’.
‘[:blank:]’ Blank characters: space and tab. (This is an extension to the POSIX standard.)
‘[:cntrl:]’ Control characters. In ASCII, these characters have octal codes 000 through 037,
and 177 (DEL). In another character set, these are the equivalent characters, if any.
‘[:digit:]’ Digits: ‘0 1 2 3 4 5 6 7 8 9’.
‘[:graph:]’ Graphical characters: ‘[:alnum:]’ and ‘[:punct:]’.
‘[:lower:]’ Lower-case letters in the current locale.
‘[:print:]’ Printable characters: ‘[:alnum:]’, ‘[:punct:]’ and space.
‘[:punct:]’ Punctuation characters: ‘! " # $ % & ' ( ) * + , - . / : ; <=
>? @ [ \ ] ^ _ ` { | } ~’.
‘[:space:]’ Space characters: tab, newline, vertical tab, form feed, carriage return, and space.
‘[:upper:]’ Upper-case letters in the current locale.
‘[:xdigit:]’ Hexadecimal digits: ‘0 1 2 3 4 5 6 7 8 9 A B C D E F a b c d
e f’.
```

For example, ‘[[:alnum:]]’ means ‘[0-9A-Za-z]’, except the latter depends upon the locale and the character encoding, whereas the former is independent of locale and character set. (Note

that the brackets in these class names are part of the symbolic names, and must be included in addition to the brackets delimiting the bracket list.) Most metacharacters lose their special meaning inside a character class. To include a literal ']', place it first in the list. Similarly, to include a literal '^', place it anywhere but first. Finally, to include a literal '-', place it first or last (or, for `perl = TRUE` only, precede it by a backslash.). (Only '^ -\ ]' are special inside character classes.)

The period '.' matches any single character. The symbol '\w' matches a 'word' character (a synonym for '[[:alnum:]]') and '\W' is its negation. Symbols '\d', '\s', '\D' and '\S' denote the digit and space classes and their negations.

The caret '^' and the dollar sign '\$' are metacharacters that respectively match the empty string at the beginning and end of a line. The symbols '<' and '>' match the empty string at the beginning and end of a word. The symbol '\b' matches the empty string at either edge of a word, and '\B' matches the empty string provided it is not at an edge of a word. (The interpretation of 'word' depends on the locale and implementation.)

A regular expression may be followed by one of several repetition quantifiers:

'?' The preceding item is optional and will be matched at most once.

'\*' The preceding item will be matched zero or more times.

'+' The preceding item will be matched one or more times.

{n}' The preceding item is matched exactly n times.

{n,}' The preceding item is matched n or more times.

{n,m}' The preceding item is matched at least n times, but not more than m times.

By default repetition is greedy, so the maximal possible number of repeats is used. This can be changed to 'minimal' by appending ? to the quantifier. (There are further quantifiers that allow approximate matching: see the TRE documentation.)

Regular expressions may be concatenated; the resulting regular expression matches any string formed by concatenating the substrings that match the concatenated subexpressions.

Two regular expressions may be joined by the infix operator '|'; the resulting regular expression matches any string matching either subexpression. For example, 'abba|cde' matches either the string abba or the string cde. Note that alternation does not work inside character classes, where '|' has its literal meaning.

Repetition takes precedence over concatenation, which in turn takes precedence over alternation. A whole subexpression may be enclosed in parentheses to override these precedence rules.

The backreference '\N', where 'N = 1 . . . 9', matches the substring previously matched by the Nth parenthesized subexpression of the regular expression. (This is an extension for extended regular expressions: POSIX defines them only for basic ones.)

### Perl-like Regular Expressions

The `perl = TRUE` argument to `grep`, `regexpr`, `gregexpr`, `sub`, `gsub` and `strsplit` switches to the PCRE library that implements regular expression pattern matching using the same syntax and semantics as Perl 5.10, with just a few differences.

For complete details please consult the man pages for PCRE, especially `man pcrepattern` and `man pcreapi`, on your system or from the sources at <http://www.pcre.org>. If PCRE support was compiled from the sources within R, the PCRE version is 8.0 as described here.

Perl regular expressions can be computed byte-by-byte or (UTF-8) character-by-character: the latter is used in all multibyte locales and if any of the inputs are marked as UTF-8 (see [Encoding](#)).

All the regular expressions described for extended regular expressions are accepted except '<' and '>': in Perl all backslashed metacharacters are alphanumeric and backslashed symbols always are

interpreted as a literal character. ‘{’ is not special if it would be the start of an invalid interval specification. There can be more than 9 backreferences (but the replacement in `sub` can only refer to the first 9).

Character ranges are interpreted in the numerical order of the characters, either as bytes in a single-byte locale or as Unicode points in UTF-8 mode. So in either case ‘[A-Za-z]’ specifies the set of ASCII letters.

In UTF-8 mode the named character classes only match ASCII characters: see ‘\p’ below for an alternative.

The construct ‘(?...)’ is used for Perl extensions in a variety of ways depending on what immediately follows the ‘?’.

Perl-like matching can work in several modes, set by the options ‘(?i)’ (caseless, equivalent to Perl’s ‘/i’), ‘(?m)’ (multiline, equivalent to Perl’s ‘/m’), ‘(?s)’ (single line, so a dot matches all characters, even new lines: equivalent to Perl’s ‘/s’) and ‘(?x)’ (extended, whitespace data characters are ignored unless escaped and comments are allowed: equivalent to Perl’s ‘/x’). These can be concatenated, so for example, ‘(?im)’ sets caseless multiline matching. It is also possible to unset these options by preceding the letter with a hyphen, and to combine setting and unsetting such as ‘(?im-sx)’. These settings can be applied within patterns, and then apply to the remainder of the pattern. Additional options not in Perl include ‘(?U)’ to set ‘ungreedy’ mode (so matching is minimal unless ‘?’ is used as part of the repetition quantifier, when it is greedy). Initially none of these options are set.

If you want to remove the special meaning from a sequence of characters, you can do so by putting them between ‘\Q’ and ‘\E’. This is different from Perl in that ‘\$’ and ‘@’ are handled as literals in ‘\Q... \E’ sequences in PCRE, whereas in Perl, ‘\$’ and ‘@’ cause variable interpolation.

The escape sequences ‘\d’, ‘\s’ and ‘\w’ represent any decimal digit, space character and ‘word’ character (letter, digit or underscore in the current locale: in UTF-8 mode only ASCII letters and digits are considered) respectively, and their upper-case versions represent their negation. Unlike POSIX, vertical tab is not regarded as a space character. Sequences ‘\h’, ‘\v’, ‘\H’ and ‘\V’ match horizontal and vertical space or the negation. (In UTF-8 mode, these do match non-ASCII Unicode points.)

There are additional escape sequences: ‘\cx’ is ‘`ctrl-x`’ for any ‘x’, ‘\ddd’ is the octal character (for up to three digits unless interpretable as a backreference, as ‘\1’ to ‘\7’ always are), and ‘\xhh’ specifies a character by two hex digits. In a UTF-8 locale, ‘\x{h...}’ specifies a Unicode point by one or more hex digits. (Note that some of these will be interpreted by R’s parser in literal character strings.)

Outside a character class, ‘\A’ matches at the start of a subject (even in multiline mode, unlike ‘^’), ‘\Z’ matches at the end of a subject or before a newline at the end, ‘\z’ matches only at end of a subject. and ‘\G’ matches at first matching position in a subject (which is subtly different from Perl’s end of the previous match). ‘\C’ matches a single byte. including a newline, but its use is warned against. In UTF-8 mode, ‘\R’ matches any Unicode newline character (not just CR), and ‘\X’ matches any number of Unicode characters that form an extended Unicode sequence.

In UTF-8 mode, some Unicode properties are supported via ‘\p{xx}’ and ‘\P{xx}’ which match characters with and without property ‘xx’ respectively. For a list of supported properties see the PCRE documentation, but for example ‘Lu’ is ‘upper case letter’ and ‘Sc’ is ‘currency symbol’.

The sequence ‘(?#’ marks the start of a comment which continues up to the next closing parenthesis. Nested parentheses are not permitted. The characters that make up a comment play no part at all in the pattern matching.

If the extended option is set, an unescaped ‘#’ character outside a character class introduces a comment that continues up to the next newline character in the pattern.

The pattern ‘(?:...)’ groups characters just as parentheses do but does not make a backreference.

Patterns `'(?=...)'` and `'(?!...)'` are zero-width positive and negative lookahead *assertions*: they match if an attempt to match the ... forward from the current position would succeed (or not), but use up no characters in the string being processed. Patterns `'(?<=...)'` and `'(?<!...)'` are the lookbehind equivalents: they do not allow repetition quantifiers nor `'\C'` in ...

Named subpatterns, atomic grouping, possessive qualifiers and conditional and recursive patterns are not covered here.

### Author(s)

This help page is based on the documentation of GNU `grep` 2.4.2, the TRE documentation and the POSIX standard, and the `pcrpattern` man page from PCRE 8.0.

### See Also

`grep`, `apropos`, `browseEnv`, `glob2rx`, `help.search`, `list.files`, `ls` and `strsplit`.

The TRE documentation at <http://laurikari.net/tre/documentation/regex-syntax/>.

The POSIX 1003.2 standard at [http://www.opengroup.org/onlinepubs/009695399/basedefs/xbd\\_chap09.html](http://www.opengroup.org/onlinepubs/009695399/basedefs/xbd_chap09.html)

The `pcrpattern` can be found as part of <http://www.pcre.org/pcr.txt>, and details of Perl's own implementation at <http://perldoc.perl.org/perlre.html>.

---

remove

*Remove Objects from a Specified Environment*

---

### Description

`remove` and `rm` can be used to remove objects. These can be specified successively as character strings, or in the character vector `list`, or through a combination of both. All objects thus specified will be removed.

If `envir` is `NULL` then the currently active environment is searched first.

If `inherits` is `TRUE` then parents of the supplied directory are searched until a variable with the given name is encountered. A warning is printed for each variable that is not found.

### Usage

```
remove(..., list = character(0L), pos = -1,
        envir = as.environment(pos), inherits = FALSE)
```

```
rm      (... , list = character(0L), pos = -1,
        envir = as.environment(pos), inherits = FALSE)
```

### Arguments

<code>...</code>	the objects to be removed, as names (unquoted) or character strings (quoted).
<code>list</code>	a character vector naming objects to be removed.
<code>pos</code>	where to do the removal. By default, uses the current environment. See the details for other possibilities.
<code>envir</code>	the <a href="#">environment</a> to use. See the details section.
<code>inherits</code>	should the enclosing frames of the environment be inspected?

## Details

The `pos` argument can specify the environment from which to remove the objects in any of several ways: as an integer (the position in the `search` list); as the character string name of an element in the search list; or as an `environment` (including using `sys.frame` to access the currently active function calls). The `envir` argument is an alternative way to specify an environment, but is primarily there for back compatibility.

It is not allowed to remove variables from the base environment and base name space, nor from any environment which is locked (see `lockEnvironment`).

Earlier versions of R incorrectly claimed that supplying a character vector in `...` removed the objects named in the character vector, but it removed the character vector. Use the `list` argument to specify objects *via* a character vector.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[ls](#), [objects](#)

## Examples

```
tmp <- 1:4
## work with tmp and cleanup
rm(tmp)

## Not run:
## remove (almost) everything in the working environment.
## You will get no warning, so don't do this unless you are really sure.
rm(list = ls())

## End(Not run)
```

---

rep

*Replicate Elements of Vectors and Lists*

---

## Description

`rep` replicates the values in `x`. It is a generic function, and the (internal) default method is described here.

`rep.int` is a faster simplified version for the most common case.

## Usage

```
rep(x, ...)
```

```
rep.int(x, times)
```

**Arguments**

<code>x</code>	a vector (of any mode including a list) or a pairlist or a factor or (except for <code>rep.int</code> ) a <code>POSIXct</code> or <code>POSIXlt</code> or date object; or also, an S4 object containing a vector of the above kind.
<code>...</code>	further arguments to be passed to or from other methods. For the internal default method these can include:  <code>times</code> A vector giving the number of times to repeat each element if of length <code>length(x)</code> , or to repeat the whole vector if of length 1. <code>length.out</code> non-negative integer. The desired length of the output vector. Ignored if NA or invalid. <code>each</code> non-negative integer. Each element of <code>x</code> is repeated <code>each</code> times. Treated as 1 if NA or invalid.
<code>times</code>	see <code>...</code>

**Details**

The default behaviour is as if the call was `rep(x, times=1, length.out=NA, each=1)`. Normally just one of the additional arguments is specified, but if `each` is specified with either of the other two, its replication is performed first, and then that implied by `times` or `length.out`.

If `times` consists of a single integer, the result consists of the whole input repeated this many times. If `times` is a vector of the same length as `x` (after replication by `each`), the result consists of `x[1]` repeated `times[1]` times, `x[2]` repeated `times[2]` times and so on.

`length.out` may be given in place of `times`, in which case `x` is repeated as many times as is necessary to create a vector of this length. If both are given, `length.out` takes priority and `times` is ignored.

Non-integer values of `times` will be truncated towards zero. If `times` is a computed quantity it is prudent to add a small fuzz.

If `x` has length zero and `length.out` is supplied and is positive, the values are filled in using the extraction rules, that is by an NA of the appropriate class for an atomic vector (0 for raw vectors) and NULL for a list.

**Value**

An object of the same type as `x` (except that `rep` will coerce pairlists to vector lists).

`rep.int` returns no attributes.

The default method of `rep` gives the result names (which will almost always contain duplicates) if `x` had names, but retains no other attributes except for factors.

**Note**

Function `rep.int` is a simple case handled by internal code, and provided as a separate function purely for S compatibility.

Function `rep` is a primitive, but (partial) matching of argument names is performed as for normal functions. You can no longer pass a missing argument to e.g. `length.out`.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.



**See Also**

[seq](#), [sequence](#), [replicate](#).

**Examples**

```
rep(1:4, 2)
rep(1:4, each = 2)      # not the same.
rep(1:4, c(2,2,2,2))   # same as second.
rep(1:4, c(2,1,2,1))
rep(1:4, each = 2, len = 4)  # first 4 only.
rep(1:4, each = 2, len = 10) # 8 integers plus two recycled 1's.
rep(1:4, each = 2, times = 3) # length 24, 3 complete replications

rep(1, 40*(1-.8)) # length 7 on most platforms
rep(1, 40*(1-.8)+1e-7) # better

## replicate a list
fred <- list(happy = 1:10, name = "squash")
rep(fred, 5)

# date-time objects
x <- .leap.seconds[1:3]
rep(x, 2)
rep(as.POSIXlt(x), rep(2, 3))

## named factor
x <- factor(LETTERS[1:4]); names(x) <- letters[1:4]
x
rep(x, 2)
rep(x, each=2)
rep.int(x, 2) # no names
```

---

replace

*Replace Values in a Vector*

---

**Description**

`replace` replaces the values in `x` with indices given in `list` by those given in `values`. If necessary, the values in `values` are recycled.

**Usage**

```
replace(x, list, values)
```

**Arguments**

<code>x</code>	vector
<code>list</code>	an index vector
<code>values</code>	replacement values

**Value**

A vector with the values replaced.

**Note**

x is unchanged: remember to assign the result.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

---

 Reserved

---

*Reserved Words in R*


---

**Description**

The reserved words in R's parser are

`if else repeat while function for in next break`

`TRUE FALSE NULL Inf NaN NA NA_integer_ NA_real_ NA_complex_ NA_character_`

`...` and `..1`, `..2` etc, which are used to refer to arguments passed down from an enclosing function.

**Details**

Reserved words outside [quotes](#) are always parsed to be references to the objects linked to in the 'Description', and hence they are not allowed as syntactic names (see [make.names](#)). They **are** allowed as non-syntactic names, e.g. inside [backtick](#) quotes.

---

 rev

---

*Reverse Elements*


---

**Description**

`rev` provides a reversed version of its argument. It is generic function with a default method for vectors and one for [dendrograms](#).

Note that this is no longer needed (nor efficient) for obtaining vectors sorted into descending order, since that is now rather more directly achievable by `sort(x, decreasing = TRUE)`.

**Usage**

```
rev(x)
```

**Arguments**

x a vector or another object for which reversal is defined.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[seq](#), [sort](#).

**Examples**

```
x <- c(1:5, 5:3)
## sort into descending order; first more efficiently:
stopifnot(sort(x, decreasing = TRUE) == rev(sort(x)))
stopifnot(rev(1:7) == 7:1) #- don't need 'rev' here
```

---

Rhome

*Return the R Home Directory*

---

**Description**

Return the R home directory.

**Usage**

```
R.home(component="home")
```

**Arguments**

`component` As well as "home" which gives the R home directory, other known values are "bin", "doc", "etc" and "share" giving the paths to the corresponding parts of an R installation.

**Details**

The R home directory is the top-level directory of the R installation being run.

The R home directory is often referred to as *R\_HOME*, and is the value of an environment variable of that name in an R session. It can be found outside an R session by R [RHOME](#).

**Value**

A character string giving the R home directory or path to a particular component. Normally the components are all subdirectories of the R home directory, but this may not be the case in a Unix-like installation.

---

rle	<i>Run Length Encoding</i>
-----	----------------------------

---

### Description

Compute the lengths and values of runs of equal values in a vector – or the reverse operation.

### Usage

```
rle(x)
inverse.rle(x, ...)

## S3 method for class 'rle':
print(x, digits = getOption("digits"), prefix = "", ...)
```

### Arguments

x	an atomic vector for <code>rle()</code> ; an object of class "rle" for <code>inverse.rle()</code> .
...	further arguments; ignored here.
digits	number of significant digits for printing, see <code>print.default</code> .
prefix	character string, prepended to each printed line.

### Details

Missing values are regarded as unequal to the previous value, even if that is also missing.

`inverse.rle()` is the inverse function of `rle()`, reconstructing `x` from the runs.

### Value

`rle()` returns an object of class "rle" which is a list with components:

lengths	an integer vector containing the length of each run.
values	a vector of the same length as <code>lengths</code> with the corresponding values.

`inverse.rle()` returns an atomic vector.

### Examples

```
x <- rev(rep(6:10, 1:5))
rle(x)
## lengths [1:5]  5 4 3 2 1
## values  [1:5] 10 9 8 7 6

z <- c(TRUE, TRUE, FALSE, FALSE, TRUE, FALSE, TRUE, TRUE, TRUE)
rle(z)
rle(as.character(z))
print(rle(z), prefix = "..| ")

N <- integer(0)
stopifnot(x == inverse.rle(rle(x)),
          identical(N, inverse.rle(rle(N))),
          z == inverse.rle(rle(z)))
```

Round

*Rounding of Numbers***Description**

`ceiling` takes a single numeric argument `x` and returns a numeric vector containing the smallest integers not less than the corresponding elements of `x`.

`floor` takes a single numeric argument `x` and returns a numeric vector containing the largest integers not greater than the corresponding elements of `x`.

`trunc` takes a single numeric argument `x` and returns a numeric vector containing the integers formed by truncating the values in `x` toward 0.

`round` rounds the values in its first argument to the specified number of decimal places (default 0).

`signif` rounds the values in its first argument to the specified number of significant digits.

**Usage**

```
ceiling(x)
floor(x)
trunc(x, ...)

round(x, digits = 0)
signif(x, digits = 6)
```

**Arguments**

<code>x</code>	a numeric vector. Or, for <code>round</code> and <code>signif</code> , a complex vector.
<code>digits</code>	integer indicating the number of decimal places ( <code>round</code> ) or significant digits ( <code>signif</code> ) to be used.
<code>...</code>	arguments to be passed to methods.

**Details**

These are generic functions: methods can be defined for them individually or via the [Math](#) group generic.

Note that for rounding off a 5, the IEC 60559 standard is expected to be used, ‘*go to the even digit*’. Therefore `round(0.5)` is 0 and `round(-1.5)` is -2. However, this is dependent on OS services and on representation error (since e.g. 0.15 is not represented exactly, the rounding rule applies to the represented number and not to the printed number, and so `round(0.15, 1)` could be either 0.1 or 0.2).

For `signif` the recognized values of `digits` are 1...22. Complex numbers are rounded to retain the specified number of digits in the larger of the components. Each element of the vector is rounded individually, unlike printing.

These are all primitive functions.

**S4 methods**

These are all (internally) S4 generic.

`ceiling`, `floor` and `trunc` are members of the `Math` group generic. As an S4 generic, `trunc` has only one argument.

`round` and `signif` are members of the `Math2` group generic.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[as.integer](#).

**Examples**

```
round(.5 + -2:4) # IEEE rounding: -2 0 0 2 2 4 4
( x1 <- seq(-2, 4, by = .5) )
round(x1)##-- IEEE rounding !
x1[trunc(x1) != floor(x1)]
x1[round(x1) != floor(x1 + .5)]
(non.int <- ceiling(x1) != floor(x1))

x2 <- pi * 100^(-1:3)
round(x2, 3)
signif(x2, 3)
```

---

round.POSIXt

*Round / Truncate Data-Time Objects*


---

**Description**

Round or truncate date-time objects.

**Usage**

```
## S3 method for class 'POSIXt':
round(x, units = c("secs", "mins", "hours", "days"))
## S3 method for class 'POSIXt':
trunc(x, units = c("secs", "mins", "hours", "days"), ...)

## S3 method for class 'Date':
round(x, ...)
## S3 method for class 'Date':
trunc(x, ...)
```

**Arguments**

`x` an object inheriting from "POSIXt" or "Date".

`units` one of the units listed. Can be abbreviated.

`...` arguments to be passed to or from other methods, notably `digits` for `round`.

### Details

The time is rounded or truncated to the second, minute, hour or day. Timezones are only relevant to days, when midnight in the current [timezone](#) is used.

The methods for class "Date" are of little use except to remove fractional days.

### Value

An object of class "POSIXlt" or "Date".

### See Also

[round](#) for the generic function and default methods.

[DateTimeClasses](#), [Date](#)

### Examples

```
round(.leap.seconds + 1000, "hour")
trunc(Sys.time(), "day")
```

---

row

*Row Indexes*

---

### Description

Returns a matrix of integers indicating their row number in a matrix-like object, or a factor indicating the row labels.

### Usage

```
row(x, as.factor = FALSE)
```

### Arguments

<code>x</code>	a matrix-like object, that is one with a two-dimensional <code>dim</code> .
<code>as.factor</code>	a logical value indicating whether the value should be returned as a factor of row labels (created if necessary) rather than as numbers.

### Value

An integer (or factor) matrix with the same dimensions as `x` and whose `i j`-th element is equal to `i` (or the `i`-th row label).

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[col](#) to get columns.

**Examples**

```
x <- matrix(1:12, 3, 4)
# extract the diagonal of a matrix
dx <- x[row(x) == col(x)]
dx

# create an identity 5-by-5 matrix
x <- matrix(0, nrow = 5, ncol = 5)
x[row(x) == col(x)] <- 1
x
```

row.names

*Get and Set Row Names for Data Frames***Description**

All data frames have a row names attribute, a character vector of length the number of rows with no duplicates nor missing values.

For convenience, these are generic functions for which users can write other methods, and there are default methods for arrays. The description here is for the `data.frame` method.

**Usage**

```
row.names(x)
row.names(x) <- value
```

**Arguments**

<code>x</code>	object of class "data.frame", or any other class for which a method has been defined.
<code>value</code>	an object to be coerced to character unless an integer vector. It should have (after coercion) the same length as the number of rows of <code>x</code> with no duplicated nor missing values. <code>NULL</code> is also allowed: see 'Details'.

**Details**

A data frame has (by definition) a vector of *row names* which has length the number of rows in the data frame, and contains neither missing nor duplicated values. Where a row names sequence has been added by the software to meet this requirement, they are regarded as 'automatic'.

Row names were character are allowed to be integer or character, but for backwards compatibility (with R <= 2.4.0) `row.names` will always return a character vector. (Use `attr(x, "row.names")` if you need an integer value.)

Using `NULL` for the value resets the row names to `seq_len(nrow(x))`, regarded as 'automatic'.

**Value**

`row.names` returns a character vector.

`row.names<-` returns a data frame with the row names changed.



**Note**

`row.names` is similar to `rownames` for arrays, and it has a method that calls `rownames` for an array argument.

Row names of the form `1:n` for  $n > 2$  are stored internally in a compact form, which might be seen from C code or by deparsing but never via `row.names` or `attr(x, "row.names")`. Additionally, some names of this sort are marked as ‘automatic’ and handled differently by `as.matrix` and `data.matrix` (and potentially other functions). (All zero-row data frames are regarded as having automatic `row.names`.)

**References**

Chambers, J. M. (1992) *Data for models*. Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

`data.frame`, `rownames`, `names`.

`.row_names_info` for the internal representations.

---

row/colnames

*Row and Column Names*


---

**Description**

Retrieve or set the row or column names of a matrix-like object.

**Usage**

```
rownames(x, do.NULL = TRUE, prefix = "row")
rownames(x) <- value
```

```
colnames(x, do.NULL = TRUE, prefix = "col")
colnames(x) <- value
```

**Arguments**

<code>x</code>	a matrix-like R object, with at least two dimensions for <code>colnames</code> .
<code>do.NULL</code>	logical. Should this create names if they are NULL?
<code>prefix</code>	for created names.
<code>value</code>	a valid value for that component of <code>dimnames(x)</code> . For a matrix or array this is either NULL or a character vector of non-zero length equal to the appropriate dimension.

## Details

The extractor functions try to do something sensible for any matrix-like object `x`. If the object has `dimnames` the first component is used as the row names, and the second component (if any) is used for the column names. For a data frame, `rownames` and `colnames` eventually call `row.names` and `names` respectively, but the latter are preferred.

If `do.NULL` is `FALSE`, a character vector (of length `NROW(x)` or `NCOL(x)`) is returned in any case, prepending `prefix` to simple numbers, if there are no `dimnames` or the corresponding component of the `dimnames` is `NULL`.

The replacement methods for arrays/matrices coerce vector and factor values of `value` to character, but do not dispatch methods for `as.character`.

For a data frame, `value` for `rownames` should be a character vector of non-duplicated and non-missing names (this is enforced), and for `colnames` a character vector of (preferably) unique syntactically-valid names. In both cases, `value` will be coerced by `as.character`, and setting `colnames` will convert the row names to character.

## See Also

`dimnames`, `case.names`, `variable.names`.

## Examples

```
m0 <- matrix(NA, 4, 0)
rownames(m0)

m2 <- cbind(1, 1:4)
colnames(m2, do.NULL = FALSE)
colnames(m2) <- c("x", "y")
rownames(m2) <- rownames(m2, do.NULL = FALSE, prefix = "Obs.")
m2
```

---

rowsum

*Give Column Sums of a Matrix or Data Frame, Based on a Grouping Variable*

---

## Description

Compute column sums across rows of a matrix-like object for each level of a grouping variable. `rowsum` is generic, with a method for data frames and a default method for vectors and matrices.

## Usage

```
rowsum(x, group, reorder = TRUE, ...)

## S3 method for class 'data.frame':
rowsum(x, group, reorder = TRUE, na.rm = FALSE, ...)

## Default S3 method:
rowsum(x, group, reorder = TRUE, na.rm = FALSE, ...)
```

**Arguments**

<code>x</code>	a matrix, data frame or vector of numeric data. Missing values are allowed. A numeric vector will be treated as a column vector.
<code>group</code>	a vector or factor giving the grouping, with one element per row of <code>x</code> . Missing values will be treated as another group and a warning will be given.
<code>reorder</code>	if <code>TRUE</code> , then the result will be in order of <code>sort(unique(group))</code> , if <code>FALSE</code> , it will be in the order that groups were encountered.
<code>na.rm</code>	logical ( <code>TRUE</code> or <code>FALSE</code> ). Should NA values be discarded?
<code>...</code>	other arguments to be passed to or from methods

**Details**

The default is to reorder the rows to agree with `tapply` as in the example below. Reordering should not add noticeably to the time except when there are very many distinct values of `group` and `x` has few columns.

The original function was written by Terry Therneau, but this is a new implementation using hashing that is much faster for large matrices.

To sum over all the rows of a matrix (ie, a single `group`) use `colSums`, which should be even faster.

**Value**

A matrix or data frame containing the sums. There will be one row per unique value of `group`.

**See Also**

[tapply](#), [aggregate](#), [rowSums](#)

**Examples**

```
require(stats)

x <- matrix(runif(100), ncol=5)
group <- sample(1:8, 20, TRUE)
(xsum <- rowsum(x, group))
## Slower versions
tapply(x, list(group[row(x)], col(x)), sum)
t(sapply(split(as.data.frame(x), group), colSums))
aggregate(x, list(group), sum)[-1]
```

**Description**

`sample` takes a sample of the specified size from the elements of `x` using either with or without replacement.

**Usage**

```
sample(x, size, replace = FALSE, prob = NULL)

sample.int(n, size = n, replace = FALSE, prob = NULL)
```

**Arguments**

<code>x</code>	Either a vector of one or more elements from which to choose, or a positive integer. See ‘Details.’
<code>n</code>	a positive number, the number of items to choose from. See ‘Details.’
<code>size</code>	a non-negative integer giving the number of items to choose.
<code>replace</code>	Should sampling be with replacement?
<code>prob</code>	A vector of probability weights for obtaining the elements of the vector being sampled.

**Details**

If `x` has length 1, is numeric (in the sense of `is.numeric`) and `x`  $\geq$  1, sampling *via* `sample` takes place from `1:x`. *Note* that this convenience feature may lead to undesired behaviour when `x` is of varying length in calls such as `sample(x)`. See the examples.

Otherwise `x` can be any R object for which `length` and subsetting by integers make sense: S3 or S4 methods for these operations will be dispatched as appropriate.

For `sample` the default for `size` is the number of items inferred from the first argument, so that `sample(x)` generates a random permutation of the elements of `x` (or `1:x`).

As from R 2.11.0 it is allowed to ask for `size = 0` samples with `n = 0` or a length-zero `x`, but otherwise `n > 0` or positive `length(x)` is required.

Non-integer positive numerical values of `n` or `x` will be truncated to the next smallest integer, which has to be no larger than `.Machine$integer.max`.

The optional `prob` argument can be used to give a vector of weights for obtaining the elements of the vector being sampled. They need not sum to one, but they should be non-negative and not all zero. If `replace` is true, Walker’s alias method (Ripley, 1987) is used when there are more than 250 reasonably probable values: this gives results incompatible with those from R < 2.2.0, and there will be a warning the first time this happens in a session.

If `replace` is false, these probabilities are applied sequentially, that is the probability of choosing the next item is proportional to the weights amongst the remaining items. The number of nonzero weights must be at least `size` in this case.

`sample.int` is a bare interface in which both `n` and `size` must be supplied as integers.

**Value**

For `sample` a vector of length `size` with elements drawn from either `x` or from the integers `1:x`.

For `sample.int`, an integer vector of length `size` with elements from `1:n`,

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Ripley, B. D. (1987) *Stochastic Simulation*. Wiley.

**See Also**

Package **sampling** for other methods of weighted sampling without replacement.

**Examples**

```
x <- 1:12
# a random permutation
sample(x)
# bootstrap resampling -- only if length(x) > 1 !
sample(x, replace=TRUE)

# 100 Bernoulli trials
sample(c(0,1), 100, replace = TRUE)

## More careful bootstrapping -- Consider this when using sample()
## programmatically (i.e., in your function or simulation)!

# sample()'s surprise -- example
x <- 1:10
  sample(x[x > 8]) # length 2
  sample(x[x > 9]) # oops -- length 10!
  sample(x[x > 10]) # length 0

## For R >= 2.11.0 only
resample <- function(x, ...) x[sample.int(length(x), ...)]
resample(x[x > 8]) # length 2
resample(x[x > 9]) # length 1
resample(x[x > 10]) # length 0
```

---

 save

*Save R Objects*


---

**Description**

`save` writes an external representation of R objects to the specified file. The objects can be read back from the file at a later date by using the function `load` (or `data` in some cases).

`save.image()` is just a short-cut for ‘save my current workspace’, i.e., `save(list = ls(all=TRUE), file = ".RData")`. It is also what happens with `q("yes")`.

**Usage**

```
save(..., list = character(0L),
      file = stop("'file' must be specified"),
      ascii = FALSE, version = NULL, envir = parent.frame(),
      compress = !ascii, compression_level,
      eval.promises = TRUE, precheck = TRUE)

save.image(file = ".RData", version = NULL, ascii = FALSE,
           compress = !ascii, safe = TRUE)
```

**Arguments**

<code>...</code>	the names of the objects to be saved (as symbols or character strings).
<code>list</code>	A character vector containing the names of objects to be saved.
<code>file</code>	a connection or the name of the file where the data will be saved. Must be a file name for workspace format version 1.
<code>ascii</code>	if <code>TRUE</code> , an ASCII representation of the data is written. The default value of <code>ascii</code> is <code>FALSE</code> which leads to a more compact binary file being written.
<code>version</code>	the workspace format version to use. <code>NULL</code> specifies the current default format. The version used from R 0.99.0 to R 1.3.1 was version 1. The default format as from R 1.4.0 is version 2.
<code>envir</code>	environment to search for objects to be saved.
<code>compress</code>	logical or character string specifying whether saving to a named file is to use compression. <code>TRUE</code> corresponds to <code>gzip</code> compression, and (from R 2.10.0) character strings <code>"gzip"</code> , <code>"bzip2"</code> or <code>"xz"</code> specify the type of compression. Ignored when <code>file</code> is a connection and for workspace format version 1.
<code>compression_level</code>	integer: the level of compression to be used. Defaults to 6 for <code>gzip</code> compression and to 9 for <code>bzip2</code> or <code>xz</code> compression.
<code>eval.promises</code>	logical: should objects which are promises be forced before saving?
<code>precheck</code>	logical: should the existence of the objects be checked before starting to save (and in particular before opening the file/connection)? Does not apply to version 1 saves.
<code>safe</code>	logical. If <code>TRUE</code> , a temporary file is used for creating the saved workspace. The temporary file is renamed to <code>file</code> if the save succeeds. This preserves an existing workspace <code>file</code> if the save fails, but at the cost of using extra disk space during the save.

**Details**

The names of the objects specified either as symbols (or character strings) in `...` or as a character vector in `list` are used to look up the objects from environment `envir`. By default `promises` are evaluated, but if `eval.promises = FALSE` promises are saved (together with their evaluation environments). (Promises embedded in objects are always saved unevaluated.)

All R platforms use the XDR (bigendian) representation of C ints and doubles in binary save-d files, and these are portable across all R platforms. (ASCII saves used to be useful for moving data between platforms but are now mainly of historical interest.)

Default values for the `ascii`, `compress`, `safe` and `version` arguments can be modified with the `save.defaults` option (used both by `save` and `save.image`), see also the example section below. If a `save.image.defaults` option is set it overrides `save.defaults` for function `save.image` (which allows this to have different defaults).

A connection that is not already open will be opened in mode `"wb"`. Only ASCII saves can be written to text-mode connections.

**Compression**

Large files can be reduced considerably in size by compression. A particular 46MB dataset was saved as 35MB without compression in 2 seconds, 22MB with `gzip` compression in 8 secs, 19MB with `bzip2` compression in 13 secs and 9.4MB with `xz` compression in 40 secs. The load times

were 1.3, 2.8, 5.5 and 5.7 seconds respectively. These results are indicative, but the relative performances do depend on the actual file and `xz` did unusually well here.

It is possible to compress later (with `gzip`, `bzip2` or `xz`) a file saved with `compress = FALSE`: the effect is the same as saving with compression. Also, a saved file can be uncompressed and re-compressed under a different compression scheme (and see [resaveRdaFiles](#) for a way to do so from within R).

### Warnings

The `...` arguments only give the *names* of the objects to be saved: they are searched for in the environment given by the `envir` argument, and the actual objects given as arguments need not be those found.

Saved R objects are binary files, even those saved with `ascii = TRUE`, so ensure that they are transferred without conversion of end of line markers and of 8-bit characters. The lines are delimited by LF on all platforms.

Although the default version has not changed since R 1.4.0, this does not mean that saved files are necessarily backwards compatible. You will be able to load a saved image into an earlier version of R unless use is made of later additions (for example, raw vectors or external pointers).

### Note

The most common reason for failure is lack of write permission in the current directory. For `save.image` and for saving at the end of a session this will shown by messages like

```
Error in gzfile(file, "wb") : unable to open connection
In addition: Warning message:
In gzfile(file, "wb") :
  cannot open compressed file '.RDataTmp',
  probable reason 'Permission denied'
```

The defaults were changed to use compressed saves for `save` in 2.3.0 and for `save.image` in 2.4.0. Any recent version of R can read compressed save files, and a compressed file can be uncompressed (by `gzip -d`) for use with very old versions of R.

### See Also

[dput](#), [dump](#), [load](#), [data](#).

### Examples

```
x <- stats::runif(20)
y <- list(a = 1, b = TRUE, c = "oops")
save(x, y, file = "xy.Rdata")
save.image()
unlink("xy.Rdata")
unlink(".RData")

# set save defaults using option:
options(save.defaults=list(ascii=TRUE, safe=FALSE))
save.image()
unlink(".RData")
```

---

`scale`*Scaling and Centering of Matrix-like Objects*

---

**Description**

`scale` is generic function whose default method centers and/or scales the columns of a numeric matrix.

**Usage**

```
scale(x, center = TRUE, scale = TRUE)
```

**Arguments**

<code>x</code>	a numeric matrix(like object).
<code>center</code>	either a logical value or a numeric vector of length equal to the number of columns of <code>x</code> .
<code>scale</code>	either a logical value or a numeric vector of length equal to the number of columns of <code>x</code> .

**Details**

The value of `center` determines how column centering is performed. If `center` is a numeric vector with length equal to the number of columns of `x`, then each column of `x` has the corresponding value from `center` subtracted from it. If `center` is `TRUE` then centering is done by subtracting the column means (omitting NAs) of `x` from their corresponding columns, and if `center` is `FALSE`, no centering is done.

The value of `scale` determines how column scaling is performed (after centering). If `scale` is a numeric vector with length equal to the number of columns of `x`, then each column of `x` is divided by the corresponding value from `scale`. If `scale` is `TRUE` then scaling is done by dividing the (centered) columns of `x` by their standard deviations, and if `scale` is `FALSE`, no scaling is done.

The standard deviation for a column is obtained by computing the square-root of the sum-of-squares of the non-missing values in the column divided by the number of non-missing values minus one (whether or not centering was done).

**Value**

For `scale.default`, the centered, scaled matrix. The numeric centering and scalings used (if any) are returned as attributes `"scaled:center"` and `"scaled:scale"`

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[sweep](#) which allows centering (and scaling) with arbitrary statistics.

For working with the scale of a plot, see [par](#).



## Examples

```
require(stats)
x <- matrix(1:10, ncol=2)
(centered.x <- scale(x, scale=FALSE))
cov(centered.scaled.x <- scale(x))# all 1
```

---

scan

*Read Data Values*

---

## Description

Read data into a vector or list from the console or file.

## Usage

```
scan(file = "", what = double(0), nmax = -1, n = -1, sep = "",
      quote = if(identical(sep, "\n")) "" else "'\"'", dec = ".",
      skip = 0, nlines = 0, na.strings = "NA",
      flush = FALSE, fill = FALSE, strip.white = FALSE,
      quiet = FALSE, blank.lines.skip = TRUE, multi.line = TRUE,
      comment.char = "", allowEscapes = FALSE,
      encoding = "unknown")
```

## Arguments

**file** the name of a file to read data values from. If the specified file is "", then input is taken from the keyboard (or whatever `stdin()` reads if input is redirected or R is embedded). (In this case input can be terminated by a blank line or an EOF signal, 'Ctrl-D' on Unix and 'Ctrl-Z' on Windows.)

Otherwise, the file name is interpreted *relative* to the current working directory (given by `getwd()`), unless it specifies an *absolute* path. Tilde-expansion is performed where supported. When running R from a script, `file="stdin"` can be used to refer to the process's `stdin` file stream.

As from R 2.10.0 this can be a compressed file (see [file](#)).

Alternatively, `file` can be a [connection](#), which will be opened if necessary, and if so closed at the end of the function call. Whatever mode the connection is opened in, any of LF, CRLF or CR will be accepted as the EOL marker for a line and so will match `sep = "\n"`.

`file` can also be a complete URL.

To read a data file not in the current encoding (for example a Latin-1 file in a UTF-8 locale or conversely) use a [file](#) connection setting the `encoding` argument.

**what** the type of what gives the type of data to be read. The supported types are logical, integer, numeric, complex, character, raw and [list](#). If `what` is a list, it is assumed that the lines of the data file are records each containing `length(what)` items ('fields') and the list components should have elements which are one of the first six types listed or NULL, see section 'Details' below.

nmax	integer: the maximum number of data values to be read, or if <code>what</code> is a list, the maximum number of records to be read. If omitted or not positive or an invalid value for an integer (and <code>nlines</code> is not set to a positive value), <code>scan</code> will read to the end of <code>file</code> .
n	integer: the maximum number of data values to be read, defaulting to no limit. Invalid values will be ignored.
sep	by default, <code>scan</code> expects to read white-space delimited input fields. Alternatively, <code>sep</code> can be used to specify a character which delimits fields. A field is always delimited by an end-of-line marker unless it is quoted. If specified this should be the empty character string (the default) or <code>NULL</code> or a character string containing just one single-byte character.
quote	the set of quoting characters as a single character string or <code>NULL</code> . In a multibyte locale the quoting characters must be ASCII (single-byte).
dec	decimal point character. This should be a character string containing just one single-byte character. ( <code>NULL</code> and a zero-length character vector are also accepted, and taken as the default.)
skip	the number of lines of the input file to skip before beginning to read data values.
nlines	if positive, the maximum number of lines of data to be read.
na.strings	character vector. Elements of this vector are to be interpreted as missing ( <code>NA</code> ) values. Blank fields are also considered to be missing values in logical, integer, numeric and complex fields.
flush	logical: if <code>TRUE</code> , <code>scan</code> will flush to the end of the line after reading the last of the fields requested. This allows putting comments after the last field, but precludes putting more than one record on a line.
fill	logical: if <code>TRUE</code> , <code>scan</code> will implicitly add empty fields to any lines with fewer fields than implied by <code>what</code> .
strip.white	vector of logical value(s) corresponding to items in the <code>what</code> argument. It is used only when <code>sep</code> has been specified, and allows the stripping of leading and trailing white space from <code>character</code> fields (numeric fields are always stripped). If <code>strip.white</code> is of length 1, it applies to all fields; otherwise, if <code>strip.white[i]</code> is <code>TRUE</code> <i>and</i> the <i>i</i> -th field is of mode <code>character</code> (because <code>what[i]</code> is) then the leading and trailing white space from field <i>i</i> is stripped.
quiet	logical: if <code>FALSE</code> (default), <code>scan()</code> will print a line, saying how many items have been read.
blank.lines.skip	logical: if <code>TRUE</code> blank lines in the input are ignored, except when counting <code>skip</code> and <code>nlines</code> .
multi.line	logical. Only used if <code>what</code> is a list. If <code>FALSE</code> , all of a record must appear on one line (but more than one record can appear on a single line). Note that using <code>fill = TRUE</code> implies that a record will terminated at the end of a line.
comment.char	character: a character vector of length one containing a single character or an empty string. Use <code>" "</code> to turn off the interpretation of comments altogether (the default).
allowEscapes	logical. Should C-style escapes such as <code>'\n'</code> be processed (the default) or read verbatim? Note that if not within quotes these could be interpreted as a delimiter (but not as a comment character).

The escapes which are interpreted are the control characters `'\a, \b, \f, \n, \r, \t, \v'` and octal and hexadecimal representations like `'\040'` and `'\0x2A'`. Any other escaped character is treated as itself, including backslash.

`encoding` encoding to be assumed for input strings. If the value is `"latin1"` or `"UTF-8"` it is used to mark character strings as known to be in Latin-1 or UTF-8: it is not used to re-encode the input. To do the latter, specify the encoding as part of the connection `con` or *via* `options(encoding=)`: see the example under [file](#).

## Details

The value of `what` can be a list of types, in which case `scan` returns a list of vectors with the types given by the types of the elements in `what`. This provides a way of reading columnar data. If any of the types is `NULL`, the corresponding field is skipped (but a `NULL` component appears in the result).

The type of `what` or its components can be one of the six atomic vector types or `NULL` (see [is.atomic](#)).

'White space' is defined for the purposes of this function as one or more contiguous characters from the set space, horizontal tab, carriage return and line feed. It does not include form feed or vertical tab, but in Latin-1 and Windows 8-bit locales 'space' includes non-breaking space.

Empty numeric fields are always regarded as missing values. Empty character fields are scanned as empty character vectors, unless `na.strings` contains `" "` when they are regarded as missing values.

The allowed input for a numeric field is optional whitespace followed either `NA` or an optional sign followed by a decimal or hexadecimal constant (see [NumericConstants](#)), or `NaN`, `Inf` or `infinity` (ignoring case). Out-of-range values are recorded as `Inf`, `-Inf` or `0`.

For an integer field the allowed input is optional whitespace, followed by either `NA` or an optional sign and one or more digits (`'0-9'`): all out-of-range values are converted to `NA_integer_`.

If `sep` is the default (`" "`), the character `'\'` in a quoted string escapes the following character, so quotes may be included in the string by escaping them.

If `sep` is non-default, the fields may be quoted in the style of `'CSV'` files where separators inside quotes (`"` or `"`) are ignored and quotes may be put inside strings by doubling them. However, if `sep = "\n"` it is assumed by default that one wants to read entire lines verbatim.

Quoting is only interpreted in character fields and in `NULL` fields (which might be skipping character fields).

Note that since `sep` is a separator and not a terminator, reading a file by `scan("foo", sep="\n", blank.lines.skip=FALSE)` will give an empty final line if the file ends in a linefeed and not if it does not. This might not be what you expected; see also [readLines](#).

If `comment.char` occurs (except inside a quoted character field), it signals that the rest of the line should be regarded as a comment and be discarded. Lines beginning with a comment character (possibly after white space with the default separator) are treated as blank lines.

There is a line-length limit of 4095 bytes when reading from the console (which may impose a lower limit: see 'An Introduction to R').

There is a check for a user interrupt every 1000 lines if `what` is a list, otherwise every 10000 items.

**Value**

if `what` is a list, a list of the same length and same names (as any) as `what`.

Otherwise, a vector of the type of `what`.

Character strings in the result will have a declared encoding if `encoding` is `"latin1"` or `"UTF-8"`.

**Note**

The default for `multi.line` differs from `S`. To read one record per line, use `flush = TRUE` and `multi.line = FALSE`. (Note that quoted character strings can still include embedded new-lines.)

If `number of items` is not specified, the internal mechanism re-allocates memory in powers of two and so could use up to three times as much memory as needed. (It needs both old and new copies.) If you can, specify either `n` or `nmax` whenever inputting a large vector, and `nmax` or `nlines` when inputting a large list.

Using `scan` on an open connection to read partial lines can lose chars: use an explicit separator to avoid this.

Having `nul` bytes in fields (including `'\0'` if `allowEscapes = TRUE`) may lead to interpretation of the field being terminated at the `nul`. They not normally present in text files – see [readBin](#).

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[read.table](#) for more user-friendly reading of data matrices; [readLines](#) to read a file a line at a time. [write](#).

[Quotes](#) for the details of C-style escape sequences.

[readChar](#) and [readBin](#) to read fixed or variable length character strings or binary representations of numbers a few at a time from a connection.

**Examples**

```
cat("TITLE extra line", "2 3 5 7", "11 13 17", file="ex.data", sep="\n")
pp <- scan("ex.data", skip = 1, quiet= TRUE)
scan("ex.data", skip = 1)
scan("ex.data", skip = 1, nlines=1) # only 1 line after the skipped one
scan("ex.data", what = list("", "", "")) # flush is F -> read "7"
scan("ex.data", what = list("", "", ""), flush = TRUE)
unlink("ex.data") # tidy up
```

---

`search`*Give Search Path for R Objects*

---

**Description**

Gives a list of [attached packages](#) (see [library](#)), and R objects, usually [data.frames](#).

**Usage**

```
search()  
searchpaths()
```

**Value**

A character vector, starting with `".GlobalEnv"`, and ending with `"package:base"` which is R's **base** package required always.

`searchpaths` gives a similar character vector, with the entries for packages being the path to the package used to load the code.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. ([search](#).)

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer. ([searchPaths](#).)

**See Also**

[.packages](#) to list just the packages on search path.

[loadedNamespaces](#) to list loaded name spaces.

[attach](#) and [detach](#) to change the search path, [objects](#) to find R objects in there.

**Examples**

```
search()  
searchpaths()
```

---

`seek`*Functions to Reposition Connections*

---

**Description**

Functions to re-position connections.

**Usage**

```
seek(con, ...)
## S3 method for class 'connection':
seek(con, where = NA, origin = "start", rw = "", ...)

isSeekable(con)

truncate(con, ...)
```

**Arguments**

<code>con</code>	a connection.
<code>where</code>	numeric. A file position (relative to the origin specified by <code>origin</code> ), or <code>NA</code> .
<code>rw</code>	character. Empty or "read" or "write", partial matches allowed.
<code>origin</code>	character. One of "start", "current", "end": see 'Details'.
<code>...</code>	further arguments passed to or from other methods.

**Details**

`seek` with `where = NA` returns the current byte offset of a connection (from the beginning), and with a non-missing `where` argument the connection is re-positioned (if possible) to the specified position. `isSeekable` returns whether the connection in principle supports `seek`: currently only (possibly gz-compressed) file connections do. `gzfile` connections do not support `origin = "end"`; the file position they use is that of the uncompressed file.

`where` is stored as a real but should represent an integer: non-integer values are likely to be truncated. Note that the possible values can exceed the largest representable number in an `R` integer on 64-bit builds, and on some 32-bit builds.

File connections can be open for both writing/appending, in which case `R` keeps separate positions for reading and writing. Which `seek` refers to can be set by its `rw` argument: the default is the last mode (reading or writing) which was used. Most files are only opened for reading or writing and so default to that state. If a file is open for both reading and writing but has not been used, the default is to give the reading position (0).

The initial file position for reading is always at the beginning. The initial position for writing is at the beginning of the file for modes "r+" and "r+b", otherwise at the end of the file. Some platforms only allow writing at the end of the file in the append modes. (The reported write position for a file opened in an append mode will typically be unreliable until the file has been written to.)

If `seek` is called with a non-`NA` value of `where`, any pushback on a text-mode connection is discarded.

`truncate` truncates a file opened for writing at its current position. It works only for file connections, and is not implemented on all platforms: on others (including Windows) it will not work for large (> 2Gb) files.

**Value**

`seek` returns the current position (before any move), as a (numeric) byte offset from the origin, if relevant, or 0 if not. Note that the position can exceed the largest representable number in an `R` integer on 64-bit builds, and on some 32-bit builds.

`truncate` returns `NULL`: it stops with an error if it fails (or is not implemented).

`isSeekable` returns a logical value, whether the connection supports `seek`.

**Warning**

Use of `seek` on Windows is discouraged. We have found so many errors in the Windows implementation of file positioning that users are advised to use it only at their own risk, and asked not to waste the R developers' time with bug reports on Windows' deficiencies.

**See Also**

[connections](#)

---

seq	<i>Sequence Generation</i>
-----	----------------------------

---

**Description**

Generate regular sequences. `seq` is a standard generic with a default method. `seq.int` is an internal generic which can be much faster but has a few restrictions. `seq_along` and `seq_len` are very fast primitives for two common cases.

**Usage**

```
seq(...)

## Default S3 method:
seq(from = 1, to = 1, by = ((to - from)/(length.out - 1)),
     length.out = NULL, along.with = NULL, ...)

seq.int(from, to, by, length.out, along.with, ...)

seq_along(along.with)
seq_len(length.out)
```

**Arguments**

<code>...</code>	arguments passed to or from methods.
<code>from, to</code>	the starting and (maximal) end value of the sequence.
<code>by</code>	number: increment of the sequence.
<code>length.out</code>	desired length of the sequence. A non-negative number, which for <code>seq</code> and <code>seq.int</code> will be rounded up if fractional.
<code>along.with</code>	take the length from the length of this argument.

**Details**

The interpretation of the unnamed arguments of `seq` and `seq.int` is *not* standard, and it is recommended always to name the arguments when programming.

Both `seq` and `seq.int` are generic, and only the default method is described here. Typical usages are

```
seq(from, to)
seq(from, to, by= )
seq(from, to, length.out= )
seq(along.with= )
seq(from)
seq(length.out= )
```

The first form generates the sequence `from, from+/-1, ..., to` (identical to `from:to`).

The second form generates `from, from+by, ..., up` to the sequence value less than or equal to `to`. Specifying `to - from` and `by` of opposite signs is an error. Note that the computed final value can go just beyond `to` to allow for rounding error, but (as from R 2.9.0) is truncated to `to`. ('Just beyond' is by up to  $10^{-10}$  times `abs(from - to)` as from R 2.11.0: previously it was  $10^{-7}$  times.)

The third generates a sequence of `length.out` equally spaced values from `from` to `to`. (`length.out` is usually abbreviated to `length` or `len`, and `seq_len` is much faster.)

The fourth form generates the integer sequence `1, 2, ..., length(along.with)`. (`along.with` is usually abbreviated to `along`, and `seq_along` is much faster.)

The fifth form generates the sequence `1, 2, ..., length(from)` (as if argument `along.with` had been specified), *unless* the argument is numeric of length 1 when it is interpreted as `1:from` (even for `seq(0)` for compatibility with S).

The final form generates the integer sequence `1, 2, ..., length.out` unless `length.out = 0`, when it generates `integer(0)`.

Very small sequences (with `from - to` of the order of  $10^{-14}$  times the larger of the ends) will return `from`.

For `seq` (only), up to two of `from`, `to` and `by` can be supplied as complex values provided `length.out` or `along.with` is specified.

`seq.int`, `seq_along` and `seq_len` are [primitive](#).

## Value

`seq.int` and the default method of `seq` return a vector of type "integer" or "double": programmers should not rely on which.

`seq_along` and `seq_length` always return an integer vector.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

The methods [seq.Date](#) and [seq.POSIXt](#).

[:](#), [rep](#), [sequence](#), [row](#), [col](#).

## Examples

```
seq(0, 1, length.out=11)
seq(stats::rnorm(20))
seq(1, 9, by = 2) # match
seq(1, 9, by = pi)# stay below
seq(1, 6, by = 3)
```



```
seq(1.575, 5.125, by=0.05)
seq(17) # same as 1:17
```

---

seq.Date

*Generate Regular Sequences of Dates*


---

### Description

The method for `seq` for objects of class `"Date"` representing calendar dates.

### Usage

```
## S3 method for class 'Date':
seq(from, to, by, length.out = NULL, along.with = NULL, ...)
```

### Arguments

<code>from</code>	starting date. Required
<code>to</code>	end date. Optional.
<code>by</code>	increment of the sequence. Optional. See 'Details'.
<code>length.out</code>	integer, optional. desired length of the sequence.
<code>along.with</code>	take the length from the length of this argument.
<code>...</code>	arguments passed to or from other methods.

### Details

`by` can be specified in several ways.

- A number, taken to be in days.
- A object of class `difftime`
- A character string, containing one of "day", "week", "month" or "year". This can optionally be preceded by a (positive or negative) integer and a space, or followed by "s". See `seq.POSIXt` for the details of "month".

### Value

A vector of class `"Date"`.

### See Also

[Date](#)

**Examples**

```
## first days of years
seq(as.Date("1910/1/1"), as.Date("1999/1/1"), "years")
## by month
seq(as.Date("2000/1/1"), by="month", length.out=12)
## quarters
seq(as.Date("2000/1/1"), as.Date("2003/1/1"), by="3 months")

## find all 7th of the month between two dates, the last being a 7th.
st <- as.Date("1998-12-17")
en <- as.Date("2000-1-7")
ll <- seq(en, st, by="-1 month")
rev(ll[ll > st & ll < en])
```

seq.POSIXt

*Generate Regular Sequences of Times***Description**

The method for `seq` for date-time classes.

**Usage**

```
## S3 method for class 'POSIXt':
seq(from, to, by, length.out = NULL, along.with = NULL, ...)
```

**Arguments**

<code>from</code>	starting date. Required.
<code>to</code>	end date. Optional.
<code>by</code>	increment of the sequence. Optional. See ‘Details’.
<code>length.out</code>	integer, optional. desired length of the sequence.
<code>along.with</code>	take the length from the length of this argument.
<code>...</code>	arguments passed to or from other methods.

**Details**

`by` can be specified in several ways.

- A number, taken to be in seconds.
- A object of class `difftime`
- A character string, containing one of "sec", "min", "hour", "day", "DSTday", "week", "month" or "year". This can optionally be preceded by a (positive or negative) integer and a space, or followed by "s".

The difference between "day" and "DSTday" is that the former ignores changes to/from daylight savings time and the latter takes the same clock time each day. ("week" ignores DST (it is a period of 144 hours), but "7 DSTdays") can be used as an alternative. "month" and "year" allow for DST.)

The [timezone](#) of the result is taken from `from`: remember that GMT means UTC (and not the timezone of Greenwich, England) and so does not have daylight savings time.

Using `"month"` first advances the month without changing the day: if this results in an invalid day of the month, it is counted forward into the next month: see the examples.

### Value

A vector of class `"POSIXct"`.

### See Also

[DateTimeClasses](#)

### Examples

```
## first days of years
seq(ISOdate(1910,1,1), ISOdate(1999,1,1), "years")
## by month
seq(ISOdate(2000,1,1), by = "month", length.out = 12)
seq(ISOdate(2000,1,31), by = "month", length.out = 4)
## quarters
seq(ISOdate(1990,1,1), ISOdate(2000,1,1), by = "3 months")
## days vs DSTdays: use c() to lose the timezone.
seq(c(ISOdate(2000,3,20)), by = "day", length.out = 10)
seq(c(ISOdate(2000,3,20)), by = "DSTday", length.out = 10)
seq(c(ISOdate(2000,3,20)), by = "7 DSTdays", length.out = 4)
```

---

sequence

*Create A Vector of Sequences*

---

### Description

For each element of `nvec` the sequence `seq_len(nvec[i])` is created. These are concatenated and the result returned.

### Usage

```
sequence(nvec)
```

### Arguments

`nvec` a non-negative integer vector each element of which specifies the end point of a sequence.

### Details

Earlier versions of `sequence` used to work for 0 or negative inputs as `seq(x) == 1:x`.

Note that `sequence <- function(nvec) unlist(lapply(nvec, seq_len))` and it mainly exists in reverence to the very early history of R.

### See Also

[gl](#), [seq](#), [rep](#).

**Examples**

```
sequence(c(3,2))# the concatenated sequences 1:3 and 1:2.
#> [1] 1 2 3 1 2
```

---

serialize	<i>Simple Serialization Interface</i>
-----------	---------------------------------------

---

**Description**

A simple low-level interface for serializing to connections.

**Usage**

```
serialize(object, connection, ascii = FALSE, refhook = NULL)
```

```
unserialize(connection, refhook = NULL)
```

**Arguments**

object	R object to serialize.
connection	an open connection or (for <code>serialize</code> ) <code>NULL</code> or (for <code>unserialize</code> ) a raw vector (see ‘Details’).
ascii	a logical. If <code>TRUE</code> , an ASCII representation is written; otherwise (default except for text-mode connections), a more compact binary one is used.
refhook	a hook function for handling reference objects.

**Details**

The function `serialize` writes `object` to the specified connection. If `connection` is `NULL` then `object` is serialized to a raw vector, which is returned as the result of `serialize`.

Sharing of reference objects is preserved within the object but not across separate calls to `serialize`.

`unserialize` reads an object (as written by `serialize`) from `connection` or a raw vector.

The `refhook` functions can be used to customize handling of non-system reference objects (all external pointers and weak references, and all environments other than name space and package environments and `.GlobalEnv`). The hook function for `serialize` should return a raw vector for references it wants to handle; otherwise it should return `NULL`. The hook for `unserialize` will be called with raw vectors supplied to `serialize` and should return an appropriate object.

For a text-mode connection, the default value of `ascii` is set to `TRUE`: only ASCII representations can be written to text-mode connections and attempting to use `ascii = FALSE` will throw an error.

The format consists of a single line followed by the data: the first line contains a single character: X for binary serialization and A for ASCII serialization, followed by a new line.

**Value**

For `serialize`, `NULL` unless `connection = NULL`, when the result is returned in a raw vector.

For `unserialize` an R object.

### Warning

These functions are still experimental. Names, interfaces and values might change in future versions (and the value of `serialize` was changed for R 2.4.0).

A raw vector is limited to  $2^{31} - 1$  bytes, but R objects can exceed this and their serializations will normally be larger than the objects.

### Examples

```
x <- serialize(list(1,2,3), NULL)
unserialize(x)
```

---

sets

*Set Operations*

---

### Description

Performs **set** union, intersection, (asymmetric!) difference, equality and membership on two vectors.

### Usage

```
union(x, y)
intersect(x, y)
setdiff(x, y)
setequal(x, y)

is.element(el, set)
```

### Arguments

`x`, `y`, `el`, `set`  
vectors (of the same mode) containing a sequence of items (conceptually) with no duplicated values.

### Details

Each of `union`, `intersect`, `setdiff` and `setequal` will discard any duplicated values in the arguments, and they apply `as.vector` to their arguments (and so in particular coerce factors to character vectors).

`is.element(x, y)` is identical to `x %in% y`.

### Value

A vector of the same `mode` as `x` or `y` for `setdiff` and `intersect`, respectively, and of a common mode for `union`.

A logical scalar for `setequal` and a logical of the same length as `x` for `is.element`.

### See Also

`%in%`

`'plotmath'` for the use of `union` and `intersect` in plot annotation.

**Examples**

```
(x <- c(sort(sample(1:20, 9)), NA))
(y <- c(sort(sample(3:23, 7)), NA))
union(x, y)
intersect(x, y)
setdiff(x, y)
setdiff(y, x)
setequal(x, y)

## True for all possible x & y :
setequal( union(x,y),
          c(setdiff(x,y), intersect(x,y), setdiff(y,x)))

is.element(x, y) # length 10
is.element(y, x) # length 8
```

---

```
setTimeLimit          Set CPU and/or Elapsed Time Limits
```

---

**Description**

Functions to set CPU and/or elapsed time limits for top-level computations or the current session.

**Usage**

```
setTimeLimit(cpu = Inf, elapsed = Inf, transient = FALSE)

setSessionTimeLimit(cpu = Inf, elapsed = Inf)
```

**Arguments**

cpu	double. Limit on total cpu time.
elapsed	double. Limit on elapsed time.
transient	logical. If TRUE, the limits apply only to the rest of the current computation.

**Details**

`setTimeLimit` sets limits which apply to each top-level computation, that is a command line (including any continuation lines) entered at the console or from a file. If it is called from within a computation the limits apply to the rest of the computation and (unless `transient = TRUE` to subsequent top-level computations.

`setSessionTimeLimit` sets limits for the rest of the session. Once a session limit is reached it is reset to `Inf`.

Setting any limit has a small overhead – well under 1% on the systems measured.

Time limits are checked whenever a user interrupt could occur. This will happen frequently in R code and during `Sys.sleep`, but only at points in compiled C and Foreign code identified by the code author.

‘Total cpu time’ includes that used by child processes where the latter is reported.

It is possible (but very unusual) to build R without support for `proc.time`, in which case these functions have no effect.

---

showConnections      *Display Connections*

---

## Description

Display aspects of connections.

## Usage

```
showConnections(all = FALSE)
getConnection(what)
closeAllConnections()

stdin()
stdout()
stderr()
```

## Arguments

all	logical: if true all connections, including closed ones and the standard ones are displayed. If false only open user-created connections are included.
what	integer: a row number of the table given by <code>showConnections</code> .

## Details

`stdin()`, `stdout()` and `stderr()` are standard connections corresponding to input, output and error on the console respectively (and not necessarily to file streams). They are text-mode connections of class "terminal" which cannot be opened or closed, and are read-only, write-only and write-only respectively. The `stdout()` and `stderr()` connections can be re-directed by `sink` (and in some circumstances the output from `stdout()` can be split: see the help page).

The encoding for `stdin()` when redirected can be set by the command-line flag '--encoding'.

`showConnections` returns a matrix of information. If a connection object has been lost or forgotten, `getConnection` will take a row number from the table and return a connection object for that connection, which can be used to close the connection, for example. However, if there is no R level object referring to the connection it will be closed automatically at the next garbage collection.

`closeAllConnections` closes (and destroys) all user connections, restoring all `sink` diversions as it does so.

## Value

`stdin()`, `stdout()` and `stderr()` return connection objects.

`showConnections` returns a character matrix of information with a row for each connection, by default only for open non-standard connections.

`getConnection` returns a connection object, or NULL.

**Note**

`stdin()` refers to the ‘console’ and not to the C-level ‘`stdin`’ of the process. The distinction matters in GUI consoles (which may not have an active ‘`stdin`’, and if they do it may not be connected to console input), and also in embedded applications. If you want access to the C-level file stream ‘`stdin`’, use `file("stdin")`.

When `R` is reading a script from a file, the *file* is the ‘console’: this is traditional usage to allow in-line data (see ‘An Introduction to R’ for an example).

**See Also**

[connections](#)

**Examples**

```
showConnections(all = TRUE)

textConnection(letters)
# oops, I forgot to record that one
showConnections()
# class      description      mode text  isopen  can read can write
#3 "letters" "textConnection" "r"  "text" "opened" "yes"    "no"
## Not run: close(getConnection(3))

showConnections()
```

---

shQuote

*Quote Strings for Use in OS Shells*


---

**Description**

Quote a string to be passed to an operating system shell.

**Usage**

```
shQuote(string, type = c("sh", "csh", "cmd"))
```

**Arguments**

<code>string</code>	a character vector, usually of length one.
<code>type</code>	character: the type of shell. Partial matching is supported. "cmd" refers to the Windows NT shell, and is the default under Windows.

**Details**

The default type of quoting supported under Unix-alikes is that for the Bourne shell `sh`. If the string does not contain single quotes, we can just surround it with single quotes. Otherwise, the string is surrounded in double quotes, which suppresses all special meanings of metacharacters except dollar, backquote and backslash, so these (and of course double quote) are preceded by backslash. This type of quoting is also appropriate for `bash`, `ksh` and `zsh`.

The other type of quoting is for the C-shell (`csh` and `tcsh`). Once again, if the string does not contain single quotes, we can just surround it with single quotes. If it does contain single quotes,



we can use double quotes provided it does not contain dollar or backquote (and we need to escape backslash, exclamation mark and double quote). As a last resort, we need to split the string into pieces not containing single quotes and surround each with single quotes, and the single quotes with double quotes.

## References

Loukides, M. et al (2002) *Unix Power Tools* Third Edition. O'Reilly. Section 27.12.  
[http://www.mhuffman.com/notes/dos/bash\\_cmd.htm](http://www.mhuffman.com/notes/dos/bash_cmd.htm)

## See Also

Quotes for quoting R code.  
[sQuote](#) for quoting English text.

## Examples

```
test <- "abc$def`gh`i\\j"
cat(shQuote(test), "\n")
## Not run: system(paste("echo", shQuote(test)))
test <- "don't do it!"
cat(shQuote(test), "\n")

tryit <- paste("use the", sQuote("-c"), "switch\nlike this")
cat(shQuote(tryit), "\n")
## Not run: system(paste("echo", shQuote(tryit)))
cat(shQuote(tryit, type="csh"), "\n")

## Windows-only example.
perlcmd <- 'print "Hello World\n";'
## Not run: shell(paste("perl -e", shQuote(perlcmd), type="cmd"))
```

---

sign

*Sign Function*

---

## Description

`sign` returns a vector with the signs of the corresponding elements of `x` (the sign of a real number is 1, 0, or  $-1$  if the number is positive, zero, or negative, respectively).

Note that `sign` does not operate on complex vectors.

## Usage

```
sign(x)
```

## Arguments

`x` a numeric vector

## Details

This is an [internal generic primitive](#) function: methods can be defined for it directly or via the [Math](#) group generic.

**See Also**[abs](#)**Examples**

```
sign(pi) # == 1
sign(-2:3) # -1 -1 0 1 1 1
```

---

Signals

*Interrupting Execution of R*

---

**Description**

On receiving SIGUSR1 R will save the workspace and quit. SIGUSR2 has the same result except that the `.Last` function and `on.exit` expressions will not be called.

**Usage**

```
kill -USR1 pid
kill -USR2 pid
```

**Arguments**

`pid`                    The process ID of the R process

**Warning**

It is possible that one or more R objects will be undergoing modification at the time the signal is sent. These objects could be saved in a corrupted form.

---

`sink`

*Send R Output to a File*

---

**Description**

`sink` diverts R output to a connection.

`sink.number()` reports how many diversions are in use.

`sink.number(type = "message")` reports the number of the connection currently being used for error messages.

**Usage**

```
sink(file = NULL, append = FALSE, type = c("output", "message"),
      split = FALSE)
```

```
sink.number(type = c("output", "message"))
```

**Arguments**

<code>file</code>	a writable connection or a character string naming the file to write to, or <code>NULL</code> to stop sink-ing.
<code>append</code>	logical. If <code>TRUE</code> , output will be appended to <code>file</code> ; otherwise, it will overwrite the contents of <code>file</code> .
<code>type</code>	character. Either the output stream or the messages stream.
<code>split</code>	logical: if <code>TRUE</code> , output will be sent to the new sink and to the current output stream, like the Unix program <code>tee</code> .

**Details**

`sink` diverts R output to a connection. If `file` is a character string, a file connection with that name will be established for the duration of the diversion.

Normal R output (to connection `stdout`) is diverted by the default `type = "output"`. Only prompts and (most) messages continue to appear on the console. Messages sent to `stderr()` (including those from `message`, `warning` and `stop`) can be diverted by `sink(type = "message")` (see below).

`sink()` or `sink(file=NULL)` ends the last diversion (of the specified type). There is a stack of diversions for normal output, so output reverts to the previous diversion (if there was one). The stack is of up to 21 connections (20 diversions).

If `file` is a connection it will be opened if necessary (in "wt" mode) and closed once it is removed from the stack of diversions.

`split = TRUE` only splits R output (via `Rvprintf`) and the default output from `writeLines`: it does not split all output that might be sent to `stdout()`.

Sink-ing the messages stream should be done only with great care. For that stream `file` must be an already open connection, and there is no stack of connections.

**Value**

`sink` returns `NULL`.

For `sink.number()` the number (0, 1, 2, ...) of diversions of output in place.

For `sink.number("message")` the connection number used for messages, 2 if no diversion has been used.

**Warning**

Do not use a connection that is open for `sink` for any other purpose. The software will stop you closing one such inadvertently.

Do not sink the messages stream unless you understand the source code implementing it and hence the pitfalls.

**Note**

`sink(split = TRUE)` is only available on systems which support the C99 function `va_copy` (or under the name `__va_copy`), but we know of no current systems which do not.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

## See Also

[capture.output](#)

## Examples

```
sink("sink-examp.txt")
i <- 1:10
outer(i, i, "*")
sink()
unlink("sink-examp.txt")
## Not run:
## capture all the output to a file.
zz <- file("all.Rout", open="wt")
sink(zz)
sink(zz, type="message")
try(log("a"))
## back to the console
sink(type="message")
sink()
try(log("a"))

## End(Not run)
```

---

slice.index

*Slice Indexes in an Array*

---

## Description

Returns a matrix of integers indicating the number of their slice in a given array.

## Usage

```
slice.index(x, MARGIN)
```

## Arguments

x	an array. If x has no dimension attribute, it is considered a one-dimensional array.
MARGIN	an integer giving the dimension number to slice by.

## Value

An integer array y with dimensions corresponding to those of x such that all elements of slice number i with respect to dimension MARGIN have value i.

**See Also**

`row` and `col` for determining row and column indexes; in fact, these are special cases of `slice.index` corresponding to `MARGIN` equal to 1 and 2, respectively when `x` is a matrix.

**Examples**

```
x <- array(1 : 24, c(2, 3, 4))
slice.index(x, 2)
```

---

`slotOp`*Extract Slots*

---

**Description**

Extract the contents of a slot in a object with a formal (S4) class structure.

**Usage**

```
object@name
```

**Arguments**

<code>object</code>	An object from a formally defined (S4) class.
<code>name</code>	The character-string name of the slot.

**Details**

This operator supports the formal classes of package **methods**, and is enabled only when **methods** is loaded (as per default). See `slot` for further details.

It is checked that `object` is an S4 object (see `isS4`), and it is an error to attempt to use `@` on any other object. (There is an exception for name `.Data` for internal useonly.)

If `name` is not a slot name, an error is thrown.

**Value**

The current contents of the slot.

**See Also**

[Extract](#), [slot](#)

---

 socketSelect

*Wait on Socket Connections*


---

### Description

Waits for the first of several socket connections to become available.

### Usage

```
socketSelect(socklist, write = FALSE, timeout = NULL)
```

### Arguments

socklist	list of open socket connections
write	logical. If TRUE wait for corresponding socket to become available for writing; otherwise wait for it to become available for reading.
timeout	numeric or NULL. Time in seconds to wait for a socket to become available; NULL means wait indefinitely.

### Details

The values in `write` are recycled if necessary to make up a logical vector the same length as `socklist`. Socket connections can appear more than once in `socklist`; this can be useful if you want to determine whether a socket is available for reading or writing.

### Value

Logical the same length as `socklist` indicating whether the corresponding socket connection is available for output or input, depending on the corresponding value of `write`.

### Examples

```
## Not run:
## test whether socket connection s is available for writing or reading
socketSelect(list(s,s),c(TRUE,FALSE),timeout=0)

## End(Not run)
```

---

 solve

*Solve a System of Equations*


---

### Description

This generic function solves the equation  $a \%*\% x = b$  for  $x$ , where  $b$  can be either a vector or a matrix.

**Usage**

```
solve(a, b, ...)

## Default S3 method:
solve(a, b, tol, LINPACK = FALSE, ...)
```

**Arguments**

a	a square numeric or complex matrix containing the coefficients of the linear system.
b	a numeric or complex vector or matrix giving the right-hand side(s) of the linear system. If missing, b is taken to be an identity matrix and solve will return the inverse of a.
tol	the tolerance for detecting linear dependencies in the columns of a. If LINPACK is TRUE the default is 1e-7, otherwise it is .Machine\$double.eps. Future versions of R may use a tighter tolerance. Not presently used with complex matrices a.
LINPACK	logical. Should LINPACK be used (for compatibility with R < 1.7.0)? Otherwise LAPACK is used.
...	further arguments passed to or from other methods

**Details**

a or b can be complex, but this uses double complex arithmetic which might not be available on all platforms and LAPACK will always be used.

The row and column names of the result are taken from the column names of a and of b respectively. If b is missing the column names of the result are the row names of a. No check is made that the column names of a and the row names of b are equal.

For back-compatibility a can be a (real) QR decomposition, although `qr.solve` should be called in that case. `qr.solve` can handle non-square systems.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`solve.qr` for the qr method, `chol2inv` for inverting from the Choleski factor `backsolve`, `qr.solve`.

**Examples**

```
hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, "+") }
h8 <- hilbert(8); h8
sh8 <- solve(h8)
round(sh8 %*% h8, 3)

A <- hilbert(4)
A[] <- as.complex(A)
## might not be supported on all platforms
try(solve(A))
```

---

 sort

*Sorting or Ordering Vectors*


---

### Description

Sort (or *order*) a vector or factor (partially) into ascending or descending order. For ordering along more than one variable, e.g., for sorting data frames, see [order](#).

### Usage

```
sort(x, decreasing = FALSE, ...)

## Default S3 method:
sort(x, decreasing = FALSE, na.last = NA, ...)

sort.int(x, partial = NULL, na.last = NA, decreasing = FALSE,
         method = c("shell", "quick"), index.return = FALSE)
```

### Arguments

<code>x</code>	for <code>sort</code> an R object with a class or a numeric, complex, character or logical vector. For <code>sort.int</code> , a numeric, complex, character or logical vector, or a factor.
<code>decreasing</code>	logical. Should the sort be increasing or decreasing? Not available for partial sorting.
<code>...</code>	arguments to be passed to or from methods or (for the default methods and objects without a class) to <code>sort.int</code> .
<code>na.last</code>	for controlling the treatment of NAs. If <code>TRUE</code> , missing values in the data are put last; if <code>FALSE</code> , they are put first; if <code>NA</code> , they are removed.
<code>partial</code>	<code>NULL</code> or an integer vector of indices for partial sorting.
<code>method</code>	character string specifying the algorithm used.
<code>index.return</code>	logical indicating if the ordering index vector should be returned as well; this is only available for a few cases, the default <code>na.last = NA</code> and full sorting of non-factors.

### Details

`sort` is a generic function for which methods can be written, and `sort.int` is the internal method which is compatible with S if only the first three arguments are used.

The default `sort` method makes use of [order](#) for classed objects, which in turn makes use of the generic function [xtfrm](#) (and can be slow unless a `xtfrm` method has been defined unless `is.numeric(x)` is true).

If `partial` is not `NULL`, it is taken to contain indices of elements of the result which are to be placed in their correct positions in the sorted array by partial sorting. For each of the result values in a specified position, any values smaller than that one are guaranteed to have a smaller index in the sorted array and any values which are greater are guaranteed to have a bigger index in the sorted array. (This is included for efficiency, and many of the options are not available for partial sorting. It is only substantially more efficient if `partial` has a handful of elements, and a full sort is done if there are more than 10.) Names are discarded for partial sorting.



Complex values are sorted first by the real part, then the imaginary part.

The sort order for character vectors will depend on the collating sequence of the locale in use: see [Comparison](#). The sort order for factors is the order of their levels (which is particularly appropriate for ordered factors).

Method "shell" uses Shellsort (an  $O(n^{4/3})$  variant from Sedgewick (1996)). If `x` has names a stable sort is used, so ties are not reordered. (This only matters if names are present.)

Method "quick" uses Singleton's Quicksort implementation and is only available when `x` is numeric (double or integer) and `partial` is `NULL`. (For other types of `x` Shellsort is used, silently.) It is normally somewhat faster than Shellsort (perhaps twice as fast on vectors of length a million) but has poor performance in the rare worst case. (Peto's modification using a pseudo-random midpoint is used to make the worst case rarer.) This is not a stable sort, and ties may be reordered.

## Value

For `sort`, the result depends on the S3 method which is dispatched. If `x` does not have a class the rest of this section applies. For classed objects which do not have a specific method the default method will be used and is equivalent to `x[order(x, ...)]`: this depends on the class having a suitable method for `[]` (and also that `order` will work, which is not the case for a class based on a list).

For `sort.int` the value is the sorted vector unless `index.return` is true, when the result is a list with components named `x` and `ix` containing the sorted numbers and the ordering index vector. In the latter case, if `method == "quick"` ties may be reversed in the ordering, unlike `sort.list`, as quicksort is not stable.

All attributes are removed from the return value (see Becker *et al*, 1988, p.146) except names, which are sorted. (If `partial` is specified even the names are removed.) Note that this means that the returned value has no class, except for factors and ordered factors (which are treated specially and whose result is transformed back to the original class).

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Sedgewick, R. (1986) A new upper bound for Shell sort. *J. Algorithms* **7**, 159–173.

Singleton, R. C. (1969) An efficient algorithm for sorting with minimal storage: Algorithm 347. *Communications of the ACM* **12**, 185–187.

## See Also

[‘Comparison’](#) for how character strings are collated.  
[order](#) for sorting on or reordering multiple variables.  
[is.unsorted.rank](#).

## Examples

```
require(stats)

x <- swiss$Education[1:25]
x; sort(x); sort(x, partial = c(10, 15))
median.default # shows you another example for 'partial'

## illustrate 'stable' sorting (of ties):
```

```

sort(c(10:3,2:12), method = "sh", index.return=TRUE) # is stable
## $x : 2 3 3 4 4 5 5 6 6 7 7 8 8 9 9 10 10 11 12
## $ix: 9 8 10 7 11 6 12 5 13 4 14 3 15 2 16 1 17 18 19
sort(c(10:3,2:12), method = "qu", index.return=TRUE) # is not
## $x : 2 3 3 4 4 5 5 6 6 7 7 8 8 9 9 10 10 11 12
## $ix: 9 10 8 7 11 6 12 5 13 4 14 3 15 16 2 17 1 18 19
##          ^^^^

x <- c(1:3, 3:5, 10)
is.unsorted(x) #-> FALSE: is sorted
is.unsorted(x, strictly=TRUE) #-> TRUE : is not (and cannot be) sorted strictly

## Not run:
## Small speed comparison simulation:
N <- 2000
Sim <- 20
rep <- 1000 # << adjust to your CPU
c1 <- c2 <- numeric(Sim)
for(is in 1:Sim){
  x <- rnorm(N)
  c1[is] <- system.time(for(i in 1:rep) sort(x, method = "shell"))[1]
  c2[is] <- system.time(for(i in 1:rep) sort(x, method = "quick"))[1]
  stopifnot(sort(x, method = "s") == sort(x, method = "q"))
}
rbind(ShellSort = c1, QuickSort = c2)
cat("Speedup factor of quick sort():\n")
summary({qq <- c1 / c2; qq[is.finite(qq)]})

## A larger test
x <- rnorm(1e7)
system.time(x1 <- sort(x, method = "shell"))
system.time(x2 <- sort(x, method = "quick"))
stopifnot(identical(x1, x2))

## End(Not run)

```

---

source

*Read R Code from a File or a Connection*


---

## Description

source causes R to accept its input from the named file or URL (the name must be quoted) or connection. Input is read and *parsed* by from that file until the end of the file is reached, then the parsed expressions are evaluated sequentially in the chosen environment.

## Usage

```

source(file, local = FALSE, echo = verbose, print.eval = echo,
       verbose = getOption("verbose"),
       prompt.echo = getOption("prompt"),
       max.deparse.length = 150, chdir = FALSE,
       encoding = getOption("encoding"),
       continue.echo = getOption("continue"),
       skip.echo = 0, keep.source = getOption("keep.source"))

```

**Arguments**

<code>file</code>	a connection or a character string giving the pathname of the file or URL to read from. "" indicates the connection <code>stdin()</code> .
<code>local</code>	if <code>local</code> is <code>FALSE</code> , the statements scanned are evaluated in the user's workspace (the global environment), otherwise in the environment calling <code>source</code> .
<code>echo</code>	logical; if <code>TRUE</code> , each expression is printed after parsing, before evaluation.
<code>print.eval</code>	logical; if <code>TRUE</code> , the result of <code>eval(i)</code> is printed for each expression <code>i</code> ; defaults to the value of <code>echo</code> .
<code>verbose</code>	if <code>TRUE</code> , more diagnostics (than just <code>echo = TRUE</code> ) are printed during parsing and evaluation of input, including extra info for <b>each</b> expression.
<code>prompt.echo</code>	character; gives the prompt to be used if <code>echo = TRUE</code> .
<code>max.deparse.length</code>	integer; is used only if <code>echo</code> is <code>TRUE</code> and gives the maximal number of characters output for the deparse of a single expression.
<code>chdir</code>	logical; if <code>TRUE</code> and <code>file</code> is a pathname, the R working directory is temporarily changed to the directory containing <code>file</code> for evaluating.
<code>encoding</code>	character vector. The encoding(s) to be assumed when <code>file</code> is a character string: see <code>file</code> . A possible value is "unknown" when the encoding is guesses: see the 'Details'.
<code>continue.echo</code>	character; gives the prompt to use on continuation lines if <code>echo = TRUE</code> .
<code>skip.echo</code>	integer; how many comment lines at the start of the file to skip if <code>echo = TRUE</code> .
<code>keep.source</code>	logical: should the source formatting be retained when echo expressions, if possible?

**Details**

Note that running code via `source` differs in a few respects from entering it at the R command line. Since expressions are not executed at the top level, auto-printing is not done. So you will need to include explicit `print` calls for things you want to be printed (and remember that this includes plotting by **lattice**, FAQ Q7.22). Since the complete file is parsed before any of it is run, syntax errors result in none of the code being run. If an error occurs in running a syntactically correct script, anything assigned into the workspace by code that has been run will be kept (just as from the command line), but diagnostic information such as `traceback()` will contain additional calls to `eval.with.vis`, an undocumented internal function.

All versions of R accept input from a connection with end of line marked by LF (as used on Unix), CRLF (as used on DOS/Windows) or CR (as used on classic Mac OS) and map this to newline. The final line can be incomplete, that is missing the final end-of-line marker.

If `options("keep.source")` is true (the default in interactive use), the source of functions is kept so they can be listed exactly as input. This imposes a limit of 128K bytes on the function size and a nesting limit of 265. Use `keep.source = FALSE` when these limits might take effect: if exceeded they generate an error.

This paragraph applies if `file` is a filename (rather than a connection). If `encoding = "unknown"`, an attempt is made to guess the encoding. The result of `localeToCharset()` is used as a guide. If `encoding` has two or more elements, they are tried in turn until the file/URL can be read without error in the trial encoding. If an actual `encoding` is specified (rather than

the default or "unknown") then character strings in the result will be translated to the current encoding and marked as such (see [Encoding](#)) in Latin-1 and UTF-8 locales.

If `file` is a connection (including one specified by "`"`", it is not possible to re-encode the input inside `source`, and so the `encoding` argument is just used to mark character strings in the parsed input: see [parse](#).

Unlike input from a console, lines in the file or on a connection can contain an unlimited number of characters.

When `skip.echo > 0`, that many comment lines at the start of the file will not be echoed. This does not affect the execution of the code at all. If there are executable lines within the first `skip.echo` lines, echoing will start with the first of them.

If `echo` is true and a deparsed expression exceeds `max.deparse.length`, that many characters are output followed by `.... [TRUNCATED]` .

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[demo](#) which uses `source`; [eval](#), [parse](#) and [scan](#); [options](#) ("keep.source").  
[sys.source](#) which is a streamlined version to source a file into an environment.

## Examples

```
## If you want to source() a bunch of files, something like
## the following may be useful:
sourceDir <- function(path, trace = TRUE, ...) {
  for (nm in list.files(path, pattern = "\\.[RrSsQq]$")) {
    if(trace) cat(nm,":")
    source(file.path(path, nm), ...)
    if(trace) cat("\n")
  }
}
```

## Description

Special mathematical functions related to the beta and gamma functions.

## Usage

```
beta(a, b)
lbeta(a, b)

gamma(x)
lgamma(x)
psigamma(x, deriv = 0)
digamma(x)
```

```

trigamma(x)

choose(n, k)
lchoose(n, k)
factorial(x)
lfactorial(x)

```

### Arguments

**a, b**                non-negative numeric vectors.  
**x, n**                numeric vectors.  
**k, deriv**           integer vectors.

### Details

The functions `beta` and `lbeta` return the beta function and the natural logarithm of the beta function,

$$B(a, b) = \frac{\Gamma(a)\Gamma(b)}{\Gamma(a+b)}.$$

The formal definition is

$$B(a, b) = \int_0^1 t^{a-1}(1-t)^{b-1} dt$$

(Abramowitz and Stegun section 6.2.1, page 258). Note that it is only defined in  $\mathbf{R}$  for non-negative  $a$  and  $b$ , and is infinite if either is zero.

The functions `gamma` and `lgamma` return the gamma function  $\Gamma(x)$  and the natural logarithm of the absolute value of the gamma function. The gamma function is defined by (Abramowitz and Stegun section 6.1.1, page 255)

$$\Gamma(x) = \int_0^\infty t^{x-1} e^{-t} dt$$

for all real  $x$  except zero and negative integers (when `NaN` is returned). There will be a warning on possible loss of precision for values which are too close (within about  $10^{-8}$ ) to a negative integer less than `-10`.

`factorial(x)` ( $x!$  for non-negative integer  $x$ ) is defined to be `gamma(x+1)` and `lfactorial` to be `lgamma(x+1)`.

The functions `digamma` and `trigamma` return the first and second derivatives of the logarithm of the gamma function. `psigamma(x, deriv)` (`deriv`  $\geq 0$ ) computes the `deriv`-th derivative of  $\psi(x)$ .

$$\text{digamma}(x) = \psi(x) = \frac{d}{dx} \ln \Gamma(x) = \frac{\Gamma'(x)}{\Gamma(x)}$$

This is often called the ‘polygamma’ function, e.g. in Abramowitz and Stegun (section 6.4.1, page 260); and higher derivatives (`deriv` = 2:4) have occasionally been called ‘tetragamma’, ‘pentagamma’, and ‘hexagamma’.

The functions `choose` and `lchoose` return binomial coefficients and the logarithms of their absolute values. Note that `choose(n, k)` is defined for all real numbers  $n$  and integer  $k$ . For  $k \geq 1$  it is defined as  $n(n-1)\cdots(n-k+1)/k!$ , as 1 for  $k = 0$  and as 0 for negative  $k$ . Non-integer values of  $k$  are rounded to an integer, with a warning.

`choose(*, k)` uses direct arithmetic (instead of `[1]gamma` calls) for small  $k$ , for speed and accuracy reasons. Note the function `combn` (package `utils`) for enumeration of all possible combinations.

The `gamma`, `lgamma`, `digamma` and `trigamma` functions are [internal generic primitive functions](#): methods can be defined for them individually or via the `Math` group generic.

**Source**

`gamma`, `lgamma`, `beta` and `lbeta` are based on C translations of Fortran subroutines by W. Fullerton of Los Alamos Scientific Laboratory (now available as part of SLATEC).

`digamma`, `trigamma` and `psigamma` are based on

Amos, D. E. (1983). A portable Fortran subroutine for derivatives of the psi function, Algorithm 610, *ACM Transactions on Mathematical Software* **9**(4), 494–502.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (For `gamma` and `lgamma`.)

Abramowitz, M. and Stegun, I. A. (1972) *Handbook of Mathematical Functions*. New York: Dover. Chapter 6: Gamma and Related Functions.

**See Also**

[Arithmetic](#) for simple, [sqrt](#) for miscellaneous mathematical functions and [Bessel](#) for the real Bessel functions.

For the incomplete gamma function see [pgamma](#).

**Examples**

```
require(graphics)

choose(5, 2)
for (n in 0:10) print(choose(n, k = 0:n))

factorial(100)
lfactorial(10000)

## gamma has 1st order poles at 0, -1, -2, ...
## this will generate loss of precision warnings, so turn off
op <- options("warn")
options(warn = -1)
x <- sort(c(seq(-3,4, length.out=201), outer(0:-3, (-1:1)*1e-6, "+")))
plot(x, gamma(x), ylim=c(-20,20), col="red", type="l", lwd=2,
      main=expression(Gamma(x)))
abline(h=0, v=-3:0, lty=3, col="midnightblue")
options(op)

x <- seq(.1, 4, length.out = 201); dx <- diff(x)[1]
par(mfrow = c(2, 3))
for (ch in c("", "l", "di", "tri", "tetra", "penta")) {
  is.deriv <- nchar(ch) >= 2
  nm <- paste(ch, "gamma", sep = "")
  if (is.deriv) {
    dy <- diff(y) / dx # finite difference
    der <- which(ch == c("di", "tri", "tetra", "penta")) - 1
    nm2 <- paste("psigamma(*, deriv = ", der, ")", sep='')
    nm <- if(der >= 2) nm2 else paste(nm, nm2, sep = " ==\n")
    y <- psigamma(x, deriv=der)
  } else {
    y <- get(nm)(x)
  }
}
```

```

plot(x, y, type = "l", main = nm, col = "red")
abline(h = 0, col = "lightgray")
if (is.deriv) lines(x[-1], dy, col = "blue", lty = 2)
}
par(mfrow = c(1, 1))

## "Extended" Pascal triangle:
fN <- function(n) formatC(n, width=2)
for (n in -4:10) cat(fN(n), ":", fN(choose(n, k= -2:max(3,n+2))), "\n")

## R code version of choose() [simplistic; warning for k < 0]:
mychoose <- function(r,k)
  ifelse(k <= 0, (k==0),
         sapply(k, function(k) prod(r:(r-k+1))) / factorial(k))
k <- -1:6
cbind(k=k, choose(1/2, k), mychoose(1/2, k))

## Binomial theorem for n=1/2 ;
## sqrt(1+x) = (1+x)^(1/2) = sum_{k=0}^Inf choose(1/2, k) * x^k :
k <- 0:10 # 10 is sufficient for ~ 9 digit precision:
sqrt(1.25)
sum(choose(1/2, k) * .25^k)

```

---

split

---

*Divide into Groups and Reassemble*


---

## Description

`split` divides the data in the vector `x` into the groups defined by `f`. The replacement forms replace values corresponding to such a division. `unsplit` reverses the effect of `split`.

## Usage

```

split(x, f, drop = FALSE, ...)
split(x, f, drop = FALSE, ...) <- value
unsplit(value, f, drop = FALSE)

```

## Arguments

<code>x</code>	vector or data frame containing values to be divided into groups.
<code>f</code>	a ‘factor’ in the sense that <code>as.factor(f)</code> defines the grouping, or a list of such factors in which case their interaction is used for the grouping.
<code>drop</code>	logical indicating if levels that do not occur should be dropped (if <code>f</code> is a factor or a list).
<code>value</code>	a list of vectors or data frames compatible with a splitting of <code>x</code> . Recycling applies if the lengths do not match.
<code>...</code>	further potential arguments passed to methods.

## Details

`split` and `split<-` are generic functions with default and `data.frame` methods. The data frame method can also be used to split a matrix into a list of matrices, and the replacement form likewise, provided they are invoked explicitly.

`unsplit` works with lists of vectors or data frames (assumed to have compatible structure, as if created by `split`). It puts elements or rows back in the positions given by `f`. In the data frame case, row names are obtained by unsplitting the row name vectors from the elements of `value`.

`f` is recycled as necessary and if the length of `x` is not a multiple of the length of `f` a warning is printed.

Any missing values in `f` are dropped together with the corresponding values of `x`.

## Value

The value returned from `split` is a list of vectors containing the values for the groups. The components of the list are named by the levels of `f` (after converting to a factor, or if already a factor and `drop=TRUE`, dropping unused levels).

The replacement forms return their right hand side. `unsplit` returns a vector or data frame for which `split(x, f)` equals `value`

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

`cut` to categorize numeric values.

`strsplit` to split strings.

## Examples

```
require(stats); require(graphics)
n <- 10; nn <- 100
g <- factor(round(n * runif(n * nn)))
x <- rnorm(n * nn) + sqrt(as.numeric(g))
xg <- split(x, g)
boxplot(xg, col = "lavender", notch = TRUE, varwidth = TRUE)
sapply(xg, length)
sapply(xg, mean)

### Calculate 'z-scores' by group (standardize to mean zero, variance one)

z <- unsplit(lapply(split(x, g), scale), g)
# check group means are zero
tapply(z, g, mean)

# or

z <- x
split(z, g) <- lapply(split(x, g), scale)
# check group sds are one
tapply(z, g, sd)
```



```
### data frame variation

## Notice that assignment form is not used since a variable is being added

g <- airquality$Month
l <- split(airquality, g)
l <- lapply(l, transform, Oz.Z = scale(Ozone))
aq2 <- unsplit(l, g)
head(aq2)
with(aq2, tapply(Oz.Z, Month, sd, na.rm=TRUE))

### Split a matrix into a list by columns
ma <- cbind(x = 1:10, y = (-4:5)^2)
split(ma, col(ma))

split(1:10, 1:2)
```

---

 sprintf

*Use C-style String Formatting Commands*


---

### Description

A wrapper for the C function `sprintf`, that returns a character vector containing a formatted combination of text and variable values.

### Usage

```
sprintf(fmt, ...)
gettextf(fmt, ..., domain = NULL)
```

### Arguments

<code>fmt</code>	a character vector of format strings, each of up to 8192 bytes.
<code>...</code>	values to be passed into <code>fmt</code> . Only logical, integer, real and character vectors are supported, but some coercion will be done: see the ‘Details’ section.
<code>domain</code>	see <a href="#">gettext</a> .

### Details

`sprintf` is a wrapper for the system `sprintf` C-library function. Attempts are made to check that the mode of the values passed match the format supplied, and R’s special values (`NA`, `Inf`, `-Inf` and `NaN`) are handled correctly.

`gettextf` is a convenience function which provides C-style string formatting with possible translation of the format string.

The arguments (including `fmt`) are recycled if possible a whole number of times to the length of the longest, and then the formatting is done in parallel. As from R 2.9.0 zero-length arguments are allowed and will give a zero-length result. All arguments are evaluated even if unused, and hence some types (e.g., `"symbol"` or `"language"`, see [typeof](#)) are not allowed.

The following is abstracted from Kernighan and Ritchie (see References). The string `fmt` contains normal characters, which are passed through to the output string, and also conversion specifications

which operate on the arguments provided through . . . . The allowed conversion specifications start with a % and end with one of the letters in the set aAdiFeEgGosxX%. These letters denote the following types:

- d, i, o, x, X Integer value, o being octal, x and X being hexadecimal (using the same case for a-f as the code). Numeric variables with exactly integer values will be coerced to integer. Formats d and i can also be used for logical variables, which will be converted to 0, 1 or NA.
- f Double precision value, in “fixed point” decimal notation of the form “[-]mmm.ddd”. The number of decimal places (“d”) is specified by the precision: the default is 6; a precision of 0 suppresses the decimal point. Non-finite values are converted to NA, NaN or (perhaps a sign followed by) Inf.
- e, E Double precision value, in “exponential” decimal notation of the form [-]m.ddde[+-]xx or [-]m.dddE[+-]xx.
- g, G Double precision value, in %e or %E format if the exponent is less than -4 or greater than or equal to the precision, and %f format otherwise. (The precision (default 6) specifies the number of *significant* digits here, whereas in %f, %e, it is the number of digits after the decimal point.)
- a, A Double precision value, in binary notation of the form [-]0xh.hhhp[+-]d. This is a binary fraction expressed in hex multiplied by a (decimal) power of 2. The number of hex digits after the decimal point is specified by the precision: the default is enough digits to represent exactly the internal binary representation. Non-finite values are converted to NA, NaN or (perhaps a sign followed by) Inf. Format %a uses lower-case for x, p and the hex values: format %A uses upper-case.  
 This might not be supported on all platforms as it is a feature of C99. The format is not uniquely defined: although it would be possible to make the leading h always zero or one, this is not always done. Most systems will suppress trailing zeros, but a few do not. On a well-written platform, for normal numbers there will be a leading one before the decimal point plus (by default) 13 hexadecimal digits, hence 53 bits. (The treatment of denormalized numbers is very platform-dependent.)
- s Character string. Character NAs are converted to "NA".
- % Literal % (none of the extra formatting characters given below are permitted in this case).

Conversion by `as.character` is used for non-character arguments with s and by `as.double` for non-double arguments with f, e, E, g, G. NB: the length is determined before conversion, so do not rely on the internal coercion if this would change the length. The coercion is done only once, so if `length(fmt) > 1` then all elements must expect the same types of arguments.

In addition, between the initial % and the terminating conversion character there may be, in any order:

- m.n Two numbers separated by a period, denoting the field width (m) and the precision (n).
- Left adjustment of converted argument in its field.
- + Always print number with sign: by default only negative numbers are printed with a sign.
- a space** Prefix a space if the first character is not a sign.
- 0 For numbers, pad to the field width with leading zeros.
- # specifies “alternate output” for numbers, its action depending on the type: For x or X, 0x or 0X will be prefixed to a non-zero result. For e, E, f, g and G, the output will always have a decimal point; for g and G, trailing zeros will not be removed.

Further, immediately after % may come 1\$ to 99\$ to refer to numbered argument: this allows arguments to be referenced out of order and is mainly intended for translators of error messages. If this is done it is best if all formats are numbered: if not the unnumbered ones process the arguments in order. See the examples. This notation allows arguments to be used more than once, in which case they must be used as the same type (integer, double or character).

A field width or precision (but not both) may be indicated by an asterisk \*: in this case an argument specifies the desired number. A negative field width is taken as a '-' flag followed by a positive field width. A negative precision is treated as if the precision were omitted. The argument should be integer, but a double argument will be coerced to integer.

There is a limit of 8192 bytes on elements of `fmt`, and on strings included from a single `%letter` conversion specification.

Field widths and precisions of %s conversions are interpreted as bytes, not characters, as described in the C standard.

### Value

A character vector of length that of the longest input. If any element of `fmt` or any character argument is declared as UTF-8, the element of the result will be in UTF-8 and have the encoding declared as UTF-8. Otherwise it will be in the current locale's encoding.

### Warning

The format string is passed down the OS's `printf` function, and incorrect formats can cause the latter to crash the R process. R does perform sanity checks on the format, and since R 2.10.0, we have not seen crashes anymore. But not all possible user errors on all platforms have been tested, and some might be terminal.

### Author(s)

Original code by Jonathan Rougier.

### References

Kernighan, B. W. and Ritchie, D. M. (1988) *The C Programming Language*. Second edition, Prentice Hall. describes the format options in table B-1 in the Appendix.

### See Also

[formatC](#) for a way of formatting vectors of numbers in a similar fashion.

[paste](#) for another way of creating a vector combining text and values.

[gettext](#) for the mechanisms for the automated translation of text.

### Examples

```
## be careful with the format: most things in R are floats
## only integer-valued reals get coerced to integer.

sprintf("%s is %f feet tall\n", "Sven", 7.1)      # OK
try(sprintf("%s is %i feet tall\n", "Sven", 7.1)) # not OK
  sprintf("%s is %i feet tall\n", "Sven", 7 )    # OK

## use a literal % :
```

```

sprintf("%.0f%% said yes (out of a sample of size %.0f)", 66.666, 3)

## various formats of pi :

sprintf("%f", pi)
sprintf("%.3f", pi)
sprintf("%1.0f", pi)
sprintf("%5.1f", pi)
sprintf("%05.1f", pi)
sprintf("%+f", pi)
sprintf("% f", pi)
sprintf("%-10f", pi) # left justified
sprintf("%e", pi)
sprintf("%E", pi)
sprintf("%g", pi)
sprintf("%g", 1e6 * pi) # -> exponential
sprintf("%.9g", 1e6 * pi) # -> "fixed"
sprintf("%G", 1e-6 * pi)

## no truncation:
sprintf("%1.f", 101)

## re-use one argument three times, show difference between %x and %X
xx <- sprintf("%1$d %1$x %1$X", 0:15)
xx <- matrix(xx, dimnames=list(rep("", 16), "%d%x%X"))
noquote(format(xx, justify="right"))

## More sophisticated:

sprintf("min 10-char string '%10s'",
       c("a", "ABC", "and an even longer one"))

n <- 1:18
sprintf(paste("e with %2d digits = %.", n, "g", sep=""), n, exp(1))

## Using arguments out of order
sprintf("second %2$1.0f, first %1$5.2f, third %3$1.0f", pi, 2, 3)

## Using asterisk for width or precision
sprintf("precision %.*f, width '%*.3f'", 3, pi, 8, pi)

## Asterisk and argument re-use, 'e' example reiterated:
sprintf("e with %1$2d digits = %2$.*1$g", n, exp(1))

## re-cycle arguments
sprintf("%s %d", "test", 1:3)

## binary output showing rounding/representation errors
x <- seq(0, 1.0, 0.1); y <- c(0, .1, .2, .3, .4, .5, .6, .7, .8, .9, 1)
cbind(x, sprintf("%a", x), sprintf("%a", y))

```

## Description

Single or double quote text by combining with appropriate single or double left and right quotation marks.

## Usage

```
sQuote(x)
dQuote(x)
```

## Arguments

`x` an R object, to be coerced to a character vector.

## Details

The purpose of the functions is to provide a simple means of markup for quoting text to be used in the R output, e.g., in warnings or error messages.

The choice of the appropriate quotation marks depends on both the locale and the available character sets. Older Unix/X11 fonts displayed the grave accent (ASCII code 0x60) and the apostrophe (0x27) in a way that they could also be used as matching open and close single quotation marks. Using modern fonts, or non-Unix systems, these characters no longer produce matching glyphs. Unicode provides left and right single quotation mark characters (U+2018 and U+2019); if Unicode markup cannot be assumed to be available, it seems good practice to use the apostrophe as a non-directional single quotation mark.

Similarly, Unicode has left and right double quotation mark characters (U+201C and U+201D); if only ASCII's typewriter characteristics can be employed, then the ASCII quotation mark (0x22) should be used as both the left and right double quotation mark.

Some other locales also have the directional quotation marks, notably on Windows. TeX uses grave and apostrophe for the directional single quotation marks, and doubled grave and doubled apostrophe for the directional double quotation marks.

What rendering is used depend on the `options` setting for `useFancyQuotes`. If this is `FALSE` then the unidirectional ASCII quotation style is used. If this is `TRUE` (the default), Unicode directional quotes are used where available (currently, UTF-8 locales on Unix-alikes and all Windows locales except C): if set to "UTF-8" UTF-8 markup is used (whatever the current locale). If set to "TeX", TeX-style markup is used. Finally, if this is set to a character vector of length four, the first two entries are used for beginning and ending single quotes and the second two for beginning and ending double quotes: this can be used to implement non-English quoting conventions such as the use of guillemets.

Where fancy quotes are used, you should be aware that they may not be rendered correctly as not all fonts include the requisite glyphs: for example some have directional single quotes but not directional double quotes.

## Value

A character vector in the current locale's encoding.

## References

Markus Kuhn, "ASCII and Unicode quotation marks". <http://www.cl.cam.ac.uk/~mgk25/ucs/quotes.html>

**See Also**

[Quotes](#) for quoting R code.

[shQuote](#) for quoting OS commands.

**Examples**

```
op <- options("useFancyQuotes")
paste("argument", sQuote("x"), "must be non-zero")
options(useFancyQuotes = FALSE)
cat("\ndistinguish plain", sQuote("single"), "and",
    dQuote("double"), "quotes\n")
options(useFancyQuotes = TRUE)
cat("\ndistinguish fancy", sQuote("single"), "and",
    dQuote("double"), "quotes\n")
options(useFancyQuotes = "TeX")
cat("\ndistinguish TeX", sQuote("single"), "and",
    dQuote("double"), "quotes\n")
if(l10n_info()$`Latin-1`) {
  options(useFancyQuotes = c("\xab", "\xbb", "\xbf", "?"))
  cat("\n", sQuote("guillemet"), "and",
      dQuote("Spanish question"), "styles\n")
} else if(l10n_info()$`UTF-8`) {
  options(useFancyQuotes = c("\xc2\xab", "\xc2\xbb", "\xc2\xbf", "?"))
  cat("\n", sQuote("guillemet"), "and",
      dQuote("Spanish question"), "styles\n")
}
options(op)
```

---

 srcfile

*References to source files*


---

**Description**

These functions are for working with source files.

**Usage**

```
srcfile(filename, encoding = getOption("encoding"), Enc = "unknown")
srcfilecopy(filename, lines)
getSrcLines(srcfile, first, last)
srcref(srcfile, lloc)
## S3 method for class 'srcfile':
print(x, ...)
## S3 method for class 'srcfile':
summary(object, ...)
## S3 method for class 'srcfile':
open(con, line, ...)
## S3 method for class 'srcfile':
close(con, ...)
## S3 method for class 'srcref':
print(x, useSource = TRUE, ...)
## S3 method for class 'srcref':
```

```
summary(object, useSource = FALSE, ...)
## S3 method for class 'srcref':
as.character(x, useSource = TRUE, ...)
.isOpen(srcfile)
```

### Arguments

filename	The name of a file
encoding	The character encoding to assume for the file
Enc	The encoding with which to make strings: see the encoding argument of <a href="#">parse</a> .
lines	A character vector of source lines. Other R objects will be coerced to character.
srcfile	A <code>srcfile</code> object.
first, last, line	Line numbers.
lloc	A vector of four or six values giving a source location; see ‘Details’.
x, object, con	An object of the appropriate class.
useSource	Whether to read the <code>srcfile</code> to obtain the text of a <code>srcref</code> .
...	Additional arguments to the methods; these will be ignored.

### Details

These functions and classes handle source code references.

The `srcfile` function produces an object of class `srcfile`, which contains the name and directory of a source code file, along with its timestamp, for use in source level debugging (not yet implemented) and source echoing. The encoding of the file is saved; see [file](#) for a discussion of encodings, and [iconvlist](#) for a list of allowable encodings on your platform.

The `srcfilecopy` function produces an object of the descendant class `srcfilecopy`, which saves the source lines in a character vector.

The `getSrcLines` function reads the specified lines from `srcfile`.

The `srcref` function produces an object of class `srcref`, which describes a range of characters in a `srcfile`. The `lloc` value gives the following values: `c(first_line, first_byte, last_line, last_byte, first_column, last_column)`. (Bytes and columns may be different due to multibyte characters. If only four values are given, the columns and bytes are assumed to match.)

Methods are defined for `print`, `summary`, `open`, and `close` for classes `srcfile` and `srcfilecopy`. The `open` method opens its internal file connection at a particular line; if it was already open, it will be repositioned to that line.

Methods are defined for `print`, `summary` and `as.character` for class `srcref`. The `as.character` method will read the associated source file to obtain the text corresponding to the reference. If an error occurs (e.g. the file no longer exists), text like `<srcref: "file" chars 1:1 to 2:10>` will be returned instead, indicating the `line:column` ranges of the first and last character. The `summary` method defaults to this type of display.

Lists of `srcref` objects may be attached to expressions as the `"srcref"` attribute. (The list of `srcref` objects should be the same length as the expression.) By default, expressions are printed by `print.default` using the associated `srcref`. To see deparsed code instead, call

`print` with argument `useSource = FALSE`. If a `srcref` object is printed with `useSource = FALSE`, the `<srcref: ...>` record will be printed.

`.isOpen` is intended for internal use: it checks whether the connection associated with a `srcfile` object is open.

### Value

`srcfile` returns a `srcfile` object.

`srcfilecopy` returns a `srcfilecopy` object.

`getSrcLines` returns a character vector of source code lines.

`srcref` returns a `srcref` object.

### Author(s)

Duncan Murdoch

### Examples

```
src <- srcfile(system.file("DESCRIPTION", package = "base"))
summary(src)
getSrcLines(src, 1, 4)
ref <- srcref(src, c(1, 1, 2, 1000))
ref
print(ref, useSource = FALSE)
```

### Description

In R, the startup mechanism is as follows.

Unless `--no-environ` was given on the command line, R searches for site and user files to process for setting environment variables. The name of the site file is the one pointed to by the environment variable `R_ENVIRON`; if this is unset or empty, `'R_HOME/etc/Renviron.site'` is used (if it exists, which it does not in a 'factory-fresh' installation). The name of the user file can be specified by the `R_ENVIRON_USER` environment variable; if this is unset, the user files searched for are `'.Renviron'` in the current or in the user's home directory (in that order). See 'Details' for how the files are read.

Then R searches for the site-wide startup profile unless the command line option `--no-site-file` was given. The name of this file is taken from the value of the `R_PROFILE` environment variable. If this variable is unset, the default is `'R_HOME/etc/Rprofile.site'`, which is used if it exists (which it does not in a 'factory-fresh' installation). This code is sourced into the **base** package. Users need to be careful not to unintentionally overwrite objects in **base**, and it is normally advisable to use `local` if code needs to be executed: see the examples.

Then, unless `--no-init-file` was given, R searches for a user profile file. The name of this file can be specified by the `R_PROFILE_USER` environment variable. If this is unset, a file called `'.Rprofile'` in the current directory or in the user's home directory (in that order) is searched for. The user profile is sourced into the user workspace.



Note that when the site and user profile files are sourced only the **base** package is loaded, so objects in other packages need to be referred to by e.g. `utils::dump.frames` or after explicitly loading the package concerned.

It then loads a saved image of the user workspace from `‘.RData’` if there is one (unless `‘--no-restore-data’` or `‘--no-restore’` was specified on the command line).

Next, if a function `.First` is found on the search path, it is executed as `.First()`. Finally, function `.First.sys()` in the **base** package is run. This calls `require` to attach the default packages specified by `options("defaultPackages")`. If the **methods** package is included, this will have been attached earlier (by function `.OptRequireMethods()`) so that name space initializations such as those from the user workspace will proceed correctly.

A function `.First` (and `.Last`) can be defined in appropriate `‘.Rprofile’` or `‘Rprofile.site’` files or have been saved in `‘.RData’`. If you want a different set of packages than the default ones when you start, insert a call to `options` in the `‘.Rprofile’` or `‘Rprofile.site’` file. For example, `options(defaultPackages = character())` will attach no extra packages on startup (only the **base** package) (or set `R_DEFAULT_PACKAGES=NULL` as an environment variable before running R). Using `options(defaultPackages = "")` or `R_DEFAULT_PACKAGES=""` enforces the R *system* default.

On front-ends which support it, the commands history is read from the file specified by the environment variable `R_HISTFILE` (default `‘.Rhistory’`) unless `‘--no-restore-history’` was specified (or `‘--no-restore’`).

The command-line flag `‘--vanilla’` implies `‘--no-site-file’`, `‘--no-init-file’`, `‘--no-restore’` and `‘--no-environ’`.

## Usage

```
.First <- function() { ..... }

.Rprofile <startup file>
```

## Details

Note that there are two sorts of files used in startup: *environment files* which contain lists of environment variables to be set, and *profile files* which contain R code.

Lines in a site or user environment file should be either comment lines starting with `#`, or lines of the form `name=value`. The latter sets the environmental variable `name` to `value`, overriding an existing value. If `value` contains an expression of the form `${foo-bar}`, the value is that of the environmental variable `foo` if that exists and is set to a non-empty value, otherwise `bar`. (If it is of the form `${foo}`, the default is `" "`.) This construction can be nested, so `bar` can be of the same form (as in `${foo-${bar-blah}}`). Note that the braces are essential: `$HOME` will not be interpreted.

Leading and trailing white space in `value` are stripped. `value` is then processed in a similar way to a Unix shell: in particular the outermost level of (single or double) quotes is stripped, and backslashes are removed except inside quotes.

On systems with sub-architectures (mainly Mac OS X), the files `‘Renviron.site’` and `‘Rprofile.site’` are looked for first in architecture-specific directories, e.g. `‘R_HOME/etc/i386/Renviron.site’`.

## Note

The file `‘R_HOME/etc/Renviron’` is always read very early in the start-up processing. It contains environment variables set by R in the configure process. Values in that file can be overridden in site

or user environment files: do not change '[R\\_HOME/etc/Renviron](#)' itself. Note that this is distinct from '[R\\_HOME/etc/Renviron.site](#)'.

### See Also

For the definition of the 'home' directory on Windows see the '[rw-FAQ](#)' Q2.14 It can be found from a running R by `Sys.getenv("R_USER")`.

[.Last](#) for final actions at the close of an R session. [commandArgs](#) for accessing the command line arguments.

There are examples of using startup files to set defaults for graphics devices in the help for [X11](#) and [quartz](#).

*An Introduction to R* for more command-line options: those affecting memory management are covered in the help file for [Memory](#).

For profiling code, see [Rprof](#).

### Examples

```
## Not run:
## Example ~/.Renviron on Unix
R_LIBS=~ /R/library
PAGER=/usr/local/bin/less

## Example .Renviron on Windows
R_LIBS=C:/R/library
MY_TCLTK="c:/Program Files/Tcl/bin"

## Example of setting R_DEFAULT_PACKAGES (from R CMD check)
R_DEFAULT_PACKAGES='utils,grDevices,graphics,stats'
# this loads the packages in the order given, so they appear on
# the search path in reverse order.

## Example of .Rprofile
options(width=65, digits=5)
options(show.signif.stars=FALSE)
setHook(packageEvent("grDevices", "onLoad"),
         function(...) grDevices::ps.options(horizontal=FALSE))
set.seed(1234)
.First <- function() cat("\n Welcome to R!\n\n")
.Last <- function() cat("\n Goodbye!\n\n")

## Example of Rprofile.site
local({
  # add MASS to the default packages, set a CRAN mirror
  old <- getOption("defaultPackages"); r <- getOption("repos")
  r["CRAN"] <- "http://my.local.cran"
  options(defaultPackages = c(old, "MASS"), repos = r)
  ## (for Unix terminal users) set the width from COLUMNS if set
  cols <- Sys.getenv("COLUMNS")
  if(nzchar(cols)) options(width = as.integer(cols))
})

## if .Renviron contains
FOOBAR="coo\bar"doh\ex"abc\"def'"

## then we get
```

```
# > cat (Sys.getenv("FOOBAR"), "\n")
# coo\bardoh\exabc"def'

## End(Not run)
```

---

 stop

*Stop Function Execution*


---

## Description

`stop` stops execution of the current expression and executes an error action.  
`geterrmessage` gives the last error message.

## Usage

```
stop(..., call. = TRUE, domain = NULL)
geterrmessage()
```

## Arguments

<code>...</code>	zero or more objects which can be coerced to character (and which are pasted together with no separator) or a single condition object.
<code>call.</code>	logical, indicating if the call should become part of the error message.
<code>domain</code>	see <a href="#">gettext</a> . If NA, messages will not be translated.

## Details

The error action is controlled by error handlers established within the executing code and by the current default error handler set by `options(error=)`. The error is first signaled as if using `signalCondition()`. If there are no handlers or if all handlers return, then the error message is printed (if `options("show.error.messages")` is true) and the default error handler is used. The default behaviour (the NULL error-handler) in interactive use is to return to the top level prompt or the top level browser, and in non-interactive use to (effectively) call `q("no", status=1, runLast=FALSE)`. The default handler stores the error message in a buffer; it can be retrieved by `geterrmessage()`. It also stores a trace of the call stack that can be retrieved by `traceback()`.

Errors will be truncated to `getOption("warning.length")` characters, default 1000.

If a condition object is supplied it should be the only argument, and further arguments will be ignored, with a warning.

## Value

`geterrmessage` gives the last error message, as a character string ending in `"\n"`.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[warning](#), [try](#) to catch errors and retry, and [options](#) for setting error handlers. [stopifnot](#) for validity testing. [tryCatch](#) and [withCallingHandlers](#) can be used to establish custom handlers while executing an expression.

[gettext](#) for the mechanisms for the automated translation of messages.

**Examples**

```
options(error = expression(NULL))
# don't stop on stop(.) << Use with CARE! >>

iter <- 12
if(iter > 10) stop("too many iterations")

tst1 <- function(...) stop("dummy error")
tst1(1:10, long, calling, expression)

tst2 <- function(...) stop("dummy error", call. = FALSE)
tst2(1:10, longcalling, expression, but.not.seen.in.Error)

options(error = NULL) # revert to default
```

---

stopifnot

*Ensure the Truth of R Expressions*


---

**Description**

If any of the expressions in `...` are not `all TRUE`, `stop` is called, producing an error message indicating the *first* of the elements of `...` which were not true.

**Usage**

```
stopifnot(...)
```

**Arguments**

`...` any number of (`logical`) R expressions, which should evaluate to `TRUE`.

**Details**

This function is intended for use in regression tests or also argument checking of functions, in particular to make them easier to read.

```
stopifnot(A, B) is conceptually equivalent to { if(any(is.na(A)) || !all(A))
stop(...) ; if(any(is.na(B)) || !all(B)) stop(...) }.
```

**Value**

(`NULL` if all statements in `...` are `TRUE`.)

**See Also**

[stop](#), [warning](#).

**Examples**

```

stopifnot(1 == 1, all.equal(pi, 3.14159265), 1 < 2) # all TRUE

m <- matrix(c(1,3,3,1), 2,2)
stopifnot(m == t(m), diag(m) == rep(1,2)) # all(.) |=> TRUE

op <- options(error = expression(NULL))
# "disable stop(.)" << Use with CARE! >>

stopifnot(all.equal(pi, 3.141593), 2 < 2, all(1:10 < 12), "a" < "b")
stopifnot(all.equal(pi, 3.1415927), 2 < 2, all(1:10 < 12), "a" < "b")

options(op) # revert to previous error handler

```

strptime

*Date-time Conversion Functions to and from Character***Description**

Functions to convert between character representations and objects of classes "POSIXlt" and "POSIXct" representing calendar dates and times.

**Usage**

```

## S3 method for class 'POSIXct':
format(x, format = "", tz = "", usetz = FALSE, ...)
## S3 method for class 'POSIXlt':
format(x, format = "", usetz = FALSE, ...)

## S3 method for class 'POSIXt':
as.character(x, ...)

strftime(x, format="", tz = "", usetz = FALSE, ...)
strptime(x, format, tz = "")

```

**Arguments**

x	An object to be converted.
tz	A timezone specification to be used for the conversion. System-specific (see <a href="#">as.POSIXlt</a> ), but "" is the current time zone, and "GMT" is UTC.
format	A character string. The default for the format methods is "%Y-%m-%d %H:%M:%S" if any component has a time component which is not midnight, and "%Y-%m-%d" otherwise. If <a href="#">options</a> ("digits.secs") is set, up to the specified number of digits will be printed for seconds.
...	Further arguments to be passed from or to other methods.
usetz	logical. Should the timezone be appended to the output? This is used in printing times, and as a workaround for problems with using "%Z" on some Linux systems.

## Details

The `format` and `as.character` methods and `strptime` convert objects from the classes `"POSIXlt"` and `"POSIXct"` (not `strptime`) to character vectors.

`strptime` converts character strings to class `"POSIXlt"`: its input `x` is first coerced to character if necessary. Each string is processed as far as necessary for the format specified: any trailing characters are ignored.

`strptime` is a wrapper for `format.POSIXlt`, and it and `format.POSIXct` first converts to class `"POSIXlt"` by calling `as.POSIXlt`. Note that only that conversion depends on the time zone.

The usual vector re-cycling rules are applied to `x` and `format` so the answer will be of length that of the longer of the vectors.

Locale-specific conversions to and from character strings are used where appropriate and available. This affects the names of the days and months, the AM/PM indicator (if used) and the separators in formats such as `%x` and `%X` (via the setting of the `LC_TIME` locale category).

The details of the formats are system-specific, but the following are defined by the ISO C99 / POSIX standard for `strptime` and are likely to be widely available. A *conversion specification* is introduced by `%`, usually followed by a single letter or `O` or `E` and then a single letter. Any character in the format string not part of a conversion specification is interpreted literally (and `%%` gives `%`). Widely implemented conversion specifications include

- `%a` Abbreviated weekday name in the current locale. (Also matches full name on input.)
- `%A` Full weekday name in the current locale. (Also matches abbreviated name on input.)
- `%b` Abbreviated month name in the current locale. (Also matches full name on input.)
- `%B` Full month name in the current locale. (Also matches abbreviated name on input.)
- `%c` Date and time. Locale-specific on output, "`%a %b %e %H:%M:%S %Y`" on input.
- `%d` Day of the month as decimal number (01–31).
- `%H` Hours as decimal number (00–23).
- `%I` Hours as decimal number (01–12).
- `%j` Day of year as decimal number (001–366).
- `%m` Month as decimal number (01–12).
- `%M` Minute as decimal number (00–59).
- `%p` AM/PM indicator in the locale. Used in conjunction with `%I` and **not** with `%H`. An empty string in some locales.
- `%S` Second as decimal number (00–61), allowing for up to two leap-seconds (but POSIX-compliant implementations will ignore leap seconds).
- `%U` Week of the year as decimal number (00–53) using Sunday as the first day 1 of the week (and typically with the first Sunday of the year as day 1 of week 1). The US convention.
- `%w` Weekday as decimal number (0–6, Sunday is 0).
- `%W` Week of the year as decimal number (00–53) using Monday as the first day of week (and typically with the first Monday of the year as day 1 of week 1). The UK convention.
- `%x` Date. Locale-specific on output, "`%y/%m/%d`" on input.
- `%X` Time. Locale-specific on output, "`%H:%M:%S`" on input.
- `%y` Year without century (00–99). Values 00 to 68 are prefixed by 20 and 69 to 99 by 19 – that is the behaviour specified by the 2004 POSIX standard, but it does also say ‘it is expected that in a future version of IEEE Std 1003.1-2001 the default century inferred from a 2-digit year will change’.

- %Y Year with century.
- %z Signed offset in hours and minutes from UTC, so `-0800` is 8 hours behind UTC.
- %Z (output only.) Time zone as a character string (empty if not available).

Where leading zeros are shown they will be used on output but are optional on input.

Also defined in the current standards but less widely implemented (e.g. not for output on Windows) are

- %C Century (00–99): the integer part of the year divided by 100.
- %D Date format such as `%m/%d/%y`: ISO C99 says it should be that exact format.
- %e Day of the month as decimal number (1–31), with a leading space for a single-digit number.
- %F Equivalent to `%Y-%m-%d` (the ISO 8601 date format).
- %g The last two digits of the week-based year (see %V). (Accepted but ignored on input.)
- %G The week-based year (see %V) as a decimal number. (Accepted but ignored on input.)
- %h Equivalent to %b.
- %k The 24-hour clock time with single digits preceded by a blank.
- %l The 12-hour clock time with single digits preceded by a blank.
- %n Newline on output, arbitrary whitespace on input.
- %r The 12-hour clock time (using the locale's AM or PM).
- %R Equivalent to `%H:%M`.
- %t Tab on output, arbitrary whitespace on input.
- %T Equivalent to `%H:%M:%S`.
- %u Weekday as a decimal number (1–7, Monday is 1).
- %V Week of the year as decimal number (00–53) as defined in ISO 8601. If the week (starting on Monday) containing 1 January has four or more days in the new year, then it is considered week 1. Otherwise, it is the last week of the previous year, and the next week is week 1. (Accepted but ignored on input.)

For output there are also `%O[dHImMUVwWy]` which may emit numbers in an alternative locale-dependent format (e.g. roman numerals), and `%E[cCYyXx]` which can use an alternative 'era' (e.g. a different religious calendar). Which of these are supported is OS-dependent. These are accepted for input, but with the standard interpretation.

Specific to R is `%OSn`, which for output gives the seconds to  $0 \leq n \leq 6$  decimal places (and if `%OS` is not followed by a digit, it uses the setting of `getOption("digits.secs")`, or if that is unset,  $n = 3$ ). Further, for `strptime` `%OS` will input seconds including fractional seconds. Note that `%S` ignores (and not rounds) fractional parts on output.

The behaviour of other conversion specifications (and even if other character sequences commencing with % are conversion specifications) is system-specific.

## Value

The format methods and `strptime` return character vectors representing the time. NA times are returned as `NA_character_`.

`strptime` turns character representations into an object of class `"POSIXlt"`. The timezone is used to set the `isdst` component and to set the `"tzzone"` attribute if `tz != ""`. If the specified time is invalid (in the specified timezone) all the components of the result are NA.

**Note**

The default formats follow the rules of the ISO 8601 international standard which expresses a day as "2001-02-28" and a time as "14:01:02" using leading zeroes as here. The ISO form uses no space to separate dates and times.

For `strptime` the input string need not specify the date completely: it is assumed that unspecified seconds, minutes or hours are zero, and an unspecified year, month or day is the current one.

If the timezone specified is invalid on your system, what happens is system-specific but it will probably be ignored.

OS facilities will probably not print years before 1CE (aka 1AD) correctly.

Remember that in most timezones some times do not occur and some occur twice because of transitions to/from summer time. What happens in those cases is OS-specific.

**References**

International Organization for Standardization (2004, 2000, 1988, 1997, ...) *ISO 8601. Data elements and interchange formats – Information interchange – Representation of dates and times*. For links to versions available on-line see (at the time of writing) <http://www.qsl.net/g1smd/isopdf.htm>; for information on the current official version, see <http://www.iso.org/iso/en/prods-services/popstds/datesandtime.html>.

**See Also**

[DateTimeClasses](#) for details of the date-time classes; [locales](#) to query or set a locale.

Your system's help pages on `strftime` and `strptime` to see how to specify their formats. (On some systems `strptime` is replaced by corrected code from 'glibc', when all the conversion specifications described here are supported, but with no alternative number representation nor era available in any locale.)

**Examples**

```
## locale-specific version of date()
format(Sys.time(), "%a %b %d %X %Y %Z")

## time to sub-second accuracy (if supported by the OS)
format(Sys.time(), "%H:%M:%OS3")

## read in date info in format 'ddmmyyyy'
## This will give NA(s) in some locales; setting the C locale
## as in the commented lines will overcome this on most systems.
## lct <- Sys.getlocale("LC_TIME"); Sys.setlocale("LC_TIME", "C")
x <- c("1jan1960", "2jan1960", "31mar1960", "30jul1960")
z <- strptime(x, "%d%b%Y")
## Sys.setlocale("LC_TIME", lct)
z

## read in date/time info in format 'm/d/y h:m:s'
dates <- c("02/27/92", "02/27/92", "01/14/92", "02/28/92", "02/01/92")
times <- c("23:03:20", "22:29:56", "01:03:30", "18:21:03", "16:56:26")
x <- paste(dates, times)
strptime(x, "%m/%d/%y %H:%M:%S")

## time with fractional seconds
z <- strptime("20/2/06 11:16:16.683", "%d/%m/%y %H:%M:%OS")
```



```

z # prints without fractional seconds
op <- options(digits.secs=3)
z
options(op)

## timezones are not portable, but 'EST5EDT' comes pretty close.
(x <- strptime(c("2006-01-08 10:07:52", "2006-08-07 19:33:02"),
               "%Y-%m-%d %H:%M:%S", tz="EST5EDT"))
attr(x, "tzone")

## An RFC 822 header (Eastern Canada, during DST)
strptime("Tue, 23 Mar 2010 14:36:38 -0400", "%a, %d %b %Y %H:%M:%S %z")

```

---

strsplit

*Split the Elements of a Character Vector*


---

### Description

Split the elements of a character vector `x` into substrings according to the matches to substring `split` within them.

### Usage

```
strsplit(x, split, fixed = FALSE, perl = FALSE, useBytes = FALSE)
```

### Arguments

<code>x</code>	character vector, each element of which is to be split. Other inputs, including a factor, will give an error.
<code>split</code>	character vector (or object which can be coerced to such) containing <a href="#">regular expression(s)</a> (unless <code>fixed = TRUE</code> ) to use for splitting. If empty matches occur, in particular if <code>split</code> has length 0, <code>x</code> is split into single characters. If <code>split</code> has length greater than 1, it is re-cycled along <code>x</code> .
<code>fixed</code>	logical. If <code>TRUE</code> match <code>split</code> exactly, otherwise use regular expressions. Has priority over <code>perl</code> and <code>extended</code> .
<code>perl</code>	logical. Should perl-compatible regexps be used? Has priority over <code>extended</code> .
<code>useBytes</code>	logical. If <code>TRUE</code> the matching is done byte-by-byte rather than character-by-character, and inputs with marked encodings are not converted.

### Details

Argument `split` will be coerced to character, so you will see uses with `split = NULL` to mean `split = character(0)`, including in the examples below.

Note that splitting into single characters can be done *via* `split = character(0)` or `split = ""`; the two are equivalent. The definition of ‘character’ here depends on the locale: in a single-byte locale it is a byte, and in a multi-byte locale it is the unit represented by a ‘wide character’ (almost always a Unicode point).

A missing value of `split` does not split the corresponding element(s) of `x` at all.

The algorithm applied to each input string is

```

repeat {
  if the string is empty
    break.
  if there is a match
    add the string to the left of the match to the output.
    remove the match and all to the left of it.
  else
    add the string to the output.
    break.
}

```

Note that this means that if there is a match at the beginning of a (non-empty) string, the first element of the output is "", but if there is a match at the end of the string, the output is the same as with the match removed.

### Value

A list of the same length as `x`, the *i*-th element of which contains the vector of splits of `x[i]`.

If any element of `x` or `split` is declared to be in UTF-8 (see [Encoding](#), all non-ASCII character strings in the result will be in UTF-8 and have their encoding declared as UTF-8. As from R 2.10.0, for `perl = TRUE`, `useBytes = FALSE` all non-ASCII strings in a multibyte locale are translated to UTF-8.

### Note

Prior to R 2.11.0 there was an argument `extended` which could be used to select ‘basic’ regular expressions: this was often used when `fixed = TRUE` would be preferable. In the actual implementation (as distinct from the POSIX standard) the only difference was that ‘?’, ‘+’, ‘{’, ‘|’, ‘(’, and ‘)’ were not interpreted as metacharacters.

### See Also

[paste](#) for the reverse, [grep](#) and [sub](#) for string search and manipulation; also [nchar](#), [substr](#).  
‘[regular expression](#)’ for the details of the pattern specification.

### Examples

```

noquote(strsplit("A text I want to display with spaces", NULL)[[1]])

x <- c(as = "asfef", qu = "qwerty", "yuiop[" , "b", "stuff.blah.yech")
# split x on the letter e
strsplit(x, "e")

unlist(strsplit("a.b.c", "."))
## [1] "" "" "" "" ""
## Note that 'split' is a regexp!
## If you really want to split on '.', use
unlist(strsplit("a.b.c", "\\."))
## [1] "a" "b" "c"
## or
unlist(strsplit("a.b.c", ".", fixed = TRUE))

## a useful function: rev() for strings

```

```

strReverse <- function(x)
  sapply(lapply(strsplit(x, NULL), rev), paste, collapse="")
strReverse(c("abc", "Statistics"))

## get the first names of the members of R-core
a <- readLines(file.path(R.home("doc"), "AUTHORS"))[-(1:8)]
a <- a[(0:2)-length(a)]
(a <- sub(" .*", "", a))
# and reverse them
strReverse(a)

## Note that final empty strings are not produced:
strsplit(paste(c("", "a", ""), collapse="#"), split="#")[[1]]
# [1] "" "a"
## and also an empty string is only produced before a definite match:
strsplit("", " ")[[1]] # character(0)
strsplit(" ", " ")[[1]] # [1] ""

```

---

strtoi

*Convert Strings to Integers*


---

## Description

Convert strings to integers according to the given base using the C function `strtol`.

## Usage

```
strtoi(x, base = 0L)
```

## Arguments

`x` a character vector, or something coercible to this by `as.character`.  
`base` an integer which is between 2 and 36 inclusive, or zero (default).

## Details

Conversion is based on the C library function `strtol`.

For the default `base = 0L`, the base chosen from the string representation of that element of `x`, so different elements can have different bases (see the first example). The standard C rules for choosing the base are that octal constants (prefix 0 not followed by `x` or `X`) and hexadecimal constants (prefix `0x` or `0X`) are interpreted as base 8 and 16; all other strings are interpreted as base 10.

For a base greater than 10, letters `a` to `z` (or `A` to `Z`) are used to represent 10 to 35.

## Value

An integer vector of the same length as `x`. Values which cannot be interpreted as integers or would overflow are returned as `NA_integer_`.

## Examples

```

strtoi(c("0xff", "077", "123"))
strtoi(c("ffff", "FFFF"), 16L)
strtoi(c("177", "377"), 8L)

```

---

`strtrim`*Trim Character Strings to Specified Widths*

---

**Description**

Trim character strings to specified display widths.

**Usage**

```
strtrim(x, width)
```

**Arguments**

<code>x</code>	a character vector, or an object which can be coerced to a character vector by <a href="#">as.character</a> .
<code>width</code>	Positive integer values: recycled to the length of <code>x</code> .

**Details**

'Width' is interpreted as the display width in a monospaced font. What happens with non-printable characters (such as backspace, tab) is implementation-dependent and may depend on the locale (e.g. they may be included in the count or they may be omitted).

Using this function rather than [substr](#) is important when there might be double-width characters in character vectors

**Value**

A character vector of the same length and with the same attributes as `x` (after possible coercion).

Elements of the result will have the encoding declared as that of the current locale (see [Encoding](#) if the corresponding input had a declared encoding and the current locale is either Latin-1 or UTF-8).

**Examples**

```
strtrim(c("abcdef", "abcdef", "abcdef"), c(1,5,10))
```

---

`structure`*Attribute Specification*

---

**Description**

`structure` returns the given object with further [attributes](#) set.

**Usage**

```
structure(.Data, ...)
```

**Arguments**

`.Data` an object which will have various attributes attached to it.  
`...` attributes, specified in `tag=value` form, which will be attached to `data`.

**Details**

Adding a class `"factor"` will ensure that numeric codes are given integer storage mode.

For historical reasons (these names are used when deparsing), attributes `".Dim"`, `".Dimnames"`, `".Names"`, `".Tsp"` and `".Label"` are renamed to `"dim"`, `"dimnames"`, `"names"`, `"tsp"` and `"levels"`.

It is possible to give the same tag more than once, in which case the last value assigned wins. As with other ways of assigning attributes, using `tag=NULL` removes attribute `tag` from `.Data` if it is present.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[attributes](#), [attr](#).

**Examples**

```
structure(1:6, dim = 2:3)
```

---

strwrap

*Wrap Character Strings to Format Paragraphs*

---

**Description**

Each character string in the input is first split into paragraphs (or lines containing whitespace only). The paragraphs are then formatted by breaking lines at word boundaries. The target columns for wrapping lines and the indentation of the first and all subsequent lines of a paragraph can be controlled independently.

**Usage**

```
strwrap(x, width = 0.9 * getOption("width"), indent = 0,
        exdent = 0, prefix = "", simplify = TRUE, initial = prefix)
```

**Arguments**

`x` a character vector, or an object which can be converted to a character vector by [as.character](#).

`width` a positive integer giving the target column for wrapping lines in the output.

`indent` a non-negative integer giving the indentation of the first line in a paragraph.

`exdent` a non-negative integer specifying the indentation of subsequent lines in paragraphs.

prefix, initial a character string to be used as prefix for each line except the first, for which initial is used.

simplify a logical. If TRUE, the result is a single character vector of line text; otherwise, it is a list of the same length as x the elements of which are character vectors of line text obtained from the corresponding element of x. (Hence, the result in the former case is obtained by unlisting that of the latter.)

### Details

Whitespace (space, tab or newline characters) in the input is destroyed. Double spaces after periods, question and explanation marks (thought as representing sentence ends) are preserved. Currently, possible sentence ends at line breaks are not considered specially.

Indentation is relative to the number of characters in the prefix string.

### Value

A character vector in the current locale's encoding.

### Examples

```
## Read in file 'THANKS'.
x <- paste(readLines(file.path(R.home("doc"), "THANKS")), collapse = "\n")
## Split into paragraphs and remove the first three ones
x <- unlist(strsplit(x, "\n[ \t\n]*\n"))[-(1:3)]
## Join the rest
x <- paste(x, collapse = "\n\n")
## Now for some fun:
writeLines(strwrap(x, width = 60))
writeLines(strwrap(x, width = 60, indent = 5))
writeLines(strwrap(x, width = 60, exdent = 5))
writeLines(strwrap(x, prefix = "THANKS> "))

## Note that messages are wrapped AT the target column indicated by
## 'width' (and not beyond it).
## From an R-devel posting by J. Hosking <jh910@juno.com>.
x <- paste(sapply(sample(10, 100, replace=TRUE),
  function(x) substring("aaaaaaaaa", 1, x)), collapse = " ")
sapply(10:40,
  function(m)
    c(target = m, actual = max(nchar(strwrap(x, m)))))
```

### Description

Return subsets of vectors, matrices or data frames which meet conditions.

## Usage

```
subset(x, ...)  
  
## Default S3 method:  
subset(x, subset, ...)  
  
## S3 method for class 'matrix':  
subset(x, subset, select, drop = FALSE, ...)  
  
## S3 method for class 'data.frame':  
subset(x, subset, select, drop = FALSE, ...)
```

## Arguments

<code>x</code>	object to be subsetted.
<code>subset</code>	logical expression indicating elements or rows to keep: missing values are taken as false.
<code>select</code>	expression, indicating columns to select from a data frame.
<code>drop</code>	passed on to <code>[</code> indexing operator.
<code>...</code>	further arguments to be passed to or from other methods.

## Details

This is a generic function, with methods supplied for matrices, data frames and vectors (including lists). Packages and users can add further methods.

For ordinary vectors, the result is simply `x[subset & !is.na(subset)]`.

For data frames, the `subset` argument works on the rows. Note that `subset` will be evaluated in the data frame, so columns can be referred to (by name) as variables in the expression (see the examples).

The `select` argument exists only for the methods for data frames and matrices. It works by first replacing column names in the selection expression with the corresponding column numbers in the data frame and then using the resulting integer vector to index the columns. This allows the use of the standard indexing conventions so that for example ranges of columns can be specified easily, or single columns can be dropped (see the examples).

The `drop` argument is passed on to the indexing method for matrices and data frames: note that the default for matrices is different from that for indexing.

## Value

An object similar to `x` contain just the selected elements (for a vector), rows and columns (for a matrix or data frame), and so on.

## Author(s)

Peter Dalgaard and Brian Ripley

## See Also

[\[, transform](#)

**Examples**

```
subset(airquality, Temp > 80, select = c(Ozone, Temp))
subset(airquality, Day == 1, select = -Temp)
subset(airquality, select = Ozone:Wind)

with(airquality, subset(Ozone, Temp > 80))

## sometimes requiring a logical 'subset' argument is a nuisance
nm <- rownames(state.x77)
start_with_M <- nm %in% grep("^M", nm, value=TRUE)
subset(state.x77, start_with_M, Illiteracy:Murder)
```

substitute

*Substituting and Quoting Expressions***Description**

`substitute` returns the parse tree for the (unevaluated) expression `expr`, substituting any variables bound in `env`.

`quote` simply returns its argument. The argument is not evaluated and can be any R expression.

**Usage**

```
substitute(expr, env)
quote(expr)
```

**Arguments**

`expr` Any syntactically valid R expression

`env` An environment or a list object. Defaults to the current evaluation environment.

**Details**

The typical use of `substitute` is to create informative labels for data sets and plots. The `myplot` example below shows a simple use of this facility. It uses the functions `deparse` and `substitute` to create labels for a plot which are character string versions of the actual arguments to the function `myplot`.

Substitution takes place by examining each component of the parse tree as follows: If it is not a bound symbol in `env`, it is unchanged. If it is a promise object, i.e., a formal argument to a function or explicitly created using `delayedAssign()`, the expression slot of the promise replaces the symbol. If it is an ordinary variable, its value is substituted, unless `env` is `.GlobalEnv` in which case the symbol is left unchanged.

These are both ‘special’ [primitive](#) functions, which do not evaluate their arguments.

**Value**

The `mode` of the result is generally `"call"` but may in principle be any type. In particular, single-variable expressions have `mode "name"` and constants have the appropriate base mode.



**Note**

Substitute works on a purely lexical basis. There is no guarantee that the resulting expression makes any sense.

Substituting and quoting often causes confusion when the argument is `expression(...)`. The result is a call to the `expression` constructor function and needs to be evaluated with `eval` to give the actual expression object.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`missing` for argument 'missingness', `bquote` for partial substitution, `sQuote` and `dQuote` for adding quotation marks to strings.

**Examples**

```
require(graphics)
(s.e <- substitute(expression(a + b), list(a = 1))) #> expression(1 + b)
(s.s <- substitute( a + b, list(a = 1))) #> 1 + b
c(mode(s.e), typeof(s.e)) # "call", "language"
c(mode(s.s), typeof(s.s)) # (the same)
# but:
(e.s.e <- eval(s.e)) #> expression(1 + b)
c(mode(e.s.e), typeof(e.s.e)) # "expression", "expression"

substitute(x <- x + 1, list(x=1)) # nonsense

myplot <- function(x, y)
  plot(x, y, xlab=deparse(substitute(x)),
       ylab=deparse(substitute(y)))

## Simple examples about lazy evaluation, etc:

f1 <- function(x, y = x) { x <- x + 1; y }
s1 <- function(x, y = substitute(x)) { x <- x + 1; y }
s2 <- function(x, y) { if(missing(y)) y <- substitute(x); x <- x + 1; y }
a <- 10
f1(a) # 11
s1(a) # 11
s2(a) # a
typeof(s2(a)) # "symbol"
```

---

 substr

*Substrings of a Character Vector*


---

**Description**

Extract or replace substrings in a character vector.

**Usage**

```
substr(x, start, stop)
substring(text, first, last = 1000000L)
substr(x, start, stop) <- value
substring(text, first, last = 1000000L) <- value
```

**Arguments**

`x`, `text` a character vector.

`start`, `first` integer. The first element to be replaced.

`stop`, `last` integer. The last element to be replaced.

`value` a character vector, recycled if necessary.

**Details**

`substring` is compatible with `S`, with `first` and `last` instead of `start` and `stop`. For vector arguments, it expands the arguments cyclically to the length of the longest *provided* none are of zero length.

When extracting, if `start` is larger than the string length then "" is returned.

For the extraction functions, `x` or `text` will be converted to a character vector by `as.character` if it is not already one.

For the replacement functions, if `start` is larger than the string length then no replacement is done. If the portion to be replaced is longer than the replacement string, then only the portion the length of the string is replaced.

If any argument is an `NA` element, the corresponding element of the answer is `NA`.

Elements of the result will have the encoding declared as that of the current locale (see [Encoding](#) if the corresponding input had a declared encoding and the current locale is either Latin-1 or UTF-8).

**Value**

For `substr`, a character vector of the same length and with the same attributes as `x` (after possible coercion).

For `substring`, a character vector of length the longest of the arguments. This will have names taken from `x` (if it has any after coercion, repeated as needed), and other attributes copied from `x` if it is the longest of the arguments).

Elements of `x` with a declared encoding (see [Encoding](#)) will be returned with the same encoding.

**Note**

The S4 version of `substring<-` ignores `last`; this version does not.

These functions are often used with `nchar` to truncate a display. That does not really work (you want to limit the width, not the number of characters, so it would be better to use `strtrim`), but at least make sure you use `nchar(type="c")` (the default since R 2.6.0).

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (`substring`.)

**See Also**

`strsplit`, `paste`, `nchar`.

**Examples**

```
substr("abcdef", 2, 4)
substring("abcdef", 1:6, 1:6)
## strsplit is more efficient ...

substr(rep("abcdef", 4), 1:4, 4:5)
x <- c("asfef", "qwerty", "yuiop[", "b", "stuff.blah.yech")
substr(x, 2, 5)
substring(x, 2, 4:6)

substring(x, 2) <- c("..", "+++")
x
```

---

sum

*Sum of Vector Elements*

---

**Description**

`sum` returns the sum of all the values present in its arguments.

**Usage**

```
sum(..., na.rm = FALSE)
```

**Arguments**

`...` numeric or complex or logical vectors.  
`na.rm` logical. Should missing values be removed?

**Details**

This is a generic function: methods can be defined for it directly or via the [Summary](#) group generic. For this to work properly, the arguments `...` should be unnamed, and `dispatch` is on the first argument.

If `na.rm` is `FALSE` an NA value in any of the arguments will cause a value of NA to be returned, otherwise NA values are ignored.

Logical true values are regarded as one, false values as zero. For historical reasons, NULL is accepted and treated as if it were `integer(0)`.

**Value**

The sum. If all of `...` are of type integer or logical, then the sum is integer, and in that case the result will be NA (with a warning) if integer overflow occurs. Otherwise it is a length-one numeric or complex vector.

**NB:** the sum of an empty set is zero, by definition.

**S4 methods**

This is part of the S4 [Summary](#) group generic. Methods for it must use the signature `x, ..., na.rm`.

'[plotmath](#)' for the use of `sum` in plot annotation.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[colSums](#) for row and column sums.

---

 summary

---

*Object Summaries*


---

**Description**

`summary` is a generic function used to produce result summaries of the results of various model fitting functions. The function invokes particular [methods](#) which depend on the [class](#) of the first argument.

**Usage**

```
summary(object, ...)

## Default S3 method:
summary(object, ..., digits = max(3, getOption("digits")-3))
## S3 method for class 'data.frame':
summary(object, maxsum = 7,
        digits = max(3, getOption("digits")-3), ...)

## S3 method for class 'factor':
summary(object, maxsum = 100, ...)

## S3 method for class 'matrix':
summary(object, ...)
```

**Arguments**

<code>object</code>	an object for which a summary is desired.
<code>maxsum</code>	integer, indicating how many levels should be shown for <a href="#">factors</a> .
<code>digits</code>	integer, used for number formatting with <a href="#">signif()</a> (for <code>summary.default</code> ) or <a href="#">format()</a> (for <code>summary.data.frame</code> ).
<code>...</code>	additional arguments affecting the summary produced.

**Details**

For `factors`, the frequency of the first `maxsum - 1` most frequent levels is shown, where the less frequent levels are summarized in "(Others)" (resulting in `maxsum` frequencies).

The functions `summary.lm` and `summary.glm` are examples of particular methods which summarize the results produced by `lm` and `glm`.

**Value**

The form of the value returned by `summary` depends on the class of its argument. See the documentation of the particular methods for details of what is produced by that method.

**References**

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

**See Also**

`anova`, `summary.glm`, `summary.lm`.

**Examples**

```
summary(attenu, digits = 4) #-> summary.data.frame(...), default precision
summary(attenu $ station, maxsum = 20) #-> summary.factor(...)

lst <- unclass(attenu$station) > 20 # logical with NAs
## summary.default() for logicals -- different from *.factor:
summary(lst)
summary(as.factor(lst))
```

---

 svd

*Singular Value Decomposition of a Matrix*


---

**Description**

Compute the singular-value decomposition of a rectangular matrix.

**Usage**

```
svd(x, nu = min(n, p), nv = min(n, p), LINPACK = FALSE)
```

```
La.svd(x, nu = min(n, p), nv = min(n, p))
```

**Arguments**

<code>x</code>	a numeric, logical or complex matrix whose SVD decomposition is to be computed.
<code>nu</code>	the number of left singular vectors to be computed. This must be between 0 and <code>n = nrow(x)</code> .
<code>nv</code>	the number of right singular vectors to be computed. This must be between 0 and <code>p = ncol(x)</code> .
<code>LINPACK</code>	logical. Should LINPACK be used (for compatibility with R < 1.7.0)? In this case <code>nu</code> must be 0, <code>nrow(x)</code> or <code>ncol(x)</code> .

## Details

The singular value decomposition plays an important role in many statistical techniques. `svd` and `La.svd` provide two slightly different interfaces. The main functions used are the LAPACK routines `DGESDD` and `ZGESVD`; `svd(LINPACK = TRUE)` provides an interface to the LINPACK routine `DSVDC`, purely for backwards compatibility.

Computing the singular vectors is the slow part for large matrices. The computation will be more efficient if  $nu \leq \min(n, p)$  and  $nv \leq \min(n, p)$ , and even more efficient if one or both are zero.

Unsuccessful results from the underlying LAPACK code will result in an error giving a positive error code: these can only be interpreted by detailed study of the FORTRAN code.

## Value

The SVD decomposition of the matrix as computed by LAPACK/LINPACK,

$$X = UDV'$$

where  $U$  and  $V$  are orthogonal,  $V'$  means  $V$  transposed, and  $D$  is a diagonal matrix with the singular values  $D_{ii}$ . Equivalently,  $D = U'XV$ , which is verified in the examples, below.

The returned value is a list with components

<code>d</code>	a vector containing the singular values of <code>x</code> , of length $\min(n, p)$ .
<code>u</code>	a matrix whose columns contain the left singular vectors of <code>x</code> , present if $nu > 0$ . Dimension $c(n, nu)$ .
<code>v</code>	a matrix whose columns contain the right singular vectors of <code>x</code> , present if $nv > 0$ . Dimension $c(p, nv)$ .

For `La.svd` the return value replaces `v` by `vt`, the (conjugated if complex) transpose of `v`.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Dongarra, J. J., Bunch, J. R., Moler, C. B. and Stewart, G. W. (1978) *LINPACK Users Guide*. Philadelphia: SIAM Publications.

Anderson. E. and ten others (1999) *LAPACK Users' Guide*. Third Edition. SIAM.

Available on-line at [http://www.netlib.org/lapack/lug/lapack\\_lug.html](http://www.netlib.org/lapack/lug/lapack_lug.html).

## See Also

[eigen](#), [qr](#).

## Examples

```
hilbert <- function(n) { i <- 1:n; 1 / outer(i - 1, i, "+") }
X <- hilbert(9)[,1:6]
(s <- svd(X))
D <- diag(s$d)
s$u %*% D %*% t(s$v) # X = U D V'
t(s$u) %*% X %*% s$v # D = U' X V
```

---

`sweep`*Sweep out Array Summaries*

---

### Description

Return an array obtained from an input array by sweeping out a summary statistic.

### Usage

```
sweep(x, MARGIN, STATS, FUN="-", check.margin=TRUE, ...)
```

### Arguments

<code>x</code>	an array.
<code>MARGIN</code>	a vector of indices giving the extents of <code>x</code> which correspond to <code>STATS</code> .
<code>STATS</code>	the summary statistic which is to be swept out.
<code>FUN</code>	the function to be used to carry out the sweep. In the case of binary operators such as <code>"/"</code> etc., the function name must be backquoted or quoted. ( <code>FUN</code> is found by a call to <code>match.fun</code> .)
<code>check.margin</code>	logical. If <code>TRUE</code> (the default), warn if the length or dimensions of <code>STATS</code> do not match the specified dimensions of <code>x</code> . Set to <code>FALSE</code> for a small speed gain when you <i>know</i> that dimensions match.
<code>...</code>	optional arguments to <code>FUN</code> .

### Details

The consistency check among `STATS`, `MARGIN` and `x` is stricter if `STATS` is an array than if it is a vector. In the vector case, some kinds of recycling are allowed without a warning. Use `sweep(x, MARGIN, as.array(STATS))` if `STATS` is a vector and you want to be warned if any recycling occurs.

### Value

An array with the same shape as `x`, but with the summary statistics swept out.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

`apply` on which `sweep` used to be based; `scale` for centering and scaling.

**Examples**

```

require(stats) # for median
med.att <- apply(attitude, 2, median)
sweep(data.matrix(attitude), 2, med.att)# subtract the column medians

## More sweeping:
A <- array(1:24, dim = 4:2)

## no warnings in normal use
sweep(A, 1, 5)
(A.min <- apply(A, 1, min)) # == 1:4
sweep(A, 1, A.min)
sweep(A, 1:2, apply(A, 1:2, median))

## warnings when mismatch
sweep(A, 1, 1:3)## STATS does not recycle
sweep(A, 1, 6:1)## STATS is longer

## exact recycling:
sweep(A, 1, 1:2)## no warning
sweep(A, 1, as.array(1:2))## warning

```

---

switch

*Select One of a List of Alternatives*


---

**Description**

switch evaluates EXPR and accordingly chooses one of the further arguments (in ...).

**Usage**

```
switch(EXPR, ...)
```

**Arguments**

EXPR	an expression evaluating to a number or a character string.
...	the list of alternatives. If it is intended that EXPR has a character-string value these will be named, perhaps except for one alternative to be used as a 'default' value.

**Details**

switch works in two distinct ways depending whether the first argument evaluates to a character string or a number.

If the value of EXPR is not a character string it is coerced to integer. If this is between 1 and `nargs() - 1` then the corresponding element of ... is evaluated and the result returned: thus if the first argument is 3 then the fourth argument is evaluated and returned.

If EXPR evaluates to a character string then that string is matched (exactly) to the names of the elements in .... If there is a match then that element is evaluated unless it is missing, in which case the next non-missing element is evaluated, so for example `switch("cc", a=1, cc=, cd=, d=2)` evaluates to 2. If there is more than one match, the first matching element is used. In



the case of no match, if there is a unnamed element of . . . its value is returned. (If there is more than one such argument the first one will be used.)

The first argument is always taken to be `EXPR`: if it is named its name must (partially) match.

This is implemented as a [primitive](#) function that only evaluates its first argument and one other if one is selected.

### Value

The value of one of the elements of . . . , or `NULL`, invisibly (whenever no element is selected).

The result has the visibility (see [invisible](#)) of the element evaluated.

### Warning

Before R 2.11.0 it was necessary to avoid partial matching: an alternative `E = foo` matched the first argument `EXPR` unless that was named.

It is possible to write calls to `switch` that can be confusing and may not work in the same way in earlier versions of R. For compatibility (and clarity), always have `EXPR` as the first argument, naming it if partial matching is a possibility. For the character-string form, have a single unnamed argument as the default after the named values.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### Examples

```
require(stats)
centre <- function(x, type) {
  switch(type,
    mean = mean(x),
    median = median(x),
    trimmed = mean(x, trim = .1))
}
x <- rcauchy(10)
centre(x, "mean")
centre(x, "median")
centre(x, "trimmed")

ccc <- c("b", "QQ", "a", "A", "bb")
# note: cat() produces no output for NULL
for(ch in ccc)
  cat(ch, ":", switch(EXPR = ch, a=1, b=2:3), "\n")
for(ch in ccc)
  cat(ch, ":", switch(EXPR = ch, a=, A=1, b=2:3, "Otherwise: last"), "\n")

## Numeric EXPR does not allow a default value to be specified
## -- it is always NULL
for(i in c(-1:3, 9)) print(switch(i, 1, 2, 3, 4))

## visibility
switch(1, invisible(pi), pi)
switch(2, invisible(pi), pi)
```

**Description**

Outlines R syntax and gives the precedence of operators

**Details**

The following unary and binary operators are defined. They are listed in precedence groups, from highest to lowest.

::	:::	access variables in a name space				
\$	@	component / slot extraction				
[	[[	indexing				
^		exponentiation (right to left)				
-	+	unary minus and plus				
:		sequence operator				
%any%		special operators				
*	/	multiply, divide				
+	-	(binary) add, subtract				
<	>	<=	>=	==	!=	ordering and comparison
!		negation				
&	&&	and				
		or				
~		as in formulae				
->	->>	rightwards assignment				
=		assignment (right to left)				
<-	<<-	assignment (right to left)				
?		help (unary and binary)				

Within an expression operators of equal precedence are evaluated from left to right except where indicated.

The binary operators ::, :::, \$ and @ require names or string constants on the right hand side, and the first two also require them on the left.

The links in the **See Also** section cover most other aspects of the basic syntax.

**Note**

There are substantial precedence differences between R and S. In particular, in S ? has the same precedence as (binary) + - and & && | || have equal precedence.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[Arithmetic](#), [Comparison](#), [Control](#), [Extract](#), [Logic](#), [NumericConstants](#), [Paren](#), [Quotes](#), [Reserved](#).

The *R Language Definition* manual.

---

 Sys.getenv

*Get Environment Variables*


---

**Description**

Sys.getenv obtains the values of the environment variables.

**Usage**

```
Sys.getenv(x = NULL, unset = "")
```

**Arguments**

x	a character vector, or NULL.
unset	a character string.

**Details**

Both arguments will be coerced to character if necessary.

Setting `unset = NA` will enable unset variables and those set to the value "" to be distinguished, if the OS does.

**Value**

A vector of the same length as `x`, with the variable names as its `names` attribute. Each element holds the value of the environment variable named by the corresponding component of `x` (or the value of `unset` if no environment variable with that name was found).

On most platforms `Sys.getenv()` will return a named vector giving the values of all the environment variables, sorted in the current locale. It may be confused by names containing `=` which some platforms allow but POSIX does not. (Windows is such a platform: there names including `=` are truncated just before the first `=`.)

**See Also**

[Sys.setenv](#), [Sys.getlocale](#) for the locale in use, [getwd](#) for the working directory.

The help for [‘environment variables’](#) lists many of the environment variables used by R.

**Examples**

```
## whether HOST is set will be shell-dependent e.g. Solaris' csh does not.
Sys.getenv(c("R_HOME", "R_PAPERSIZE", "R_PRINTCMD", "HOST"))

names(s <- Sys.getenv()) # all settings (the values could be very long)

## Language and Locale settings -- but rather use Sys.getlocale()
s[grep("^L(C|ANG)", names(s))]
```

---

`Sys.getpid`*Get the Process ID of the R Session*

---

**Description**

Get the process ID of the R Session. It is guaranteed by the operating system that two R sessions running simultaneously will have different IDs, but it is possible that R sessions running at different times will have the same ID.

**Usage**

```
Sys.getpid()
```

**Value**

An integer, usually an integer between 1 and 32767 under Unix-alikes and a small positive integer under Windows.

**Examples**

```
Sys.getpid()
```

---

`Sys.glob`*Wildcard Expansion on File Paths*

---

**Description**

Function to do wildcard expansion (also known as ‘globbing’) on file paths.

**Usage**

```
Sys.glob(paths, dirmark = FALSE)
```

**Arguments**

<code>paths</code>	character vector of patterns for relative or absolute filepaths. Missing values will be ignored.
<code>dirmark</code>	logical: should matches to directories from patterns that do not already end in / have a slash appended? May not be supported on all platforms.

**Details**

This expands wildcards in file paths. For precise details, see your system’s documentation on the glob system call. There is a POSIX 1003.2 standard (see <http://www.opengroup.org/onlinepubs/009695399/functions/glob.html>) but some OSes will go beyond this. The R implementation will always do tilde-expansion (see [path.expand](#)).

All systems should interpret \* (match zero or more characters), ? (match a single character) and (probably) [ (begin a character class or range). If a filename starts with . this must be matched explicitly. By default paths ending in / will be accepted and matched only to directories.

The rest of these details are indicative (and based on the POSIX standard).

[ begins a character class. If the first character in [ . . . ] is not !, this is a character class which matches a single character against any of the characters specified. The class cannot be empty, so ] can be included provided it is first. If the first character is !, the character class matches a single character which is *none* of the specified characters.

Character classes can include ranges such as [A-Z]: include – as a character by having it first or last in a class. (The interpretation of ranges should be locale-specific, so the example is not a good idea in an Estonian locale.)

One can remove the special meaning of ?, \* and [ by preceding them by a backslash (except within a character class).

### Value

A character vector of matched file paths. The order is system-specific (but in the order of the elements of `paths`): it is normally collated in either the current locale or in byte (ASCII) order; however, on Windows collation is in the order of Unicode points.

Directory errors are normally ignored, so the matches are to accessible file paths (but not necessarily accessible files).

### See Also

[path.expand](#).

[Quotes](#) for handling backslashes in character strings.

### Examples

```
## Not run:
Sys.glob(file.path(R.home(), "library", "*", "R", "*.rdx"))

## End(Not run)
```

---

Sys.info

*Extract System and User Information*

---

### Description

Reports system and user information.

### Usage

```
Sys.info()
```

### Details

This function is not implemented on all R platforms, and returns `NULL` when not available. Where possible it is based on POSIX system calls. (Under Windows, it is obtained from Windows system calls.)

`Sys.info()` returns details of the platform R is running on, whereas [R.version](#) gives details of the platform R was built on: they may well be different.

**Value**

A character vector with fields

sysname	The operating system.
release	The OS release.
version	The OS version.
nodename	A name by which the machine is known on the network (if any).
machine	A concise description of the hardware.
login	The user's login name, or "unknown" if it cannot be ascertained.
user	The name of the real user ID, or "unknown" if it cannot be ascertained.

The first five fields come from the `uname(2)` system call. The login name comes from `getlogin(2)`, and the user name from `getpwuid(getuid())`

**Note**

The meaning of OS 'release' and 'version' is system-dependent and there is no guarantee that the node or login or user names will be what you might reasonably expect. (In particular on some Linux distributions the login name is unknown from sessions with re-directed inputs.)

**See Also**

`.Platform`, and `R.version.sessionInfo()` gives a synopsis of both your system and the R session.

**Examples**

```
Sys.info()
## An alternative (and probably better) way to get the login name on Unix
Sys.getenv("LOGNAME")
```

---

Sys.localeconv	<i>Find Details of the Numerical and Monetary Representations in the Current Locale</i>
----------------	---

---

**Description**

Get details of the numerical and monetary representations in the current locale.

**Usage**

```
Sys.localeconv()
```

**Details**

These settings are usually controlled by the environment variables `LC_NUMERIC` and `LC_MONETARY` and if not set the values of `LC_ALL` or `LANG`.

Normally R is run without looking at the value of `LC_NUMERIC`, so the decimal point remains `'.'`. So the first three of these components will not be useful unless you have set `LC_NUMERIC` in the current R session.

**Value**

A character vector with 18 named components. See your ISO C documentation for details of the meaning.

It is possible to compile R without support for locales, in which case the value will be `NULL`.

**See Also**

[Sys.setlocale](#) for ways to set locales.

**Examples**

```

Sys.localeconv()
## The results in the C locale are
##   decimal_point      thousands_sep      grouping      int_curr_symbol
##   "."                ""                ""                ""
##   currency_symbol  mon_decimal_point  mon_thousands_sep  mon_grouping
##   ""                ""                ""                ""
##   positive_sign    negative_sign      int_frac_digits     frac_digits
##   ""                ""                "127"             "127"
##   p_cs_precedes    p_sep_by_space     n_cs_precedes        n_sep_by_space
##   "127"            "127"             "127"             "127"
##   p_sign_posn      n_sign_posn
##   "127"            "127"

## Now try your default locale (which might be "C").
## Not run: old <- Sys.getlocale()
Sys.setlocale(locale = "")
Sys.localeconv()
Sys.setlocale(locale = old)
## End(Not run)

## Not run: read.table("foo", dec=Sys.localeconv()["decimal_point"])

```

---

sys.parent

*Functions to Access the Function Call Stack*

---

**Description**

These functions provide access to [environments](#) ('frames' in S terminology) associated with functions further up the calling stack.

**Usage**

```

sys.call(which = 0)
sys.frame(which = 0)
sys.nframe()
sys.function(which = 0)
sys.parent(n = 1)

sys.calls()
sys.frames()
sys.parents()

```

```

sys.on.exit()
sys.status()
parent.frame(n = 1)

```

### Arguments

`which`            the frame number if non-negative, the number of frames to go back if negative.  
`n`                 the number of generations to go back. (See the ‘Details’ section.)

### Details

`.GlobalEnv` is given number 0 in the list of frames. Each subsequent function evaluation increases the frame stack by 1 and the call, function definition and the environment for evaluation of that function are returned by `sys.call`, `sys.function` and `sys.frame` with the appropriate index.

`sys.call`, `sys.frame` and `sys.function` accept integer values for the argument `which`. Non-negative values of `which` are frame numbers whereas negative values are counted back from the frame number of the current evaluation.

The parent frame of a function evaluation is the environment in which the function was called. It is not necessarily numbered one less than the frame number of the current evaluation, nor is it the environment within which the function was defined. `sys.parent` returns the number of the parent frame if `n` is 1 (the default), the grandparent if `n` is 2, and so on. See also the Note.

`sys.nframe` returns an integer, the number of the current frame as described in the first paragraph.

`sys.calls` and `sys.frames` give a pairlist of all the active calls and frames, respectively, and `sys.parents` returns an integer vector of indices of the parent frames of each of those frames.

Notice that even though the `sys.xxx` functions (except `sys.status`) are interpreted, their contexts are not counted nor are they reported. There is no access to them.

`sys.status()` returns a list with components `sys.calls`, `sys.parents` and `sys.frames`, the results of calls to those three functions (which this will include the call to `sys.status`: see the first example).

`sys.on.exit()` returns the expression stored for use by `on.exit` in the function currently being evaluated. (Note that this differs from S, which returns a list of expressions for the current frame and its parents.)

`parent.frame(n)` is a convenient shorthand for `sys.frame(sys.parent(n))` (implemented slightly more efficiently).

### Value

`sys.call` returns a call, `sys.function` a function definition, and `sys.frame` and `parent.frame` return an environment.

For the other functions, see the ‘Details’ section.

### Note

Strictly, `sys.parent` and `parent.frame` refer to the *context* of the parent interpreted function. So internal functions (which may or may not set contexts and so may or may not appear on the call stack) are not counted, and S3 methods can also do surprising things.



## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (not `parent.frame()`.)

## See Also

[eval](#) for a usage of `sys.frame` and `parent.frame`.

## Examples

```
require(utils)

## Note: the first two examples will give different results
## if run by example().
ff <- function(x) gg(x)
gg <- function(y) sys.status()
str(ff(1))

gg <- function(y) {
  ggg <- function() {
    cat("current frame is", sys.nframe(), "\n")
    cat("parents are", sys.parents(), "\n")
    print(sys.function(0)) # ggg
    print(sys.function(2)) # gg
  }
  if(y > 0) gg(y-1) else ggg()
}
gg(3)

t1 <- function() {
  aa <- "here"
  t2 <- function() {
    ## in frame 2 here
    cat("current frame is", sys.nframe(), "\n")
    str(sys.calls()) ## list with two components t1() and t2()
    cat("parents are frame numbers", sys.parents(), "\n") ## 0 1
    print(ls(envir=sys.frame(-1))) ## [1] "aa" "t2"
    invisible()
  }
  t2()
}
t1()

test.sys.on.exit <- function() {
  on.exit(print(1))
  ex <- sys.on.exit()
  str(ex)
  cat("exiting...\n")
}
test.sys.on.exit()
## gives 'language print(1)', prints 1 on exit

## An example where the parent is not the next frame up the stack
## since method dispatch uses a frame.
as.double.foo <- function(x)
{
```

```
    str(sys.calls())
    print(sys.frames())
    print(sys.parents())
    print(sys.frame(-1)); print(parent.frame())
  }
  x
}
t2 <- function(x) as.double(x)
a <- structure(pi, class = "foo")
t2(a)
```

---

Sys.readlink

*Read File Symbolic Links*

---

### Description

Find out if a file path is a symbolic link, and if so what it is linked to, *via* the system call `readlink`. Symbolic links are a Unix concept, not implemented on Windows.

### Usage

```
Sys.readlink(paths)
```

### Arguments

`paths` character vector of file paths.

### Value

A character vector of the the same length as `paths`. The entries are the path of the file linked to, "" if the path is not a symbolic link, and NA if there is an error (e.g., the path does not exist).

### See Also

[file.symlink](#), [file.info](#)

---

Sys.setenv

*Set or Unset Environment Variables*

---

### Description

`Sys.setenv` sets environment variables (for other processes called from within R or future calls to [Sys.getenv](#) from this R process).

`Sys.unsetenv` removes environment variables.

### Usage

```
Sys.setenv(...)
```

```
Sys.unsetenv(x)
```

**Arguments**

- . . .            named arguments with values coercible to a character string.
- x                a character vector, or an object coercible to character.

**Details**

The names `setenv` and `putenv` come from different Unix traditions: R also has `Sys.putenv`, but this is now deprecated. The internal code uses `setenv` if available, otherwise `putenv`.

Non-standard R names must be quoted in `Sys.setenv`: see the examples. Most platforms (and POSIX) do not allow names containing `"="`. Windows does, but the facilities provided by R may not handle these correctly so they should be avoided.

There may be system-specific limits on the maximum length of the values of individual environment variables or of all environment variables.

**Value**

A logical vector, with elements being true if (un)setting the corresponding variable succeeded. (For `Sys.unsetenv` this includes attempting to remove a non-existent variable.)

**Note**

Not all systems need support `Sys.setenv` (although all known current platforms do) nor `Sys.unsetenv`. If `Sys.unsetenv` is not supported, it will at least try to set the value of the environment variable to `" "`, with a warning.

**See Also**

[Sys.getenv](#), [Startup](#) for ways to set environment variables for the R session.

[setwd](#) for the working directory.

The help for [‘environment variables’](#) lists many of the environment variables used by R.

**Examples**

```
print(Sys.setenv(R_TEST="testit", "A+C"=123)) # `A+C` could also be used
Sys.getenv("R_TEST")
Sys.unsetenv("R_TEST") # may warn and not succeed
Sys.getenv("R_TEST", unset=NA)
```

---

Sys.sleep

*Suspend Execution for a Time Interval*

---

**Description**

Suspend execution of R expressions for a given number of seconds

**Usage**

```
Sys.sleep(time)
```

**Arguments**

`time`            The time interval to suspend execution for, in seconds.

**Details**

Using this function allows R to be given very low priority and hence not to interfere with more important foreground tasks. A typical use is to allow a process launched from R to set itself up and read its input files before R execution is resumed.

The intention is that this function suspends execution of R expressions but wakes the process up often enough to respond to GUI events, typically every 0.5 seconds.

There is no guarantee that the process will sleep for the whole of the specified interval, and it may well take slightly longer in real time to resume execution. The resolution of the time interval is system-dependent, but will normally be down to 0.02 secs or better. (On modern Unix-alikes it will be better than 1ms.)

**Value**

Invisible NULL.

**Note**

This function may not be implemented on all systems.

**Examples**

```
testit <- function(x)
{
  p1 <- proc.time()
  Sys.sleep(x)
  proc.time() - p1 # The cpu usage should be negligible
}
testit(3.7)
```

---

sys.source

*Parse and Evaluate Expressions from a File*

---

**Description**

Parses expressions in the given file, and then successively evaluates them in the specified environment.

**Usage**

```
sys.source(file, envir = baseenv(), chdir = FALSE,
           keep.source = getOption("keep.source.pkgs"))
```

**Arguments**

<code>file</code>	a character string naming the file to be read from
<code>envir</code>	an R object specifying the environment in which the expressions are to be evaluated. May also be a list or an integer. The default value <code>NULL</code> corresponds to evaluation in the base environment. This is probably not what you want; you should typically supply an explicit <code>envir</code> argument.
<code>chdir</code>	logical; if <code>TRUE</code> , the R working directory is changed to the directory containing <code>file</code> for evaluating.
<code>keep.source</code>	logical. If <code>TRUE</code> , functions keep their source including comments, see <a href="#">options</a> ( <code>keep.source = *</code> ) for more details.

**Details**

For large files, `keep.source = FALSE` may save quite a bit of memory.

In order for the code being evaluated to use the correct environment (for example, in global assignments), source code in packages should call `topenv()`, which will return the name space, if any, the environment set up by `sys.source`, or the global environment if a saved image is being used.

**See Also**

[source](#), and [library](#) which uses `sys.source`.

**Examples**

```
## a simple way to put some objects in an environment
## high on the search path
tmp <- tempfile()
writeLines("aaa <- pi", tmp)
env <- attach(NULL, name = "myenv")
sys.source(tmp, env)
unlink(tmp)
search()
aaa
detach("myenv")
```

---

Sys.time

*Get Current Date and Time*

---

**Description**

`Sys.time` and `Sys.Date` returns the system's idea of the current date with and without time.

**Usage**

```
Sys.time()
Sys.Date()
```

**Details**

`Sys.time` returns an absolute date-time value which can be converted to various time zones and may return different days.

`Sys.Date` returns the current day in the current [timezone](#).

**Value**

`Sys.time` returns an object of class "POSIXct" (see [DateTimeClasses](#)). On almost all systems it will have sub-second accuracy: on systems conforming to POSIX 1003.1-2001 the time will be reported in microsecond increments. On Windows it increments in clock ticks (1/60 of a second) reported to millisecond accuracy.

`Sys.Date` returns an object of class "Date" (see [Date](#)).

**Note**

`Sys.time` may return fractional seconds, but they are ignored by the default conversions (e.g. printing) for class "POSIXct". See the examples and `format.POSIXct` for ways to reveal them.

**See Also**

`date` for the system time in a fixed-format character string; the elapsed time component of `proc.time` for possibly finer resolution in changes in time.

`Sys.timezone`.

**Examples**

```

Sys.time()
## print with possibly greater accuracy:
op <- options(digits.secs=6)
Sys.time()
options(op)

## locale-specific version of date()
format(Sys.time(), "%a %b %d %X %Y")

Sys.Date()

```

---

Sys.which

*Find Full Paths of Executables*


---

**Description**

This is an interface to the system command `which`.

**Usage**

```

Sys.which(names)

```

**Arguments**

`names`                      Character vector of names of possible executables.

**Details**

The system command `which` reports on the full names of an executable (including an executable script) found on the current path.

**Value**

A character vector of the same length as `names`, named by `names`. The elements are either the full path to the executable/script or some indication that no executable of that name was found. Typically the indication is "", but this does depend on the OS (and is a message on Solaris).

**Examples**

```
## the first two are likely to exist everywhere
## texi2dvi exists on most Unix-alikes and under MiKTeX
Sys.which(c("ftp", "ping", "texi2dvi", "this-does-not-exist"))
```

---

system

*Invoke a System Command*


---

**Description**

`system` invokes the OS command specified by `command`.

**Usage**

```
system(command, intern = FALSE, ignore.stderr = FALSE,
        wait = TRUE, input = NULL, show.output.on.console = TRUE,
        minimized = FALSE, invisible = TRUE)
```

**Arguments**

<code>command</code>	the system command to be invoked, as a string.
<code>intern</code>	a logical (not NA) which indicates whether to make the output of the command an R object. Not available unless <code>popen</code> is supported on the platform (which it almost always is).
<code>ignore.stderr</code>	a logical (not NA) indicating whether error messages written to 'stderr' should be ignored.
<code>wait</code>	a logical (not NA) indicating whether the R interpreter should wait for the command to finish, or run it asynchronously. This will be ignored (and the interpreter will always wait) if <code>intern = TRUE</code> .
<code>input</code>	if a character vector is supplied, this is copied one string per line to a temporary file, and the standard input of <code>command</code> is redirected to the file.
<code>show.output.on.console</code> , <code>minimized</code> , <code>invisible</code>	arguments that are accepted on Windows but ignored on this platform, with a warning.

**Details**

`command` is parsed as a command plus arguments separated by spaces. So if the path to the command (or a filepath argument) contains spaces, it must be quoted e.g. by `shQuote`.

How the command is run differs by platform: Unix-alikes use a shell (normally `/bin/sh`), and Windows executes the command directly (extensions `.exe`, `.com`) or as a batch file (extensions `.cmd` and `.bat`). This means that redirection, pipes, ... cannot be used on Windows, which has a function `shell` for use when shell facilities are needed.

If `intern` is `TRUE` then `popen` is used to invoke the command and the output collected, line by line, into an R [character](#) vector. If `intern` is `FALSE` then the C function `system` is used to invoke the command.

The ordering of arguments after the first two has changed from time to time: it is recommended to name all arguments after the first.

### Value

If `intern = TRUE`, a character vector giving the output of the command, one line per character string. (Output lines of more than 8095 characters will be split.) If the command could not be run or gives an error this will be reported on the shell's `'stderr'` (unless `popen` is not supported, when there is an R error).

If `intern = FALSE`, the return value is an error code (0 for success), given the invisible attribute (so needs to be printed explicitly). If the command could not be run for any reason, the value is  $256 \times 127 = 52512$ . Otherwise if `wait = TRUE` the value is 256 times the error code returned by the command, and if `wait = FALSE` it is 0 (the conventional success value).

### Stdout and stderr

Error messages written to `'stderr'` will be sent by the shell to the terminal unless `ignore.stderr = TRUE`. They can be captured (in the most likely shells) by

```
system("some command 2>&1", intern=TRUE)
```

What happens to output sent to `'stdout'` and `'stderr'` if `intern = FALSE` is interface-specific, and it is unsafe to assume that such messages will appear on a console (they do on the Mac OS X console, but not on some others).

### Note

`wait` is implemented by appending `&` to the command: this is shell-dependent, but required by POSIX and so widely supported.

### See Also

[.Platform](#) for platform-specific variables.  
[pipe](#) to set up a pipe connection.

### Examples

```
# list all files in the current directory using the -F flag
## Not run: system("ls -F")

# t1 is a character vector, each one
# representing a separate line of output from who
# (if the platform has popen and who)
t1 <- try(system("who", intern = TRUE))

try(system("ls fizzlepuzzli", intern = TRUE, ignore.stderr = TRUE))
# empty since file doesn't exist
```



---

system.file	<i>Find Names of R System Files</i>
-------------	-------------------------------------

---

**Description**

Finds the full file names of files in packages etc.

**Usage**

```
system.file(..., package = "base", lib.loc = NULL)
```

**Arguments**

...	character strings, specifying subdirectory and file(s) within some package. The default, none, returns the root of the package. Wildcards are not supported.
package	a character string with the name of a single package. An error occurs if more than one package name is given.
lib.loc	a character vector with path names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries.

**Value**

A character vector of positive length, containing the file names that matched ..., or the empty string, "", if none matched. If matching the root of a package, there is no trailing separator.

As a special case, `system.file()` gives the root of the **base** package only.

**See Also**

[R.home](#) for the root directory of the R installation, [list.files](#)

**Examples**

```
system.file()                # The root of the 'base' package
system.file(package = "stats") # The root of package 'stats'
system.file("INDEX")
system.file("help", "AnIndex", package = "splines")
```

---

system.time	<i>CPU Time Used</i>
-------------	----------------------

---

**Description**

Return CPU (and other) times that `expr` used.

**Usage**

```
system.time(expr, gcFirst = TRUE)
unix.time(expr, gcFirst = TRUE)
```

**Arguments**

<code>expr</code>	Valid R expression to be timed.
<code>gcFirst</code>	Logical - should a garbage collection be performed immediately before the timing? Default is TRUE.

**Details**

`system.time` calls the function `proc.time`, evaluates `expr`, and then calls `proc.time` once more, returning the difference between the two `proc.time` calls.

`unix.time` is an alias of `system.time`, for compatibility with S.

Timings of evaluations of the same expression can vary considerably depending on whether the evaluation triggers a garbage collection. When `gcFirst` is TRUE a garbage collection (`gc`) will be performed immediately before the evaluation of `expr`. This will usually produce more consistent timings.

**Value**

A object of class "proc\_time": see `proc.time` for details.

**Note**

It is possible to compile R without support for `system.time`, when the function will throw an error.

**See Also**

`proc.time`, `time` which is for time series.

**Examples**

```
require(stats)
system.time(for(i in 1:100) mad(runif(1000)))
## Not run:
exT <- function(n = 10000) {
  # Purpose: Test if system.time works ok; n: loop size
  system.time(for(i in 1:n) x <- mean(rt(1000, df=4)))
}
#-- Try to interrupt one of the following (using Ctrl-C / Escape):
exT()          #- about 4 secs on a 2.5GHz Xeon
system.time(exT())  #~ +/- same

## End(Not run)
```

**Description**

Given a matrix or `data.frame` `x`, `t` returns the transpose of `x`.

**Usage**

```
t(x)
```

**Arguments**

`x` a matrix or data frame, typically.

**Details**

This is a generic function for which methods can be written. The description here applies to the default and "data.frame" methods.

A data frame is first coerced to a matrix: see [as.matrix](#). When `x` is a vector, it is treated as a column, i.e., the result is a 1-row matrix.

**Value**

A matrix, with `dim` and `dimnames` constructed appropriately from those of `x`, and other attributes except names copied across.

**Note**

The *conjugate* transpose of a complex matrix  $A$ , denoted  $A^H$  or  $A^*$ , is computed as `Conj(t(A))`.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[aperm](#) for permuting the dimensions of arrays.

**Examples**

```
a <- matrix(1:30, 5, 6)
ta <- t(a) ##-- i.e., a[i, j] == ta[j, i] for all i, j :
for(j in seq(ncol(a)))
  if(! all(a[, j] == ta[j, ])) stop("wrong transpose")
```

---

table	<i>Cross Tabulation and Table Creation</i>
-------	--

---

**Description**

`table` uses the cross-classifying factors to build a contingency table of the counts at each combination of factor levels.

**Usage**

```

table(..., exclude = if (useNA == "no") c(NA, NaN), useNA = c("no",
  "ifany", "always"), dnn = list.names(...), deparse.level = 1)

as.table(x, ...)
is.table(x)

## S3 method for class 'table':
as.data.frame(x, row.names = NULL, ...,
  responseName = "Freq", stringsAsFactors = TRUE)

```

**Arguments**

`...` one or more objects which can be interpreted as factors (including character strings), or a list (or data frame) whose components can be so interpreted. (For `as.table` and `as.data.frame`, arguments passed to specific methods.)

`exclude` levels to remove from all factors in `...`. If set to `NULL`, it implies `useNA="always"`.

`useNA` whether to include extra NA levels in the table.

`dnn` the names to be given to the dimensions in the result (the *dimnames names*).

`deparse.level` controls how the default `dnn` is constructed. See details.

`x` an arbitrary R object, or an object inheriting from class "table" for the `as.data.frame` method.

`row.names` a character vector giving the row names for the data frame.

`responseName` The name to be used for the column of table entries, usually counts.

`stringsAsFactors` logical: should the classifying factors be returned as factors (the default) or character vectors?

**Details**

If the argument `dnn` is not supplied, the internal function `list.names` is called to compute the 'dimname names'. If the arguments in `...` are named, those names are used. For the remaining arguments, `deparse.level = 0` gives an empty name, `deparse.level = 1` uses the supplied argument if it is a symbol, and `deparse.level = 2` will deparse the argument.

Only when `exclude` is specified and non-NULL (i.e., not by default), will `table` potentially drop levels of factor arguments.

Both `exclude` and `useNA` operate on an "all or none" basis. If you want to control the dimensions of a multiway table separately, modify each argument using `factor` or `addNA`.

The summary method for class "table" (used for objects created by `table` or `xtabs`) which gives basic information and performs a chi-squared test for independence of factors (note that the function `chisq.test` currently only handles 2-d tables).

**Value**

`table()` returns a *contingency table*, an object of class "table", an array of integer values. Note that unlike S the result is always an array, a 1D array if one factor is given.

`as.table` and `is.table` coerce to and test for contingency table, respectively.

The `as.data.frame` method for objects inheriting from class "table" can be used to convert the array-based representation of a contingency table to a data frame containing the classifying factors and the corresponding entries (the latter as component named by `responseName`). This is the inverse of `xtabs`.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

`tabulate` is the underlying function and allows finer control.

Use `fTable` for printing (and more) of multidimensional tables. `margin.table`, `prop.table`, `addmargins`.

## Examples

```
require(stats) # for rpois and xtabs
## Simple frequency distribution
table(rpois(100,5))
## Check the design:
with(warpbreaks, table(wool, tension))
table(state.division, state.region)

# simple two-way contingency table
with(airquality, table(cut(Temp, quantile(Temp)), Month))

a <- letters[1:3]
table(a, sample(a)) # dnn is c("a", "")
table(a, sample(a), deparse.level = 0) # dnn is c("", "")
table(a, sample(a), deparse.level = 2) # dnn is c("a", "sample(a)")

## xtabs() <-> as.data.frame.table() :
UCBAdmissions ## already a contingency table
DF <- as.data.frame(UCBAdmissions)
class(tab <- xtabs(Freq ~ ., DF)) # xtabs & table
## tab *is* "the same" as the original table:
all(tab == UCBAdmissions)
all.equal(dimnames(tab), dimnames(UCBAdmissions))

a <- rep(c(NA, 1/0:3), 10)
table(a)
table(a, exclude=NULL)
b <- factor(rep(c("A", "B", "C"), 10))
table(b)
table(b, exclude="B")
d <- factor(rep(c("A", "B", "C"), 10), levels=c("A", "B", "C", "D", "E"))
table(d, exclude="B")
print(table(b,d), zero.print = ".")

## NA counting:
is.na(d) <- 3:4
d. <- addNA(d)
d.[1:7]
table(d.) # ", exclude = NULL" is not needed
```

```
## i.e., if you want to count the NA's of 'd', use
table(d, useNA="ifany")

## Two-way tables with NA counts. The 3rd variant is absurd, but shows
## something that cannot be done using exclude or useNA.
with(airquality,
     table(OzHi=Ozone > 80, Month, useNA="ifany"))
with(airquality,
     table(OzHi=Ozone > 80, Month, useNA="always"))
with(airquality,
     table(OzHi=Ozone > 80, addNA(Month)))
```

---

tabulate

*Tabulation for Vectors*


---

### Description

`tabulate` takes the integer-valued vector `bin` and counts the number of times each integer occurs in it.

### Usage

```
tabulate(bin, nbins = max(1, bin), na.rm = TRUE)
```

### Arguments

`bin` a numeric vector (of positive integers), or a factor.  
`nbins` the number of bins to be used.

### Details

`tabulate` is used as the basis of the `table` function.

If `bin` is a factor, its internal integer representation is tabulated.

If the elements of `bin` are numeric but not integers, they are truncated to the nearest integer.

### Value

An integer vector (without names). There is a bin for each of the values 1, ..., `nbins`; values outside that range and NAs are (silently) ignored.

### See Also

`table`, `factor`.

### Examples

```
tabulate(c(2,3,5))
tabulate(c(2,3,3,5), nbins = 10)
tabulate(c(-2,0,2,3,3,5)) # -2 and 0 are ignored
tabulate(c(-2,0,2,3,3,5), nbins = 3)
tabulate(factor(letters[1:10]))
```

tapply

*Apply a Function Over a Ragged Array***Description**

Apply a function to each cell of a ragged array, that is to each (non-empty) group of values given by a unique combination of the levels of certain factors.

**Usage**

```
tapply(X, INDEX, FUN = NULL, ..., simplify = TRUE)
```

**Arguments**

X	an atomic object, typically a vector.
INDEX	list of factors, each of same length as X. The elements are coerced to factors by <code>as.factor</code> .
FUN	the function to be applied, or NULL. In the case of functions like <code>+</code> , <code>%*%</code> , etc., the function name must be backquoted or quoted. If FUN is NULL, tapply returns a vector which can be used to subscript the multi-way array tapply normally produces.
...	optional arguments to FUN: the Note section.
simplify	If FALSE, tapply always returns an array of mode "list". If TRUE (the default), then if FUN always returns a scalar, tapply returns an array with the mode of the scalar.

**Value**

If FUN is not NULL, it is passed to `match.fun`, and hence it can be a function or a symbol or character string naming a function.

When FUN is present, tapply calls FUN for each cell that has any data in it. If FUN returns a single atomic value for each such cell (e.g., functions `mean` or `var`) and when `simplify` is TRUE, tapply returns a multi-way [array](#) containing the values, and NA for the empty cells. The array has the same number of dimensions as INDEX has components; the number of levels in a dimension is the number of levels (`nlevels()`) in the corresponding component of INDEX. Note that if the return value has a class (e.g. an object of class "Date") the class is discarded.

Note that contrary to S, `simplify = TRUE` always returns an array, possibly 1-dimensional.

If FUN does not return a single atomic value, tapply returns an array of mode `list` whose components are the values of the individual calls to FUN, i.e., the result is a list with a `dim` attribute.

When there is an array answer, its `dimnames` are named by the names of INDEX and are based on the levels of the grouping factors (possibly after coercion).

For a list result, the elements corresponding to empty cells are NULL.

**Note**

Optional arguments to FUN supplied by the `...` argument are not divided into cells. It is therefore inappropriate for FUN to expect additional arguments with the same length as X.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

the convenience functions [by](#) and [aggregate](#) (using [tapply](#)); [apply](#), [lapply](#) with its versions [sapply](#) and [mapply](#).

## Examples

```
require(stats)
groups <- as.factor(rbinom(32, n = 5, prob = 0.4))
tapply(groups, groups, length) #- is almost the same as
table(groups)

## contingency table from data.frame : array with named dimnames
tapply(warpbreaks$breaks, warpbreaks[,-1], sum)
tapply(warpbreaks$breaks, warpbreaks[, 3, drop = FALSE], sum)

n <- 17; fac <- factor(rep(1:3, length = n), levels = 1:5)
table(fac)
tapply(1:n, fac, sum)
tapply(1:n, fac, sum, simplify = FALSE)
tapply(1:n, fac, range)
tapply(1:n, fac, quantile)

## example of ... argument: find quarterly means
tapply(presidents, cycle(presidents), mean, na.rm = TRUE)

ind <- list(c(1, 2, 2), c("A", "A", "B"))
table(ind)
tapply(1:3, ind) #-> the split vector
tapply(1:3, ind, sum)
```

---

taskCallback

*Add or Remove a Top-Level Task Callback*

---

## Description

`addTaskCallback` registers an R function that is to be called each time a top-level task is completed.

`removeTaskCallback` un-registers a function that was registered earlier via `addTaskCallback`.

These provide low-level access to the internal/native mechanism for managing task-completion actions. One can use [taskCallbackManager](#) at the S-language level to manage S functions that are called at the completion of each task. This is easier and more direct.

## Usage

```
addTaskCallback(f, data = NULL, name = character(0))
removeTaskCallback(id)
```



**Arguments**

<code>f</code>	the function that is to be invoked each time a top-level task is successfully completed. This is called with 5 or 4 arguments depending on whether <code>data</code> is specified or not, respectively. The return value should be a logical value indicating whether to keep the callback in the list of active callbacks or discard it.
<code>data</code>	if specified, this is the 5-th argument in the call to the callback function <code>f</code> .
<code>id</code>	a string or an integer identifying the element in the internal callback list to be removed. Integer indices are 1-based, i.e the first element is 1. The names of currently registered handlers is available using <code>getTaskCallbackNames</code> and is also returned in a call to <code>addTaskCallback</code> .
<code>name</code>	character: names to be used.

**Details**

Top-level tasks are individual expressions rather than entire lines of input. Thus an input line of the form `expression1 ; expression2` will give rise to 2 top-level tasks.

A top-level task callback is called with the expression for the top-level task, the result of the top-level task, a logical value indicating whether it was successfully completed or not (always TRUE at present), and a logical value indicating whether the result was printed or not. If the `data` argument was specified in the call to `addTaskCallback`, that value is given as the fifth argument.

The callback function should return a logical value. If the value is FALSE, the callback is removed from the task list and will not be called again by this mechanism. If the function returns TRUE, it is kept in the list and will be called on the completion of the next top-level task.

**Value**

`addTaskCallback` returns an integer value giving the position in the list of task callbacks that this new callback occupies. This is only the current position of the callback. It can be used to remove the entry as long as no other values are removed from earlier positions in the list first.

`removeTaskCallback` returns a logical value indicating whether the specified element was removed. This can fail (i.e., return FALSE) if an incorrect name or index is given that does not correspond to the name or position of an element in the list.

**Note**

This is an experimental feature and the interface may be changed in the future.

There is also C-level access to top-level task callbacks to allow C routines rather than R functions be used.

**See Also**

`getTaskCallbackNames`      `taskCallbackManager`      <http://developer.r-project.org/TaskHandlers.pdf>

**Examples**

```
times <- function(total = 3, str="Task a") {
  ctr <- 0

  function(expr, value, ok, visible) {
```

```

    ctr <- ctr + 1
    cat(str, ctr, "\n")
    if(ctr == total) {
      cat("handler removing itself\n")
    }
    return(ctr < total)
  }
}

# add the callback that will work for
# 4 top-level tasks and then remove itself.
n <- addTaskCallback(times(4))

# now remove it, assuming it is still first in the list.
removeTaskCallback(n)

## Not run:
# There is no point in running this
# as
addTaskCallback(times(4))

sum(1:10)
sum(1:10)
sum(1:10)
sum(1:10)
sum(1:10)

## End(Not run)

```

---

```
taskCallbackManager
```

*Create an R-level Task Callback Manager*

---

## Description

This provides an entirely S-language mechanism for managing callbacks or actions that are invoked at the conclusion of each top-level task. Essentially, we register a single R function from this manager with the underlying, native task-callback mechanism and this function handles invoking the other R callbacks under the control of the manager. The manager consists of a collection of functions that access shared variables to manage the list of user-level callbacks.

## Usage

```
taskCallbackManager(handlers = list(), registered = FALSE,
  verbose = FALSE)
```

## Arguments

`handlers` this can be a list of callbacks in which each element is a list with an element named "f" which is a callback function, and an optional element named "data" which is the 5-th argument to be supplied to the callback when it is invoked. Typically this argument is not specified, and one uses `add` to register callbacks after the manager is created.

registered	a logical value indicating whether the <code>evaluate</code> function has already been registered with the internal task callback mechanism. This is usually <code>FALSE</code> and the first time a callback is added via the <code>add</code> function, the <code>evaluate</code> function is automatically registered. One can control when the function is registered by specifying <code>TRUE</code> for this argument and calling <code>addTaskCallback</code> manually.
verbose	a logical value, which if <code>TRUE</code> , causes information to be printed to the console about certain activities this dispatch manager performs. This is useful for debugging callbacks and the handler itself.

### Value

A list containing 6 functions:

<code>add</code>	register a callback with this manager, giving the function, an optional 5-th argument, an optional name by which the callback is stored in the list, and a <code>register</code> argument which controls whether the <code>evaluate</code> function is registered with the internal C-level dispatch mechanism if necessary.
<code>remove</code>	remove an element from the manager's collection of callbacks, either by name or position/index.
<code>evaluate</code>	the 'real' callback function that is registered with the C-level dispatch mechanism and which invokes each of the R-level callbacks within this manager's control.
<code>suspend</code>	a function to set the suspend state of the manager. If it is suspended, none of the callbacks will be invoked when a task is completed. One sets the state by specifying a logical value for the <code>status</code> argument.
<code>register</code>	a function to register the <code>evaluate</code> function with the internal C-level dispatch mechanism. This is done automatically by the <code>add</code> function, but can be called manually.
<code>callbacks</code>	returns the list of callbacks being maintained by this manager.

### Note

This is an experimental feature and the interface may be changed in the future.

### See Also

`addTaskCallback`, `removeTaskCallback`, `getTaskCallbackNames` \ <http://developer.r-project.org/TaskHandlers.pdf>

### Examples

```
# create the manager
h <- taskCallbackManager()

# add a callback
h$add(function(expr, value, ok, visible) {
  cat("In handler\n")
  return(TRUE)
}, name = "simpleHandler")

# look at the internal callbacks.
getTaskCallbackNames()
```

```
# look at the R-level callbacks
names(h$callbacks())

getTaskCallbackNames()
removeTaskCallback("R-taskCallbackManager")
```

---

taskCallbackNames *Query the Names of the Current Internal Top-Level Task Callbacks*

---

## Description

This provides a way to get the names (or identifiers) for the currently registered task callbacks that are invoked at the conclusion of each top-level task. These identifiers can be used to remove a callback.

## Usage

```
getTaskCallbackNames()
```

## Value

A character vector giving the name for each of the registered callbacks which are invoked when a top-level task is completed successfully. Each name is the one used when registering the callbacks and returned as the in the call to [addTaskCallback](#).

## Note

One can use [taskCallbackManager](#) to manage user-level task callbacks, i.e., S-language functions, entirely within the S language and access the names more directly.

## See Also

[addTaskCallback](#), [removeTaskCallback](#), [taskCallbackManager](#)\ <http://developer.r-project.org/TaskHandlers.pdf>

## Examples

```
n <- addTaskCallback(function(expr, value, ok, visible) {
  cat("In handler\n")
  return(TRUE)
}, name = "simpleHandler")

getTaskCallbackNames()

# now remove it by name
removeTaskCallback("simpleHandler")

h <- taskCallbackManager()
h$add(function(expr, value, ok, visible) {
  cat("In handler\n")
  return(TRUE)
}, name = "simpleHandler")
getTaskCallbackNames()
removeTaskCallback("R-taskCallbackManager")
```

---

`tempfile`*Create Names for Temporary Files*

---

**Description**

`tempfile` returns a vector of character strings which can be used as names for temporary files.

**Usage**

```
tempfile(pattern = "file", tmpdir = tmpdir())
tmpdir()
```

**Arguments**

<code>pattern</code>	a non-empty character vector giving the initial part of the name.
<code>tmpdir</code>	a non-empty character vector giving the directory name

**Details**

If `pattern` has length greater than one then the result is of the same length giving a temporary file name for each component of `pattern`.

The names are very likely to be unique among calls to `tempfile` in an R session and across simultaneous R sessions. The filenames are guaranteed not to be currently in use.

The file name is made of the `pattern` and a random suffix in hex. By default, the filenames will be in the directory given by `tmpdir()`. This will be a subdirectory of the temporary directory found by the following rule. The environment variables `TMPDIR`, `TMP` and `TEMP` are checked in turn and the first found which points to a writable directory is used: if none succeeds `/tmp` is used.

**Value**

For `tempfile` a character vector giving the names of possible (temporary) files. Note that no files are generated by `tempfile`.

For `tmpdir`, the path of the per-session temporary directory.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[unlink](#) for deleting files.

**Examples**

```
tempfile(c("ab", "a b c")) # give file name with spaces in!
tmpdir() # working on all platforms with quite platform dependent result
```

---

textConnection      *Text Connections*


---

## Description

Input and output text connections.

## Usage

```
textConnection(object, open = "r", local = FALSE,
               encoding = c("", "bytes", "UTF-8"))
```

```
textConnectionValue(con)
```

## Arguments

object	character. A description of the connection. For an input this is an R character vector object, and for an output connection the name for the R character vector to receive the output, or NULL (for none).
open	character. Either "r" (or equivalently "") for an input connection or "w" or "a" for an output connection.
local	logical. Used only for output connections. If TRUE, output is assigned to a variable in the calling environment. Otherwise the global environment is used.
encoding	character. Used only for input connections. How marked strings in object should be handled: converted to the current locale, used byte-by-byte or translated to UTF-8.
con	An output text connection.

## Details

An input text connection is opened and the character vector is copied at time the connection object is created, and `close` destroys the copy.

An output text connection is opened and creates an R character vector of the given name in the user's workspace or in the calling environment, depending on the value of the `local` argument. This object will at all times hold the completed lines of output to the connection, and `isIncomplete` will indicate if there is an incomplete final line. Closing the connection will output the final line, complete or not. (A line is complete once it has been terminated by end-of-line, represented by "\n" in R.) The output character vector has locked bindings (see `lockBinding`) until `close` is called on the connection. The character vector can also be retrieved *via* `textConnectionValue`, which is the only way to do so if `object = NULL`. If the current locale is detected as Latin-1 or UTF-8, non-ASCII elements of the character vector will be marked accordingly (see `Encoding`).

Opening a text connection with `mode = "a"` will attempt to append to an existing character vector with the given name in the user's workspace or the calling environment. If none is found (even if an object exists of the right name but the wrong type) a new character vector will be created, with a warning.

You cannot `seek` on a text connection, and `seek` will always return zero as the position.

**Value**

For `textConnection`, a connection object of class `"textConnection"` which inherits from class `"connection"`.

For `textConnectionValue`, a character vector.

**Note**

As output text connections keep the character vector up to date line-by-line, they are relatively expensive to use, and it is often better to use an anonymous `file()` connection to collect output.

On (rare) platforms where `vsprintf` does not return the needed length of output there is a 100,000 character limit on the length of line for output connections: longer lines will be truncated with a warning.

**References**

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.  
[S has input text connections only.]

**See Also**

[connections](#), [showConnections](#), [pushBack](#), [capture.output](#).

**Examples**

```
zz <- textConnection(LETTERS)
readLines(zz, 2)
scan(zz, "", 4)
pushBack(c("aa", "bb"), zz)
scan(zz, "", 4)
close(zz)

zz <- textConnection("foo", "w")
writeLines(c("testit1", "testit2"), zz)
cat("testit3 ", file=zz)
isIncomplete(zz)
cat("testit4\n", file=zz)
isIncomplete(zz)
close(zz)
foo

## Not run: # capture R output: use part of example from help(lm)
zz <- textConnection("foo", "w")
ctl <- c(4.17, 5.58, 5.18, 6.11, 4.5, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)
sink(zz)
anova(lm.D9 <- lm(weight ~ group))
cat("\nSummary of Residuals:\n\n")
summary(resid(lm.D9))
sink()
close(zz)
cat(foo, sep = "\n")

## End(Not run)
```

---

tilde	<i>Tilde Operator</i>
-------	-----------------------

---

### Description

Tilde is used to separate the left- and right-hand sides in model formula.

### Usage

```
y ~ model
```

### Arguments

`y`, `model`      symbolic expressions.

### Details

The left-hand side is optional, and one-sided formulae are used in some contexts.

### References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models*. Chapter 2 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

### See Also

[formula](#)

---

timezones	<i>Time Zones</i>
-----------	-------------------

---

### Description

Information about time zones in R. `Sys.timezone` returns the current time zone.

### Usage

```
Sys.timezone()
```

### Details

Time zones are a system-specific topic, but in recent versions of R almost all R platforms use the same underlying code, used by Linux, Mac OS X, Solaris, AIX, FreeBSD, Sun Java  $\geq 1.4$  and Tcl  $\geq 8.5$ , and supplied with R on Windows.

It is not in general possible to retrieve the system's own name(s) for the current timezone, but `Sys.timezone` will retrieve the name it uses for the current time (and the name may differ depending on whether daylight saving time is in effect).

On most platforms it is possible to set the time zone via the environment variable `TZ`: see the section on 'Time zone names' for suitable values.



Note that the principal difficulty with time zones is their individual history: over the last 100 years places have changed their affiliation between major time zones, have opted out of (or in to) DST in various years or adopted rule changes late or not at all. This often involves tiny administrative units in the US/Canada: Iowa had 23 different implementations of DST in the 1960's!

Time zones did not come into use until the second half of the nineteenth century, and DST was first introduced in the early twentieth century, most widely during the First World War (in 1916). The most common implementation of `POSIXct` is a signed 32-bit integers and so only goes back to the end of 1901: on such systems `R` assumes that dates prior to that are in the same time zone as they were in 1902.

### Value

`Sys.timezone` returns an OS-specific character string, possibly an empty string. Typically this is an abbreviation such as "EST".

### Time zone names

Where OSes describe their valid time zones can be obscure. The help for the C function `tzset` can be helpful, but it can also be inaccurate. There is a cumbersome POSIX specification (listed under environment variable `TZ` at [http://www.opengroup.org/onlinepubs/009695399/basedefs/xbd\\_chap08.html](http://www.opengroup.org/onlinepubs/009695399/basedefs/xbd_chap08.html)), which is often at least partially supported, but there usually are other more user-friendly ways to specify timezones.

Many systems make use of a timezone database compiled by Arthur Olson, in which the preferred way to refer to a time zone by a location (typically of a city) e.g. `Europe/London`, `America/Los_Angeles`, `Pacific/Easter`. Some traditional designations are also allowed such as `EST5EDT` or `GB`. (Beware that some of these designations may not be what you think: in particular `EST` is a time zone used in Canada *without* daylight savings time, and not `EST5EDT` nor (Australian) Eastern Standard Time.) The designation can also be an optional colon prepended to the path to a file giving compiled zone information (and the examples above are all files in a system-specific location). See <http://www.twinsun.com/tz/tz-link.htm> for more details and references.

For most Unix-alikes use the Olson databases. The system-specific default location in the file system varies, e.g. `‘/usr/share/zoneinfo’`, `‘/usr/etc/zoneinfo’`, `‘/usr/lib/zoneinfo’` or `‘/usr/share/lib/zoneinfo’`.

### Note

There is currently (2007/8) considerable disruption over changes to the timings of the DST transitions, aimed at energy conservation. These often have short notice and time zone databases may not be up to date (even if the OS has been updated recently).

Note that except on Windows, the operation of time zones is an OS service, and even on Windows a third-party database is used and can be updated (see the section on ‘Time zone names’). Incorrect results will never be an `R` issue, so please ensure that you have the courtesy not to blame `R` for them.

### See Also

`Sys.time`, `as.POSIXlt`.

[http://en.wikipedia.org/wiki/Time\\_zone](http://en.wikipedia.org/wiki/Time_zone) and <http://www.twinsun.com/tz/tz-link.htm> for extensive sets of links.

**Examples**

```
Sys.timezone()
```

---

`toString`*Convert an R Object to a Character String*

---

**Description**

This is a helper function for `format` to produce a single character string describing an R object.

**Usage**

```
toString(x, ...)  
  
## Default S3 method:  
toString(x, width = NULL, ...)
```

**Arguments**

<code>x</code>	The object to be converted.
<code>width</code>	Suggestion for the maximum field width. Values of <code>NULL</code> or <code>0</code> indicate no maximum. The minimum value accepted is 6 and smaller values are taken as 6.
<code>...</code>	Optional arguments passed to or from methods.

**Details**

This is a generic function for which methods can be written: only the default method is described here. Most methods should honor the `width` argument to specify the maximum display width (as measured by `nchar(type = "width")` of the result.

The default method first converts `x` to character and then concatenates the elements separated by `", "`. If `width` is supplied and is not `NULL`, the default method returns the first `width - 4` characters of the result with `....` appended, if the full result would use more than `width` characters.

**Value**

A character vector of length 1 is returned.

**Author(s)**

Robert Gentleman

**See Also**

`format`

**Examples**

```
x <- c("a", "b", "aaaaaaaaaa")  
toString(x)  
toString(x, width=8)
```

---

 trace
 

---

*Interactive Tracing and Debugging of Calls to a Function or Method*


---

**Description**

A call to `trace` allows you to insert debugging code (e.g., a call to `browser` or `recover`) at chosen places in any function. A call to `untrace` cancels the tracing. Specified methods can be traced the same way, without tracing all calls to the function. Trace code can be any R expression. Tracing can be temporarily turned on or off globally by calling `tracingState`.

**Usage**

```
trace(what, tracer, exit, at, print, signature,
      where = topenv(parent.frame()), edit = FALSE)
untrace(what, signature = NULL, where = topenv(parent.frame()))

tracingState(on = NULL)
.doTrace(expr, msg)
```

**Arguments**

<code>what</code>	The name (quoted or not) of a function to be traced or untraced. For <code>untrace</code> or for <code>trace</code> with more than one argument, more than one name can be given in the quoted form, and the same action will be applied to each one.
<code>tracer</code>	Either a function or an unevaluated expression. The function will be called or the expression will be evaluated either at the beginning of the call, or before those steps in the call specified by the argument <code>at</code> . See the details section.
<code>exit</code>	Either a function or an unevaluated expression. The function will be called or the expression will be evaluated on exiting the function. See the details section.
<code>at</code>	optional numeric vector or list. If supplied, <code>tracer</code> will be called just before the corresponding step in the body of the function. See the details section.
<code>print</code>	If <code>TRUE</code> (as per default), a descriptive line is printed before any trace expression is evaluated.
<code>signature</code>	If this argument is supplied, it should be a signature for a method for function <code>what</code> . In this case, the method, and <i>not</i> the function itself, is traced.
<code>edit</code>	For complicated tracing, such as tracing within a loop inside the function, you will need to insert the desired calls by editing the body of the function. If so, supply the <code>edit</code> argument either as <code>TRUE</code> , or as the name of the editor you want to use. Then <code>trace()</code> will call <code>edit</code> and use the version of the function after you edit it. See the details section for additional information.
<code>where</code>	where to look for the function to be traced; by default, the top-level environment of the call to <code>trace</code> .  An important use of this argument is to trace a function when it is called from a package with a name space. The current name space mechanism imports the functions to be called (with the exception of functions in the base package). The functions being called are <i>not</i> the same objects seen from the top-level (in general, the imported packages may not even be attached). Therefore, you must ensure that the correct versions are being traced. The way to do this is to set argument <code>where</code> to a function in the name space. The tracing computations

	will then start looking in the environment of that function (which will be the name space of the corresponding package). (Yes, it's subtle, but the semantics here are central to how name spaces work in R.)
on	logical; a call to the support function <code>tracingState</code> returns <code>TRUE</code> if tracing is globally turned on, <code>FALSE</code> otherwise. An argument of one or the other of those values sets the state. If the tracing state is <code>FALSE</code> , none of the trace actions will actually occur (used, for example, by debugging functions to shut off tracing during debugging).
expr, msg	arguments to the support function <code>.doTrace</code> , calls to which are inserted into the modified function or method: <code>expr</code> is the tracing action (such as a call to <code>browser()</code> ), and <code>msg</code> is a string identifying the place where the trace action occurs.

## Details

The `trace` function operates by constructing a revised version of the function (or of the method, if signature is supplied), and assigning the new object back where the original was found. If only the `what` argument is given, a line of trace printing is produced for each call to the function (back compatible with the earlier version of `trace`).

The object constructed by `trace` is from a class that extends "function" and which contains the original, untraced version. A call to `untrace` re-assigns this version.

If the argument `tracer` or `exit` is the name of a function, the tracing expression will be a call to that function, with no arguments. This is the easiest and most common case, with the functions `browser` and `recover` the likeliest candidates; the former browses in the frame of the function being traced, and the latter allows browsing in any of the currently active calls.

The `tracer` or `exit` argument can also be an unevaluated expression (such as returned by a call to `quote` or `substitute`). This expression itself is inserted in the traced function, so it will typically involve arguments or local objects in the traced function. An expression of this form is useful if you only want to interact when certain conditions apply (and in this case you probably want to supply `print=FALSE` in the call to `trace` also).

When the `at` argument is supplied, it can be a vector of integers referring to the substeps of the body of the function (this only works if the body of the function is enclosed in `{ ... }`). In this case `tracer` is *not* called on entry, but instead just before evaluating each of the steps listed in `at`. (Hint: you don't want to try to count the steps in the printed version of a function; instead, look at `as.list(body(f))` to get the numbers associated with the steps in function `f`.)

The `at` argument can also be a list of integer vectors. In this case, each vector refers to a step nested within another step of the function. For example, `at = list(c(3, 4))` will call the tracer just before the fourth step of the third step of the function. See the example below.

An intrinsic limitation in the `exit` argument is that it won't work if the function itself uses `on.exit`, since the existing calls will override the one supplied by `trace`.

Tracing does not nest. Any call to `trace` replaces previously traced versions of that function or method (except for edited versions as discussed below), and `untrace` always restores an untraced version. (Allowing nested tracing has too many potentials for confusion and for accidentally leaving traced versions behind.)

When the `edit` argument is used repeatedly with no call to `untrace` on the same function or method in between, the previously edited version is retained. If you want to throw away all the previous tracing and then edit, call `untrace` before the next call to `trace`. Editing may be combined with automatic tracing; just supply the other arguments such as `tracer`, and the `edit` argument as well. The `edit=TRUE` argument uses the default editor (see `edit`).

Tracing primitive functions (builtins and specials) from the base package works, but only by a special mechanism and not very informatively. Tracing a primitive causes the primitive to be replaced by a function with argument ... (only). You can get a bit of information out, but not much. A warning message is issued when `trace` is used on a primitive.

The practice of saving the traced version of the function back where the function came from means that tracing carries over from one session to another, *if* the traced function is saved in the session image. (In the next session, `untrace` will remove the tracing.) On the other hand, functions that were in a package, not in the global environment, are not saved in the image, so tracing expires with the session for such functions.

Tracing a method is basically just like tracing a function, with the exception that the traced version is stored by a call to `setMethod` rather than by direct assignment, and so is the untraced version after a call to `untrace`.

The version of `trace` described here is largely compatible with the version in S-Plus, although the two work by entirely different mechanisms. The S-Plus `trace` uses the session frame, with the result that tracing never carries over from one session to another (R does not have a session frame). Another relevant distinction has nothing directly to do with `trace`: The browser in S-Plus allows changes to be made to the frame being browsed, and the changes will persist after exiting the browser. The R browser allows changes, but they disappear when the browser exits. This may be relevant in that the S-Plus version allows you to experiment with code changes interactively, but the R version does not. (A future revision may include a ‘destructive’ browser for R.)

### Value

In the simple version (just the first argument), invisible `NULL`. Otherwise, the traced function(s) name(s). The relevant consequence is the assignment that takes place.

### Note

The version of function tracing that includes any of the arguments except for the function name requires the **methods** package (because it uses special classes of objects to store and restore versions of the traced functions).

If `methods` dispatch is not currently on, `trace` will load the `methods` name space, but will not put the `methods` package on the search list.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

`browser` and `recover`, the likeliest tracing functions; also, `quote` and `substitute` for constructing general expressions.

### Examples

```
require(graphics)

## Very simple use
trace(sum)
hist(stats::rnorm(100)) # shows about 3-4 calls to sum()
untrace(sum)
```

```

if(.isMethodsDispatchOn()) { # non-simple use needs 'methods' package

f <- function(x, y) {
  y <- pmax(y, 0.001)
  if (x > 0) x ^ y else stop("x must be positive")
}

## arrange to call the browser on entering and exiting
## function f
trace("f", quote(browser(skipCalls=4)), exit = quote(browser(skipCalls=4)))

## instead, conditionally assign some data, and then browse
## on exit, but only then. Don't bother me otherwise

trace("f", quote(if(any(y < 0)) yOrig <- y),
      exit = quote(if(exists("yOrig")) browser(skipCalls=4)),
      print = FALSE)

## Enter the browser just before stop() is called. First, find
## the step numbers

as.list(body(f))
as.list(body(f)[[3]])

## Now call the browser there

trace("f", quote(browser(skipCalls=4)), at=list(c(3,4)))

## trace a utility function, with recover so we
## can browse in the calling functions as well.

trace("as.matrix", recover)

## turn off the tracing

untrace(c("f", "as.matrix"))

## Not run:
## trace calls to the function lm() that come from
## the nlme package.
## (The function nlme is in that package, and the package
## has a name space, so the where= argument must be used
## to get the right version of lm)

trace(lm, exit = recover, where = nlme)

## End(Not run)
}

```

---

traceback

---

*Print Call Stacks*


---

### Description

By default `traceback()` prints the call stack of the last uncaught error, i.e., the sequence of calls that lead to the error. This is useful when an error occurs with an unidentifiable error message. It

can also be used to print arbitrary lists of deparsed calls.

### Usage

```
traceback(x = NULL, max.lines = getOption("deparse.max.lines"))
```

### Arguments

`x` NULL (default, meaning `.Traceback`), or a list or pairlist of deparsed calls.  
`max.lines` The maximum number of lines to be printed *per call*. The default is unlimited.

### Details

The stack of the last uncaught error is stored as a list of deparsed calls in `.Traceback`, which `traceback` prints in a user-friendly format. The stack of deparsed calls always contains all function calls and all foreign function calls (such as `.Call`): if profiling is in progress it will include calls to some primitive functions. (Calls to builtins are included, but not to specials.)

Errors which are caught *via* `try` or `tryCatch` do not generate a traceback, so what is printed is the call sequence for the last uncaught error, and not necessarily for the last error.

### Value

`traceback()` returns nothing, but prints the deparsed call stack deepest call first. The calls may print on more than one line, and the first line for each call is labelled by the frame number. The number of lines printed per call can be limited via `max.lines`.

### Warning

It is undocumented where `.Traceback` is stored nor that it is visible, and this is subject to change. Prior to R 2.4.0 it was stored in the workspace, but no longer.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### Examples

```
foo <- function(x) { print(1); bar(2) }
bar <- function(x) { x + a.variable.which.does.not.exist }
## Not run:
foo(2) # gives a strange error
traceback()
## End(Not run)
## 2: bar(2)
## 1: foo(2)
bar
## Ah, this is the culprit ...
```

---

`tracemem`*Trace Copying of Objects*

---

### Description

This function marks an object so that a message is printed whenever the internal function `duplicate` is called. This happens when two objects share the same memory and one of them is modified. It is a major cause of hard-to-predict memory use in R.

### Usage

```
tracemem(x)
untracemem(x)
retracemem(x, previous = NULL)
```

### Arguments

<code>x</code>	An R object, not a function or environment or <code>NULL</code> .
<code>previous</code>	A value as returned by <code>tracemem</code> or <code>retracemem</code> .

### Details

This functionality is optional, determined at compilation, because it makes R run a little more slowly even when no objects are being traced. `tracemem` and `untracemem` give errors when R is not compiled with memory profiling; `retracemem` does not (so it can be left in code during development).

When an object is traced any copying of the object by the C function `duplicate` or by arithmetic or mathematical operations produces a message to standard output. The message consists of the string `tracemem`, the identifying strings for the object being copied and the new object being created, and a stack trace showing where the duplication occurred. `retracemem()` is used to indicate that a variable should be considered a copy of a previous variable (e.g. after subscripting).

The messages can be turned off with `tracingState`.

It is not possible to trace functions, as this would conflict with `trace` and it is not useful to trace `NULL`, environments, promises, weak references, or external pointer objects, as these are not duplicated.

These functions are [primitive](#).

### Value

A character string for identifying the object in the trace output (an address in hex enclosed in angle brackets), or `NULL` (invisibly).

### See Also

[trace](#), [Rprofmem](#)

<http://developer.r-project.org/memory-profiling.html>



**Examples**

```
## Not run:
a <- 1:10
tracemem(a)
## b and a share memory
b <- a
b[1] <- 1
untracemem(a)

## copying in lm
d <- stats::rnorm(10)
tracemem(d)
lm(d ~ a+log(b))

## f is not a copy and is not traced
f <- d[-1]
f+1
## indicate that f should be traced as a copy of d
retracemem(f, retracemem(d))
f+1

## End(Not run)
```

---

transform

*Transform an Object, for Example a Data Frame*


---

**Description**

`transform` is a generic function, which—at least currently—only does anything useful with data frames. `transform.default` converts its first argument to a data frame if possible and calls `transform.data.frame`.

**Usage**

```
transform(`_data`, ...)
```

**Arguments**

<code>_data</code>	The object to be transformed
<code>...</code>	Further arguments of the form <code>tag=value</code>

**Details**

The `...` arguments to `transform.data.frame` are tagged vector expressions, which are evaluated in the data frame `_data`. The tags are matched against names (`_data`), and for those that match, the value replace the corresponding variable in `_data`, and the others are appended to `_data`.

**Value**

The modified value of `_data`.

**Note**

Prior to R 2.3.0, the first argument was named `x`, but this caused trouble if people wanted to create a variable of that name. Names starting with an underscore are syntactically invalid, so the current choice should be less problematic.

If some of the values are not vectors of the appropriate length, you deserve whatever you get!

**Author(s)**

Peter Dalgaard

**See Also**

[subset](#), [list](#), [data.frame](#)

**Examples**

```
transform(airquality, Ozone = -Ozone)
transform(airquality, new = -Ozone, Temp = (Temp-32)/1.8)

attach(airquality)
transform(Ozone, logOzone = log(Ozone)) # marginally interesting ...
detach(airquality)
```

---

Trig

*Trigonometric Functions*

---

**Description**

These functions give the obvious trigonometric functions. They respectively compute the cosine, sine, tangent, arc-cosine, arc-sine, arc-tangent, and the two-argument arc-tangent.

**Usage**

```
cos(x)
sin(x)
tan(x)
acos(x)
asin(x)
atan(x)
atan2(y, x)
```

**Arguments**

`x`, `y`            numeric or complex vectors.

**Details**

The arc-tangent of two arguments `atan2(y, x)` returns the angle between the x-axis and the vector from the origin to  $(x, y)$ , i.e., for positive arguments `atan2(y, x) == atan(y/x)`.

Angles are in radians, not degrees (i.e., a right angle is  $\pi/2$ ).

All except `atan2` are [internal generic primitive](#) functions: methods can be defined for them individually or via the [Math](#) group generic.

### Complex values

For the inverse trigonometric functions, branch cuts are defined as in Abramowitz and Stegun, figure 4.4, page 79. Continuity on the branch cuts is standard.

For `asin()` and `acos()`, there are two cuts, both along the real axis:  $(-\infty, -1]$  and  $[1, \infty)$ . Functions `asin()` and `acos()` are continuous from above on the interval  $(-\infty, -1]$  and continuous from below on  $[1, \infty)$ .

For `atan()` there are two cuts, both along the pure imaginary axis:  $(-\infty i, -1i]$  and  $[1i, \infty i)$ . It is continuous from the left on the interval  $(-\infty i, -1i]$  and from the right on the interval  $[1i, \infty i)$ .

### S4 methods

All except `atan2` are S4 generic functions: methods can be defined for them individually or via the `Math` group generic.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Abramowitz, M. and Stegun, I. A. (1972). *Handbook of Mathematical Functions*, New York: Dover. Chapter 4. Elementary Transcendental Functions: Logarithmic, Exponential, Circular and Hyperbolic Functions

---

try

*Try an Expression Allowing Error Recovery*

---

### Description

`try` is a wrapper to run an expression that might fail and allow the user's code to handle error-recovery.

### Usage

```
try(expr, silent = FALSE)
```

### Arguments

<code>expr</code>	an R expression to try.
<code>silent</code>	logical: should the report of error messages be suppressed?

### Details

`try` evaluates an expression and traps any errors that occur during the evaluation. If an error occurs then the error message is printed to the `stderr` connection unless `options("show.error.messages")` is false or the call includes `silent = TRUE`. The error message is also stored in a buffer where it can be retrieved by `geterrmessage`. (This should not be needed as the value returned in case of an error contains the error message.)

`try` is implemented using `tryCatch`; for programming, instead of `try(expr, silent=TRUE)`, something like `tryCatch(expr, error = function(e) e)` (or other simple error handler functions) may be more efficient and flexible.

**Value**

The value of the expression if `expr` is evaluated without error, but an invisible object of class "try-error" containing the error message if it fails.

**See Also**

[options](#) for setting error handlers and suppressing the printing of error messages; [geterrmessage](#) for retrieving the last error message. [tryCatch](#) provides another means of catching and handling errors.

**Examples**

```
## this example will not work correctly in example(try), but
## it does work correctly if pasted in
options(show.error.messages = FALSE)
try(log("a"))
print(.Last.value)
options(show.error.messages = TRUE)

## alternatively,
print(try(log("a"), TRUE))

## run a simulation, keep only the results that worked.
set.seed(123)
x <- stats::rnorm(50)
doit <- function(x)
{
  x <- sample(x, replace=TRUE)
  if(length(unique(x)) > 30) mean(x)
  else stop("too few unique points")
}
## alternative 1
res <- lapply(1:100, function(i) try(doit(x), TRUE))
## alternative 2
## Not run: res <- vector("list", 100)
for(i in 1:100) res[[i]] <- try(doit(x), TRUE)
## End(Not run)
unlist(res[sapply(res, function(x) !inherits(x, "try-error"))])
```

---

typeof

*The Type of an Object*

---

**Description**

`typeof` determines the (R internal) type or storage mode of any object

**Usage**

```
typeof(x)
```

**Arguments**

`x` any R object.

**Value**

A character string. The possible values are listed in the structure `TypeTable` in `'src/main/util.c'`. Current values are the vector types `"logical"`, `"integer"`, `"double"`, `"complex"`, `"character"`, `"raw"` and `"list"`, `"NULL"`, `"closure"` (function), `"special"` and `"builtin"` (basic functions and operators), `"environment"`, `"S4"` (some S4 objects) and others that are unlikely to be seen at user level (`"symbol"`, `"pairlist"`, `"promise"`, `"language"`, `"char"`, `"..."`, `"any"`, `"expression"`, `"externalptr"`, `"bytecode"` and `"weakref"`).

**See Also**

[mode](#), [storage.mode](#).

[isS4](#) to determine if an object has an S4 class.

**Examples**

```
typeof(2)
mode(2)
```

---

unique

*Extract Unique Elements*

---

**Description**

`unique` returns a vector, data frame or array like `x` but with duplicate elements/rows removed.

**Usage**

```
unique(x, incomparables = FALSE, ...)

## Default S3 method:
unique(x, incomparables = FALSE, fromLast = FALSE, ...)

## S3 method for class 'matrix':
unique(x, incomparables = FALSE, MARGIN = 1,
       fromLast = FALSE, ...)

## S3 method for class 'array':
unique(x, incomparables = FALSE, MARGIN = 1,
       fromLast = FALSE, ...)
```

**Arguments**

<code>x</code>	a vector or a data frame or an array or <code>NULL</code> .
<code>incomparables</code>	a vector of values that cannot be compared. <code>FALSE</code> is a special value, meaning that all values can be compared, and may be the only value accepted for methods other than the default. It will be coerced internally to the same type as <code>x</code> .
<code>fromLast</code>	logical indicating if duplication should be considered from the last, i.e., the last (or rightmost) of identical elements will be kept. This only matters for <a href="#">names</a> or <a href="#">dimnames</a> .

... arguments for particular methods.  
 MARGIN the array margin to be held fixed: a single integer.

### Details

This is a generic function with methods for vectors, data frames and arrays (including matrices).

The array method calculates for each element of the dimension specified by `MARGIN` if the remaining dimensions are identical to those for an earlier element (in row-major order). This would most commonly be used for matrices to find unique rows (the default) or columns (with `MARGIN = 2`).

Note that unlike the Unix command `uniq` this omits *duplicated* and not just *repeated* elements/rows. That is, an element is omitted if it is equal to any previous element and not just if it is equal the immediately previous one. (For the latter, see [rle](#)).

Missing values are regarded as equal, but `NaN` is not equal to `NA_real_`. Character strings are regarded as equal if they are in different encodings but would agree when translated to UTF-8.

Values in `incomparables` will never be marked as duplicated. This is intended to be used for a fairly small set of values and will not be efficient for a very large set.

### Value

For a vector, an object of the same type of `x`, but with only one copy of each duplicated element. No attributes are copied (so the result has no names).

For a data frame, a data frame is returned with the same columns but possibly fewer rows (and with row names from the first occurrences of the unique rows).

A matrix or array is subsetted by `[, drop = FALSE]`, so dimensions and dimnames are copied appropriately, and the result always has the same number of dimensions as `x`.

### Warning

Using this for lists is potentially slow, especially if the elements are not atomic vectors (see [vector](#)) or differ only in their attributes. In the worst case it is  $O(n^2)$ .

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[duplicated](#) which gives the indices of duplicated elements.

[rle](#) which is the equivalent of the Unix `uniq -c` command.

### Examples

```
x <- c(3:5, 11:8, 8 + 0:5)
(ux <- unique(x))
(u2 <- unique(x, fromLast = TRUE)) # different order
stopifnot(identical(sort(ux), sort(u2)))

length(unique(sample(100, 100, replace=TRUE)))
## approximately 100(1 - 1/e) = 63.21

unique(iris)
```

---

`unlink`*Delete Files and Directories*

---

**Description**

`unlink` deletes the file(s) or directories specified by `x`.

**Usage**

```
unlink(x, recursive = FALSE)
```

**Arguments**

<code>x</code>	a character vector with the names of the file(s) or directories to be deleted. Wildcards (normally <code>*</code> and <code>?</code> ) are allowed.
<code>recursive</code>	logical. Should directories be deleted recursively?

**Details**

If `recursive = FALSE` directories are not deleted, not even empty ones.

On most platforms `file` includes symbolic links, fifos and sockets. Some earlier versions of R would not try to remove broken symbolic links.

Wildcard expansion is done by the internal code of `Sys.glob`. Wildcards never match a leading `.` in the filename, and files `.` and `..` will never be considered for deletion. Wildcards will only be expanded if the system supports it. Most systems will support not only `*` and `?` but character classes such as `[a-z]` (see the man pages for `glob`). The metacharacters `*` `?` `[` can occur in Unix filenames, and this makes it difficult to use `unlink` to delete such files (see `file.remove`), although escaping the metacharacters by backslashes usually works. If a metacharacter matches nothing it is considered as a literal character.

`recursive = TRUE` is not supported on all platforms, and may be ignored, with a warning.

**Value**

0 for success, 1 for failure. Not deleting a non-existent file is not a failure, nor is being unable to delete a directory if `recursive = FALSE`. However, missing values in `x` are regarded as failures.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[file.remove](#).

---

unlist	<i>Flatten Lists</i>
--------	----------------------

---

### Description

Given a list structure `x`, `unlist` simplifies it to produce a vector which contains all the atomic components which occur in `x`.

### Usage

```
unlist(x, recursive = TRUE, use.names = TRUE)
```

### Arguments

<code>x</code>	an R object, typically a list or vector.
<code>recursive</code>	logical. Should unlisting be applied to list components of <code>x</code> ?
<code>use.names</code>	logical. Should names be preserved?

### Details

`unlist` is generic: you can write methods to handle specific classes of objects, see [InternalMethods](#), and note, e.g., `relist` with the `unlist` method for `relistable` objects.

If `recursive = FALSE`, the function will not recurse beyond the first level items in `x`.

Factors are treated specially. If all non-list elements of `x` are factors (or ordered factors) then the result will be a factor with levels the union of the level sets of the elements, in the order the levels occur in the level sets of the elements (which means that if all the elements have the same level set, that is the level set of the result).

`x` can be an atomic vector, but then `unlist` does nothing useful, not even drop names.

By default, `unlist` tries to retain the naming information present in `x`. If `use.names = FALSE` all naming information is dropped.

Where possible the list elements are coerced to a common mode during the unlisting, and so the result often ends up as a character vector. Vectors will be coerced to the highest type of the components in the hierarchy `NULL < raw < logical < integer < real < complex < character < list < expression`: pairlists are treated as lists.

A list is a (generic) vector, and the simplified vector might still be a list (and might be unchanged). Non-vector elements of the list (for example language elements such as names, formulas and calls) are not coerced, and so a list containing one or more of these remains a list. (The effect of unlisting an `lm` fit is a list which has individual residuals as components.)

### Value

`NULL` or an expression or a vector of an appropriate mode to hold the list components.

The output type is determined from the highest type of the components in the hierarchy `NULL < raw < logical < integer < real < complex < character < list < expression`, after coercion of pairlists to lists.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.



**See Also**

`c`, `as.list`, `relist`.

**Examples**

```
unlist(options())
unlist(options(), use.names=FALSE)

l.ex <- list(a = list(1:5, LETTERS[1:5]), b = "z", c = NA)
unlist(l.ex, recursive = FALSE)
unlist(l.ex, recursive = TRUE)

l1 <- list(a="a", b=2, c=pi+2i)
unlist(l1) # a character vector
l2 <- list(a="a", b=as.name("b"), c=pi+2i)
unlist(l2) # remains a list
```

---

unname

*Remove 'names' or 'dimnames'*


---

**Description**

Remove the `names` or `dimnames` attribute of an R object.

**Usage**

```
unname(obj, force = FALSE)
```

**Arguments**

<code>obj</code>	an R object.
<code>force</code>	logical; if true, the <code>dimnames</code> are even removed from <code>data.frames</code> . <i>This argument is currently <b>experimental</b> and hence might change!</i>

**Value**

Object as `obj` but without `names` or `dimnames`.

**Examples**

```
require(graphics); require(stats)

## Answering a question on R-help (14 Oct 1999):
col3 <- 750+ 100*rt(1500, df = 3)
breaks <- factor(cut(col3,breaks=360+5*(0:155)))
z <- table(breaks)
z[1:5] # The names are larger than the data ...
barplot(unname(z), axes= FALSE)
```

UseMethod

Class Methods

**Description**

R possesses a simple generic function mechanism which can be used for an object-oriented style of programming. Method dispatch takes place based on the class(es) of the first argument to the generic function or of the object supplied as an argument to `UseMethod` or `NextMethod`.

**Usage**

```
UseMethod(generic, object)
```

```
NextMethod(generic = NULL, object = NULL, ...)
```

**Arguments**

<code>generic</code>	a character string naming a function (and not a built-in operator). Required for <code>UseMethod</code> .
<code>object</code>	for <code>UseMethod</code> : an object whose class will determine the method to be dispatched. Defaults to the first argument of the enclosing function.
<code>...</code>	further arguments to be passed to the next method.

**Details**

An R object is a data object which has a `class` attribute (and this can be tested by `is.object`). A class attribute is a character vector giving the names of the classes from which the object *inherits*. If the object does not have a class attribute, it has an implicit class. Matrices and arrays have class `"matrix"` or `"array"` followed by the class of the underlying vector. Most vectors have class the result of `mode(x)`, except that integer vectors have class `c("integer", "numeric")` and real vectors have class `c("double", "numeric")`.

When a function calling `UseMethod("fun")` is applied to an object with class attribute `c("first", "second")`, the system searches for a function called `fun.first` and, if it finds it, applies it to the object. If no such function is found a function called `fun.second` is tried. If no class name produces a suitable function, the function `fun.default` is used, if it exists, or an error results.

Function `methods` can be used to find out about the methods for a particular generic function or class.

`UseMethod` is a primitive function but (as from R 2.11.0) uses standard argument matching. It is not the only means of dispatch of methods, for there are [internal generic](#) and [group generic](#) functions. `UseMethod` currently dispatches on the implicit class even for arguments that are not objects, but the other means of dispatch do not.

`NextMethod` invokes the next method (determined by the class vector, either of the object supplied to the generic, or of the first argument to the function containing `NextMethod` if a method was invoked directly). Normally `NextMethod` is used with only one argument, `generic`, but if further arguments are supplied these modify the call to the next method.

`NextMethod` should not be called except in methods called by `UseMethod` or from internal generics (see [InternalGenerics](#)). In particular it will not work inside anonymous calling functions (e.g. `get("print.ts")` (`AirPassengers`)).

Name spaces can register methods for generic functions. To support this, `UseMethod` and `NextMethod` search for methods in two places: first in the environment in which the generic function is called, and then in the registration data base for the environment in which the generic is defined (typically a name space). So methods for a generic function need to be available in the environment of the call to the generic, or they must be registered. (It does not matter whether they are visible in the environment in which the generic is defined.)

### Technical Details

Now for some obscure details that need to appear somewhere. These comments will be slightly different than those in Chambers(1992). (See also the draft 'R Language Definition'.) `UseMethod` creates a new function call with arguments matched as they came in to the generic. Any local variables defined before the call to `UseMethod` are retained (unlike S). Any statements after the call to `UseMethod` will not be evaluated as `UseMethod` does not return. `UseMethod` can be called with more than two arguments: a warning will be given and additional arguments ignored. (They are not completely ignored in S.) If it is called with just one argument, the class of the first argument of the enclosing function is used as `object`: unlike S this is the first actual argument passed and not the current value of the object of that name.

`NextMethod` works by creating a special call frame for the next method. If no new arguments are supplied, the arguments will be the same in number, order and name as those to the current method but their values will be promises to evaluate their name in the current method and environment. Any named arguments matched to `...` are handled specially: they either replace existing arguments of the same name or are appended to the argument list. They are passed on as the promise that was supplied as an argument to the current environment. (S does this differently!) If they have been evaluated in the current (or a previous environment) they remain evaluated. (This is a complex area, and subject to change: see the draft 'R Language Definition'.)

The search for methods for `NextMethod` is slightly different from that for `UseMethod`. Finding no `fun.default` is not necessarily an error, as the search continues to the generic itself. This is to pick up an [internal generic](#) like `[]` which has no separate default method, and succeeds only if the generic is a [primitive](#) function or a wrapper for a `.Internal` function of the same name. (When a primitive is called as the default method, argument matching may not work as described above due to the different semantics of primitives.)

You will see objects such as `.Generic`, `.Method`, and `.Class` used in methods. These are set in the environment within which the method is evaluated by the dispatch mechanism, which is as follows:

1. Find the context for the calling function (the generic): this gives us the unevaluated arguments for the original call.
2. Evaluate the object (usually an argument) to be used for dispatch, and find a method (possibly the default method) or throw an error.
3. Create an environment for evaluating the method and insert special variables (see below) into that environment. Also copy any variables in the environment of the generic that are not formal (or actual) arguments.
4. Fix up the argument list to be the arguments of the call matched to the formals of the method.

`.Generic` is a length-one character vector naming the generic function.

`.Method` is a character vector (normally of length one) naming the method function. (For functions in the group generic `Ops` it is of length two.)

`.Class` is a character vector of classes used to find the next method. `NextMethod` adds an attribute "previous" to `.Class` giving the `.Class` last used for dispatch, and shifts `.Class` along to that used for dispatch.

`.GenericCallEnv` and `.GenericDefEnv` are the environments of the call to be generic and defining the generic respectively. (The latter is used to find methods registered for the generic.)

Note that `.Class` is set when the generic is called, and is unchanged if the class of the dispatching argument is changed in a method. It is possible to change the method that `NextMethod` would dispatch by manipulating `.Class`, but ‘this is not recommended unless you understand the inheritance mechanism thoroughly’ (Chambers & Hastie, 1992, p. 469).

### Note

This scheme is called *S3* (S version 3). For new projects, it is recommended to use the more flexible and robust *S4* scheme provided in the **methods** package.

### References

Chambers, J. M. (1992) *Classes and methods: object-oriented programming in S*. Appendix A of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

### See Also

The draft ‘R Language Definition’.

[methods](#), [class](#), [getS3method](#), [is.object](#).

---

userhooks

*Functions to Get and Set Hooks for Load, Attach, Detach and Unload*

---

### Description

These functions allow users to set actions to be taken before packages are attached/detached and name spaces are (un)loaded.

### Usage

```
getHook(hookName)
setHook(hookName, value,
        action = c("append", "prepend", "replace"))

packageEvent(pkgname,
             event = c("onLoad", "attach", "detach", "onUnload"))
```

### Arguments

<code>hookName</code>	character string: the hook name
<code>pkgname</code>	character string: the package/name space name.
<code>event</code>	character string: an event for the package
<code>value</code>	A function, or for <code>action="replace"</code> , NULL.
<code>action</code>	The action to be taken. The names can be abbreviated.

## Details

`setHook` provides a general mechanism for users to register hooks, a list of functions to be called from system (or user) functions. The initial set of hooks is associated with events on packages/name spaces: these hooks are named via calls to `packageEvent`.

To remove a hook completely, call `setHook(hookName, NULL, "replace")`.

When an R package is attached by `library`, it can call initialization code via a function `.First.lib`, and when it is `detach`-ed it can tidy up via a function `.Last.lib`. Users can add their own initialization code via the hooks provided by these functions, functions which will be called as `funname(pkgname, pkgpath)` inside a `try` call. (The attach hook is called after `.First.lib` and the detach hook before `.Last.lib`.)

If a package has a name space, there are two further actions, when the name space is loaded (before being attached and after `.onLoad` is called) and when it is unloaded (after being detached and before `.onUnload`). Note that code in these hooks is run without the package being on the search path, so objects in the package need to be referred to using the double colon operator as in the example. (Unlike `.onLoad`, the user hook is run after the name space has been sealed.)

Hooks are normally run in the order shown by `getHook`, but the "detach" and "onUnload" hooks are run in reverse order so the default for package events is to add hooks 'inside' existing ones.

Note that when an R session is finished, packages are not detached and name spaces are not unloaded, so the corresponding hooks will not be run.

The hooks are stored in the environment `.userHooksEnv` in the base package, with 'mangled' names.

## Value

For `getHook` function, a list of functions (possible empty). For `setHook` function, no return value. For `packageEvent`, the derived hook name (a character string).

## See Also

`library`, `detach`, `loadNamespace`.

Other hooks may be added later: `plot.new` and `persp` already have them.

## Examples

```
setHook(packageEvent("grDevices", "onLoad"),
        function(...) grDevices::ps.options(horizontal=FALSE))
```

---

utf8Conversion

*Convert to or from UTF-8-encoded Character Vectors*

---

## Description

Conversion of UTF-8 encoded character vectors to and from integer vectors.

## Usage

```
utf8ToInt(x)
intToUtf8(x, multiple = FALSE)
```

**Arguments**

<code>x</code>	object to be converted.
<code>multiple</code>	logical: should the conversion be to a single character string or multiple individual characters?

**Details**

These will work in any locale, including on machines that do not otherwise support multi-byte character sets.

**Value**

`utf8ToInt` converts a length-one character string encoded in UTF-8 to an integer vector of (numeric) UTF-8 code points.

`intToUtf8` converts a vector of (numeric) UTF-8 code points either to a single character string or a character vector of single characters. (For a single character string 0 is silently omitted: otherwise 0 is mapped to "". Non-integral numeric values are truncated to integers.) The `Encoding` is declared as "UTF-8".

As from R 2.11.0 NA inputs are mapped to NA output.

**Examples**

```
## Not run:
## will only display in some locales and fonts
intToUtf8(0x03B2L) # Greek beta

## End(Not run)
```

---

vector

*Vectors*


---

**Description**

`vector` produces a vector of the given length and mode.

`as.vector`, a generic, attempts to coerce its argument into a vector of mode `mode` (the default is to coerce to whichever mode is most convenient).

`is.vector` returns TRUE if `x` is a vector of the specified mode having no attributes other than names. It returns FALSE otherwise.

**Usage**

```
vector(mode = "logical", length = 0)
as.vector(x, mode = "any")
is.vector(x, mode = "any")
```

**Arguments**

<code>mode</code>	A character string giving an atomic mode or "list", or (not for <code>vector</code> ) "any".
<code>length</code>	A non-negative integer specifying the desired length.
<code>x</code>	An object.

## Details

The atomic modes are "logical", "integer", "numeric", "complex", "character" and "raw".

If `mode = "any"`, `is.vector` returns TRUE for modes logical, integer, real, complex, character, raw, list or expression. It returns FALSE if `x` has any attributes except names. (This is incompatible with S.) On the other hand, `as.vector` removes *all* attributes including names for results of atomic mode.

Note that factors are *not* vectors; `is.vector` returns FALSE and `as.vector` converts to a character vector for `mode = "any"`.

`is.vector` is a [primitive](#) function.

## Value

For `vector`, a vector of the given length and mode. Logical vector elements are initialized to FALSE, numeric vector elements to 0, character vector elements to "", raw vector elements to nul bytes and list elements to NULL.

All attributes are removed from the answer if it is of an atomic mode.

## Note

`as.vector` and `is.vector` are quite distinct from the meaning of the formal class "vector" in the **methods** package, and hence `as(x, "vector")` and `is(x, "vector")`.

modes of "symbol", "pairlist" and "expression" are allowed but have long been undocumented.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

`c`, `is.numeric`, `is.list`, etc.

## Examples

```
df <- data.frame(x=1:3, y=5:7)
## Not run: ## Error:
  as.vector(data.frame(x=1:3, y=5:7), mode="numeric")

## End(Not run)

x <- c(a = 1, b = 2)
is.vector(x)
as.vector(x)
all.equal(x, as.vector(x)) ## FALSE

###-- All the following are TRUE:
is.list(df)
! is.vector(df)
! is.vector(df, mode="list")
```

```
is.vector(list(), mode="list")
is.vector(NULL, mode="NULL")
```

---

warning

*Warning Messages*


---

## Description

Generates a warning message that corresponds to its argument(s) and (optionally) the expression or function from which it was called.

## Usage

```
warning(..., call. = TRUE, immediate. = FALSE, domain = NULL)
suppressWarnings(expr)
```

## Arguments

...	zero or more objects which can be coerced to character (and which are pasted together with no separator) or a single condition object.
call.	logical, indicating if the call should become part of the warning message.
immediate.	logical, indicating if the call should be output immediately, even if <code>getOption("warn") &lt;= 0</code> .
expr	expression to evaluate.
domain	see <code>gettext</code> . If NA, messages will not be translated.

## Details

The result *depends* on the value of `getOption("warn")` and on handlers established in the executing code.

If a condition object is supplied it should be the only argument, and further arguments will be ignored, with a message.

`warning` signals a warning condition by (effectively) calling `signalCondition`. If there are no handlers or if all handlers return, then the value of `warn = getOption("warn")` is used to determine the appropriate action. If `warn` is negative warnings are ignored; if it is zero they are stored and printed after the top-level function has completed; if it is one they are printed as they occur and if it is 2 (or larger) warnings are turned into errors. Calling `warning(immediate. = TRUE)` turns `warn <= 0` into `warn = 1` for this call only.

If `warn` is zero (the default), a read-only variable `last.warning` is created. It contains the warnings which can be printed via a call to `warnings`.

Warnings will be truncated to `getOption("warning.length")` characters, default 1000, indicated by `[... truncated]`.

While the warning is being processed, a `muffleWarning` restart is available. If this restart is invoked with `invokeRestart`, then `warning` returns immediately.

An attempt is made to coerce other types of inputs to `warning` to character vectors.

`suppressWarnings` evaluates its expression in a context that ignores all warnings.



**Value**

The warning message as `character` string, invisibly.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`stop` for fatal errors, `message` for diagnostic messages, `warnings`, and `options` with argument `warn=`.

`gettext` for the mechanisms for the automated translation of messages.

**Examples**

```
testit <- function() warning("testit")
testit() ## shows call
testit <- function() warning("problem in testit", call. = FALSE)
testit() ## no call
suppressWarnings(warning("testit"))
```

---

warnings

*Print Warning Messages*

---

**Description**

`warnings` and its `print` method print the variable `last.warning` in a pleasing form.

**Usage**

```
warnings(...)
```

**Arguments**

`...` arguments to be passed to `cat`.

**Details**

See the description of `options("warn")` for the circumstances under which there is a `last.warning` object and `warnings()` is used. In essence this is if `options(warn = 0)` and `warning` has been called at least once.

It is possible that `last.warning` refers to the last recorded warning and not to the last warning, for example if `options(warn)` has been changed or if a catastrophic error occurred.

**Warning**

It is undocumented where `last.warning` is stored nor that it is visible, and this is subject to change. Prior to R 2.4.0 it was stored in the workspace, but no longer.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[warning](#).

**Examples**

```
## NB this example is intended to be pasted in,
##   rather than run by example()
ow <- options("warn")
for(w in -1:1) {
  options(warn = w); cat("\n warn =",w,"\n")
  for(i in 1:3) { cat(i,"..\n"); m <- matrix(1:7, 3,4) }
}
warnings()
options(ow) # reset
```

---

weekdays

---

*Extract Parts of a POSIXt or Date Object*


---

**Description**

Extract the weekday, month or quarter, or the Julian time (days since some origin). These are generic functions: the methods for the internal date-time classes are documented here.

**Usage**

```
weekdays(x, abbreviate)
## S3 method for class 'POSIXt':
weekdays(x, abbreviate = FALSE)
## S3 method for class 'Date':
weekdays(x, abbreviate = FALSE)

months(x, abbreviate)
## S3 method for class 'POSIXt':
months(x, abbreviate = FALSE)
## S3 method for class 'Date':
months(x, abbreviate = FALSE)

quarters(x, abbreviate)
## S3 method for class 'POSIXt':
quarters(x, ...)
## S3 method for class 'Date':
quarters(x, ...)

julian(x, ...)
## S3 method for class 'POSIXt':
julian(x, origin = as.POSIXct("1970-01-01", tz="GMT"), ...)
## S3 method for class 'Date':
julian(x, origin = as.Date("1970-01-01"), ...)
```

**Arguments**

`x` an object inheriting from class "POSIXt" or "Date".  
`abbreviate` logical. Should the names be abbreviated?  
`origin` an length-one object inheriting from class "POSIXt" or "Date".  
`...` arguments for other methods.

**Value**

`weekdays` and `months` return a character vector of names in the locale in use.  
`quarters` returns a character vector of "Q1" to "Q4".  
`julian` returns the number of days (possibly fractional) since the origin, with the origin as a "origin" attribute.

**Note**

Other components such as the day of the month or the year are very easy to compute: just use `as.POSIXlt` and extract the relevant component. Alternatively (especially if the components are desired as character strings), use `strftime`.

**See Also**

[DateTimeClasses](#), [Date](#)

**Examples**

```
weekdays(.leap.seconds)
months(.leap.seconds)
quarters(.leap.seconds)

## Julian Day Number (JDN, http://en.wikipedia.org/wiki/Julian_day)
## is the number of days since noon UTC on the first day of 4317 BC.
julian(Sys.Date(), -2440588) # for a day
floor(as.numeric(julian(Sys.time()))) + 2440587.5 # for a date-time
```

---

which

*Which indices are TRUE?*

---

**Description**

Give the TRUE indices of a logical object, allowing for array indices.

**Usage**

```
which(x, arr.ind = FALSE)
arrayInd(ind, .dim, .dimnames = NULL)
```

**Arguments**

<code>x</code>	a <a href="#">logical</a> vector or array. <a href="#">NAs</a> are allowed and omitted (treated as if FALSE).
<code>arr.ind</code>	logical; should <b>array indices</b> be returned when <code>x</code> is an array?
<code>ind</code>	integer-valued index vector, as resulting from <code>which(x)</code> .
<code>.dim</code>	<a href="#">dim(.)</a> integer vector
<code>.dimnames</code>	optional list of character <a href="#">dimnames(.)</a> , of which only <code>.dimnames[[1]]</code> is used.

**Value**

If `arr.ind == FALSE` (the default), an integer vector with length equal to `sum(x)`, i.e., to the number of TRUEs in `x`; Basically, the result is `(1:length(x))[x]`.

If `arr.ind == TRUE` and `x` is an [array](#) (has a `dim` attribute), the result is `arrayInd(which(x), dim(x), dimnames(x))`, namely a matrix whose rows each are the indices of one element of `x`; see Examples below.

**Author(s)**

Werner Stahel and Peter Holzer <holzer@stat.math.ethz.ch>, for the array case.

**See Also**

[Logic](#), [which.min](#) for the index of the minimum or maximum, and [match](#) for the first index of an element in a vector, i.e., for a scalar `a`, `match(a, x)` is equivalent to `min(which(x == a))` but much more efficient.

**Examples**

```
which(LETTERS == "R")
which(ll <- c(TRUE, FALSE, TRUE, NA, FALSE, FALSE, TRUE)) #> 1 3 7
names(ll) <- letters[seq(ll)]
which(ll)
which((1:12)%%2 == 0) # which are even?
which(1:10 > 3, arr.ind=TRUE)

( m <- matrix(1:12, 3, 4) )
which(m %% 3 == 0)
which(m %% 3 == 0, arr.ind=TRUE)
rownames(m) <- paste("Case", 1:3, sep="_")
which(m %% 5 == 0, arr.ind=TRUE)

dim(m) <- c(2, 2, 3); m
which(m %% 3 == 0, arr.ind=FALSE)
which(m %% 3 == 0, arr.ind=TRUE)

vm <- c(m)
dim(vm) <- length(vm) #-- funny thing with length(dim(...)) == 1
which(vm %% 3 == 0, arr.ind=TRUE)
```

---

`which.min`*Where is the Min() or Max() ?*

---

**Description**

Determines the location, i.e., index of the (first) minimum or maximum of a numeric vector.

**Usage**

```
which.min(x)
which.max(x)
```

**Arguments**

`x` numeric (integer or double) vector, whose `min` or `max` is searched for.

**Value**

Missing and NaN values are discarded.

an `integer` of length 1 or 0 (iff `x` has no non-NAs), giving the index of the *first* minimum or maximum respectively of `x`.

If this extremum is unique (or empty), the results are the same as (but more efficient than) `which(x == min(x))` or `which(x == max(x))` respectively.

**Author(s)**

Martin Maechler

**See Also**

`which`, `max.col`, `max`, etc.

`which.is.max` in package `nnet` differs in breaking ties at random (and having a ‘fuzz’ in the definition of ties).

**Examples**

```
x <- c(1:4, 0:5, 11)
which.min(x)
which.max(x)

## it *does* work with NA's present, by discarding them:
presidents[1:30]
range(presidents, na.rm = TRUE)
which.min(presidents) # 28
which.max(presidents) # 2
```

---

with	<i>Evaluate an Expression in a Data Environment</i>
------	---

---

### Description

Evaluate an R expression in an environment constructed from data, possibly modifying the original data.

### Usage

```
with(data, expr, ...)  
within(data, expr, ...)
```

### Arguments

data	data to use for constructing an environment. For the default <code>with</code> method this may be an environment, a list, a data frame, or an integer as in <code>sys.call</code> . For <code>within</code> , it can be a list or a data frame.
expr	expression to evaluate.
...	arguments to be passed to future methods.

### Details

`with` is a generic function that evaluates `expr` in a local environment constructed from `data`. The environment has the caller's environment as its parent. This is useful for simplifying calls to modeling functions. (Note: if `data` is already an environment then this is used with its existing parent.)

Note that assignments within `expr` take place in the constructed environment and not in the user's workspace.

`within` is similar, except that it examines the environment after the evaluation of `expr` and makes the corresponding modifications to `data` (this may fail in the data frame case if objects are created which cannot be stored in a data frame), and returns it. `within` can be used as an alternative to `transform`.

### Value

For `with`, the value of the evaluated `expr`. For `within`, the modified object.

### See Also

[evalq](#), [attach](#), [assign](#), [transform](#).

### Examples

```
require(stats); require(graphics)  
#examples from glm:  
## Not run:  
library(MASS)  
with(anorexia, {  
  anorex.1 <- glm(Postwt ~ Prewt + Treat + offset(Prewt),  
                 family = gaussian)
```

```

summary(anorex.1)
})

## End(Not run)

aq <- within(airquality, {      # Notice that multiple vars can be changed
  lOzone<-log(Ozone)
  Month<-factor(month.abb[Month])
  cTemp <- round((Temp - 32) * 5/9, 1) # From Fahrenheit to Celsius
  rm(Day, Temp)
})
head(aq)

with(data.frame(u = c(5,10,15,20,30,40,60,80,100),
               lot1 = c(118,58,42,35,27,25,21,19,18),
               lot2 = c(69,35,26,21,18,16,13,12,12)),
      list(summary(glm(lot1 ~ log(u), family = Gamma)),
            summary(glm(lot2 ~ log(u), family = Gamma))))

# example from boxplot:
with(ToothGrowth, {
  boxplot(len ~ dose, boxwex = 0.25, at = 1:3 - 0.2,
          subset = (supp == "VC"), col = "yellow",
          main = "Guinea Pigs' Tooth Growth",
          xlab = "Vitamin C dose mg",
          ylab = "tooth length", ylim = c(0,35))
  boxplot(len ~ dose, add = TRUE, boxwex = 0.25, at = 1:3 + 0.2,
          subset = supp == "OJ", col = "orange")
  legend(2, 9, c("Ascorbic acid", "Orange juice"),
        fill = c("yellow", "orange"))
})

# alternate form that avoids subset argument:
with(subset(ToothGrowth, supp == "VC"),
     boxplot(len ~ dose, boxwex = 0.25, at = 1:3 - 0.2,
            col = "yellow", main = "Guinea Pigs' Tooth Growth",
            xlab = "Vitamin C dose mg",
            ylab = "tooth length", ylim = c(0,35)))
with(subset(ToothGrowth, supp == "OJ"),
     boxplot(len ~ dose, add = TRUE, boxwex = 0.25, at = 1:3 + 0.2,
            col = "orange"))
legend(2, 9, c("Ascorbic acid", "Orange juice"),
      fill = c("yellow", "orange"))

```

---

withVisible

*Return both a value and its visibility*


---

## Description

This function evaluates an expression, returning it in a two element list containing its value and a flag showing whether it would automatically print.

**Usage**

```
withVisible(x)
```

**Arguments**

`x` An expression to be evaluated.

**Details**

The argument is evaluated in the caller's context.

This is a [primitive](#) function.

**Value**

`value` The value of `x` after evaluation.

`visible` logical; whether the value would auto-print.

**See Also**

[invisible](#), [eval](#)

**Examples**

```
x <- 1
withVisible(x <- 1)
x
withVisible(x)

# Wrap the call in evalq() for special handling

df <- data.frame(a=1:5, b=1:5)
evalq(withVisible(a + b), envir=df)
```

---

write

*Write Data to a File*

---

**Description**

The data (usually a matrix) `x` are written to file `file`. If `x` is a two-dimensional matrix you need to transpose it to get the columns in `file` the same as those in the internal representation.

**Usage**

```
write(x, file = "data",
      ncolumns = if(is.character(x)) 1 else 5,
      append = FALSE, sep = " ")
```



**Arguments**

x	the data to be written out.
file	A connection, or a character string naming the file to write to. If "", print to the standard output connection. If it is "  cmd", the output is piped to the command given by 'cmd'.
ncolumns	the number of columns to write the data in.
append	if TRUE the data x are appended to the connection.
sep	a string used to separate columns. Using sep = "\t" gives tab delimited output; default is " ".

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

write is a wrapper for [cat](#), which gives further details on the format used.  
[save](#) for writing any R objects, [write.table](#) for data frames, and [scan](#) for reading data.

**Examples**

```
# create a 2 by 5 matrix
x <- matrix(1:10,ncol=5)

# the file data contains x, two rows, five cols
# 1 3 5 7 9 will form the first row
write(t(x))

# Writing to the "console" 'tab-delimited'
# two rows, five cols but the first row is 1 2 3 4 5
write(x, "", sep = "\t")
unlink("data") # tidy up
```

---

writeLines

---

*Write Lines to a Connection*


---

**Description**

Write text lines to a connection.

**Usage**

```
writeLines(text, con = stdout(), sep = "\n", useBytes = FALSE)
```

**Arguments**

text	A character vector
con	A connection object or a character string.
sep	character. A string to be written to the connection after each line of text.
useBytes	logical. See 'Details'.

**Details**

If the `con` is a character string, the function calls `file` to obtain a file connection which is opened for the duration of the function call.

If the connection is open it is written from its current position. If it is not open, it is opened for the duration of the call in "wt" mode and then closed again.

Normally `writeLines` is used with a text-mode connection, and the default separator is converted to the normal separator for that platform (LF on Unix/Linux, CRLF on Windows). For more control, open a binary connection and specify the precise value you want written to the file in `sep`. For even more control, use `writeChar` on a binary connection.

`useBytes` is for expert use. Normally (when false) character strings with marked encodings are converted to the current encoding before being passed to the connection (which might do further re-encoding). `useBytes = TRUE` suppresses the re-encoding of marked strings so they are passed byte-by-byte to the connection.: this can be useful when strings have already been re-encoded by e.g. `iconv`.

**See Also**

[connections](#), [writeChar](#), [writeBin](#), [readLines](#), [cat](#)

---

 xtfrm

*Auxiliary Function for Sorting and Ranking*


---

**Description**

A generic auxiliary function that produces a numeric vector which will sort in the same order as `x`.

**Usage**

```
xtfrm(x)
```

**Arguments**

`x` an R object.

**Details**

This is a special case of ranking, but as a less general function than `rank` is more suitable to be made generic. The default method is similar to `rank(x, ties.method="min", na.last="keep")`, so NA values are given rank NA and all tied values are given equal integer rank.

The `factor` method extracts the codes. The `Surv` method sorts first on times and then on status code(s).

The default method will unclass the object if `is.numeric(x)` is true but otherwise make use of `==` and `>` methods for the class of `x[i]` (for integers `i`), and the `is.na` method for the class of `x`, but might be rather slow when doing so.

This is an [internal generic primitive](#), so S3 or S4 methods can be written for it.

**Value**

A numeric (usually integer) vector of the same length as `x`.

**See Also**

[rank](#), [sort](#), [order](#).

---

zapsmall

*Rounding of Numbers*


---

**Description**

`zapsmall` determines a `digits` argument `dr` for calling `round(x, digits = dr)` such that values close to zero (compared with the maximal absolute value) are ‘zapped’, i.e., treated as 0.

**Usage**

```
zapsmall(x, digits = getOption("digits"))
```

**Arguments**

`x` a numeric or complex vector.  
`digits` integer indicating the precision to be used.

**References**

Chambers, J. M. (1998) *Programming with Data. A Guide to the S Language*. Springer.

**Examples**

```
x2 <- pi * 100^(-1:3)
print(x2 / 1000, digits=4)
zapsmall(x2 / 1000, digits=4)

zapsmall(exp(1i*0:4*pi/2))
```

---

zpackages

*Listing of Packages*


---

**Description**

`.packages` returns information about package availability.

**Usage**

```
.packages(all.available = FALSE, lib.loc = NULL)
```

**Arguments**

`all.available` logical; if TRUE return a character vector of all available packages in `lib.loc`.  
`lib.loc` a character vector describing the location of R library trees to search through, or NULL. The default value of NULL corresponds to all libraries currently known.

**Details**

`.packages()` returns the names of the currently attached packages *invisibly* whereas `.packages(all.available = TRUE)` gives (visibly) *all* packages available in the library location path `lib.loc`.

For a package to be regarded as being available it must have valid metadata (and hence be an installed package).

**Value**

A character vector of package base names, invisible unless `all.available = TRUE`.

**Author(s)**

R core; Guido Masarotto for the `all.available=TRUE` part of `.packages`.

**See Also**

[library](#), [.libPaths](#).

**Examples**

```
.packages() # maybe just "base"  
.packages(all.available = TRUE) # return all available as character vector  
require(splines)  
.packages() # "splines", too  
detach("package:splines")
```

---

zutils

*Miscellaneous Internal/Programming Utilities*

---

**Description**

Miscellaneous internal/programming utilities.

**Usage**

```
.standard_regexps()
```

**Details**

`.standard_regexps` returns a list of ‘standard’ regexps, including elements named `valid_package_name` and `valid_package_version` with the obvious meanings. The regexps are not anchored.



## Chapter 2

# The datasets package

---

`datasets`-package    *The R Datasets Package*

---

### Description

Base R datasets

### Details

This package contains a variety of datasets. For a complete list, use `library(help="datasets")`.

### Author(s)

R Development Core Team and contributors worldwide

Maintainer: R Core Team <R-core@r-project.org>

---

`ability.cov`    *Ability and Intelligence Tests*

---

### Description

Six tests were given to 112 individuals. The covariance matrix is given in this object.

### Usage

`ability.cov`

**Details**

The tests are described as

**general:** a non-verbal measure of general intelligence using Cattell's culture-fair test.

**picture:** a picture-completion test

**blocks:** block design

**maze:** mazes

**reading:** reading comprehension

**vocab:** vocabulary

Bartholomew gives both covariance and correlation matrices, but these are inconsistent. Neither are in the original paper.

**Source**

Bartholomew, D. J. (1987) *Latent Variable Analysis and Factor Analysis*. Griffin.

Bartholomew, D. J. and Knott, M. (1990) *Latent Variable Analysis and Factor Analysis*. Second Edition, Arnold.

**References**

Smith, G. A. and Stanley G. (1983) Clocking *g*: relating intelligence and measures of timed performance. *Intelligence*, **7**, 353–368.

**Examples**

```
require(stats)
(ability.FA <- factanal(factors = 1, covmat=ability.cov))
update(ability.FA, factors=2)
update(ability.FA, factors=2, rotation="promax")
```

---

airmiles

---

*Passenger Miles on Commercial US Airlines, 1937–1960*


---

**Description**

The revenue passenger miles flown by commercial airlines in the United States for each year from 1937 to 1960.

**Usage**

```
airmiles
```

**Format**

A time series of 24 observations; yearly, 1937–1960.

**Source**

F.A.A. Statistical Handbook of Aviation.

## References

Brown, R. G. (1963) *Smoothing, Forecasting and Prediction of Discrete Time Series*. Prentice-Hall.

## Examples

```
require(graphics)
plot(airmiles, main = "airmiles data",
     xlab = "Passenger-miles flown by U.S. commercial airlines", col = 4)
```

---

AirPassengers

*Monthly Airline Passenger Numbers 1949-1960*

---

## Description

The classic Box & Jenkins airline data. Monthly totals of international airline passengers, 1949 to 1960.

## Usage

```
AirPassengers
```

## Format

A monthly time series, in thousands.

## Source

Box, G. E. P., Jenkins, G. M. and Reinsel, G. C. (1976) *Time Series Analysis, Forecasting and Control*. Third Edition. Holden-Day. Series G.

## Examples

```
## Not run:
## These are quite slow and so not run by example(AirPassengers)

## The classic 'airline model', by full ML
(fit <- arima(log10(AirPassengers), c(0, 1, 1),
             seasonal = list(order=c(0, 1, 1), period=12)))
update(fit, method = "CSS")
update(fit, x=window(log10(AirPassengers), start = 1954))
pred <- predict(fit, n.ahead = 24)
tl <- pred$pred - 1.96 * pred$se
tu <- pred$pred + 1.96 * pred$se
ts.plot(AirPassengers, 10^tl, 10^tu, log = "y", lty = c(1,2,2))

## full ML fit is the same if the series is reversed, CSS fit is not
ap0 <- rev(log10(AirPassengers))
attributes(ap0) <- attributes(AirPassengers)
arima(ap0, c(0, 1, 1), seasonal = list(order=c(0, 1, 1), period=12))
arima(ap0, c(0, 1, 1), seasonal = list(order=c(0, 1, 1), period=12),
     method = "CSS")

## Structural Time Series
```



```

ap <- log10(AirPassengers) - 2
(fit <- StructTS(ap, type= "BSM"))
par(mfrow=c(1,2))
plot(cbind(ap, fitted(fit)), plot.type = "single")
plot(cbind(ap, tsSmooth(fit)), plot.type = "single")

## End(Not run)

```

---

airquality

*New York Air Quality Measurements*


---

### Description

Daily air quality measurements in New York, May to September 1973.

### Usage

```
airquality
```

### Format

A data frame with 154 observations on 6 variables.

[, 1]	Ozone	numeric	Ozone (ppb)
[, 2]	Solar.R	numeric	Solar R (lang)
[, 3]	Wind	numeric	Wind (mph)
[, 4]	Temp	numeric	Temperature (degrees F)
[, 5]	Month	numeric	Month (1–12)
[, 6]	Day	numeric	Day of month (1–31)

### Details

Daily readings of the following air quality values for May 1, 1973 (a Tuesday) to September 30, 1973.

- **Ozone:** Mean ozone in parts per billion from 1300 to 1500 hours at Roosevelt Island
- **Solar.R:** Solar radiation in Langleys in the frequency band 4000–7700 Angstroms from 0800 to 1200 hours at Central Park
- **Wind:** Average wind speed in miles per hour at 0700 and 1000 hours at LaGuardia Airport
- **Temp:** Maximum daily temperature in degrees Fahrenheit at La Guardia Airport.

### Source

The data were obtained from the New York State Department of Conservation (ozone data) and the National Weather Service (meteorological data).

### References

Chambers, J. M., Cleveland, W. S., Kleiner, B. and Tukey, P. A. (1983) *Graphical Methods for Data Analysis*. Belmont, CA: Wadsworth.

**Examples**

```
require(graphics)
pairs(airquality, panel = panel.smooth, main = "airquality data")
```

anscombe

*Anscombe's Quartet of "Identical" Simple Linear Regressions***Description**

Four  $x$ - $y$  datasets which have the same traditional statistical properties (mean, variance, correlation, regression line, etc.), yet are quite different.

**Usage**

```
anscombe
```

**Format**

A data frame with 11 observations on 8 variables.

```
x1 == x2 == x3  the integers 4:14, specially arranged
                x4  values 8 and 19
y1, y2, y3, y4  numbers in (3, 12.5) with mean 7.5 and sdev 2.03
```

**Source**

Tufte, Edward R. (1989) *The Visual Display of Quantitative Information*, 13–14. Graphics Press.

**References**

Anscombe, Francis J. (1973) Graphs in statistical analysis. *American Statistician*, **27**, 17–21.

**Examples**

```
require(stats); require(graphics)
summary(anscombe)

##-- now some "magic" to do the 4 regressions in a loop:
ff <- y ~ x
for(i in 1:4) {
  ff[2:3] <- lapply(paste(c("y","x"), i, sep=""), as.name)
  ## or  ff[[2]] <- as.name(paste("y", i, sep=""))
  ##      ff[[3]] <- as.name(paste("x", i, sep=""))
  assign(paste("lm.",i,sep=""), lmi <- lm(ff, data= anscombe))
  print(anova(lmi))
}

## See how close they are (numerically!)
sapply(objects(pattern="lm\\. [1-4]$", function(n) coef(get(n)))
lapply(objects(pattern="lm\\. [1-4]$",
              function(n) coef(summary(get(n))))

## Now, do what you should have done in the first place: PLOTS
```

```

op <- par(mfrow=c(2,2), mar=.1+c(4,4,1,1), oma= c(0,0,2,0))
for(i in 1:4) {
  ff[2:3] <- lapply(paste(c("y","x"), i, sep=""), as.name)
  plot(ff, data =anscombe, col="red", pch=21, bg = "orange", cex = 1.2,
       xlim=c(3,19), ylim=c(3,13))
  abline(get(paste("lm.", i, sep="")), col="blue")
}
mtext("Anscombe's 4 Regression data sets", outer = TRUE, cex=1.5)
par(op)

```

attenu

*The Joyner–Boore Attenuation Data***Description**

This data gives peak accelerations measured at various observation stations for 23 earthquakes in California. The data have been used by various workers to estimate the attenuating affect of distance on ground acceleration.

**Usage**

attenu

**Format**

A data frame with 182 observations on 5 variables.

[,1]	event	numeric	Event Number
[,2]	mag	numeric	Moment Magnitude
[,3]	station	factor	Station Number
[,4]	dist	numeric	Station-hypocenter distance (km)
[,5]	accel	numeric	Peak acceleration (g)

**Source**

Joyner, W.B., D.M. Boore and R.D. Porcella (1981). Peak horizontal acceleration and velocity from strong-motion records including records from the 1979 Imperial Valley, California earthquake. USGS Open File report 81-365. Menlo Park, Ca.

**References**

- Boore, D. M. and Joyner, W.B.(1982) The empirical prediction of ground motion, *Bull. Seism. Soc. Am.*, **72**, S269–S268.
- Bolt, B. A. and Abrahamson, N. A. (1982) New attenuation relations for peak and expected accelerations of strong ground motion, *Bull. Seism. Soc. Am.*, **72**, 2307–2321.
- Bolt B. A. and Abrahamson, N. A. (1983) Reply to W. B. Joyner & D. M. Boore’s “Comments on: New attenuation relations for peak and expected accelerations for peak and expected accelerations of strong ground motion”, *Bull. Seism. Soc. Am.*, **73**, 1481–1483.
- Brillinger, D. R. and Preisler, H. K. (1984) An exploratory analysis of the Joyner-Boore attenuation data, *Bull. Seism. Soc. Am.*, **74**, 1441–1449.

Brillinger, D. R. and Preisler, H. K. (1984) *Further analysis of the Joyner-Boore attenuation data*. Manuscript.

### Examples

```
require(graphics)
## check the data class of the variables
sapply(attenu, data.class)
summary(attenu)
pairs(attenu, main = "attenu data")
coplot(accel ~ dist | as.factor(event), data = attenu, show.given = FALSE)
coplot(log(accel) ~ log(dist) | as.factor(event),
       data = attenu, panel = panel.smooth, show.given = FALSE)
```

---

attitude

*The Chatterjee-Price Attitude Data*

---

### Description

From a survey of the clerical employees of a large financial organization, the data are aggregated from the questionnaires of the approximately 35 employees for each of 30 (randomly selected) departments. The numbers give the percent proportion of favourable responses to seven questions in each department.

### Usage

```
attitude
```

### Format

A dataframe with 30 observations on 7 variables. The first column are the short names from the reference, the second one the variable names in the data frame:

Y	rating	numeric	Overall rating
X[1]	complaints	numeric	Handling of employee complaints
X[2]	privileges	numeric	Does not allow special privileges
X[3]	learning	numeric	Opportunity to learn
X[4]	raises	numeric	Raises based on performance
X[5]	critical	numeric	Too critical
X[6]	advancel	numeric	Advancement

### Source

Chatterjee, S. and Price, B. (1977) *Regression Analysis by Example*. New York: Wiley. (Section 3.7, p.68ff of 2nd ed.(1991).)

### Examples

```
require(stats); require(graphics)
pairs(attitude, main = "attitude data")
summary(attitude)
summary(fml <- lm(rating ~ ., data = attitude))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
```

```

      mar = c(4.1, 4.1, 2.1, 1.1))
plot(fm1)
summary(fm2 <- lm(rating ~ complaints, data = attitude))
plot(fm2)
par(opar)

```

---

austres

*Quarterly Time Series of the Number of Australian Residents*


---

### Description

Numbers (in thousands) of Australian residents measured quarterly from March 1971 to March 1994. The object is of class "ts".

### Usage

```
austres
```

### Source

P. J. Brockwell and R. A. Davis (1996) *Introduction to Time Series and Forecasting*. Springer

---

beavers

*Body Temperature Series of Two Beavers*


---

### Description

Reynolds (1994) describes a small part of a study of the long-term temperature dynamics of beaver *Castor canadensis* in north-central Wisconsin. Body temperature was measured by telemetry every 10 minutes for four females, but data from a one period of less than a day for each of two animals is used there.

### Usage

```

beaver1
beaver2

```

### Format

The `beaver1` data frame has 114 rows and 4 columns on body temperature measurements at 10 minute intervals.

The `beaver2` data frame has 100 rows and 4 columns on body temperature measurements at 10 minute intervals.

The variables are as follows:

**day** Day of observation (in days since the beginning of 1990), December 12–13 (`beaver1`) and November 3–4 (`beaver2`).

**time** Time of observation, in the form 0330 for 3:30am

**temp** Measured body temperature in degrees Celsius.

**activ** Indicator of activity outside the retreat.

**Note**

The observation at 22:20 is missing in `beaver1`.

**Source**

P. S. Reynolds (1994) Time-series analyses of beaver body temperatures. Chapter 11 of Lange, N., Ryan, L., Billard, L., Brillinger, D., Conquest, L. and Greenhouse, J. eds (1994) *Case Studies in Biometry*. New York: John Wiley and Sons.

**Examples**

```
require(graphics)
(y1 <- range(beaver1$temp, beaver2$temp))

beaver.plot <- function(bdat, ...) {
  nam <- deparse(substitute(bdat))
  with(bdat, {
    # Hours since start of day:
    hours <- time %% 100 + 24*(day - day[1]) + (time %% 100)/60
    plot(hours, temp, type = "l", ...,
         main = paste(nam, "body temperature"))
    abline(h = 37.5, col = "gray", lty = 2)
    is.act <- activ == 1
    points(hours[is.act], temp[is.act], col = 2, cex = .8)
  })
}
op <- par(mfrow = c(2,1), mar = c(3,3,4,2), mgp = .9* 2:0)
beaver.plot(beaver1, ylim = y1)
beaver.plot(beaver2, ylim = y1)
par(op)
```

---

 BJsales

*Sales Data with Leading Indicator*


---

**Description**

The sales time series `BJsales` and leading indicator `BJsales.lead` each contain 150 observations. The objects are of class `"ts"`.

**Usage**

```
BJsales
BJsales.lead
```

**Source**

The data are given in Box & Jenkins (1976). Obtained from the Time Series Data Library at <http://www-personal.buseco.monash.edu.au/~hyndman/TSDL/>

## References

- G. E. P. Box and G. M. Jenkins (1976): *Time Series Analysis, Forecasting and Control*, Holden-Day, San Francisco, p. 537.
- P. J. Brockwell and R. A. Davis (1991): *Time Series: Theory and Methods*, Second edition, Springer Verlag, NY, pp. 414.

---

BOD

*Biochemical Oxygen Demand*

---

## Description

The BOD data frame has 6 rows and 2 columns giving the biochemical oxygen demand versus time in an evaluation of water quality.

## Usage

BOD

## Format

This data frame contains the following columns:

**Time** A numeric vector giving the time of the measurement (days).

**demand** A numeric vector giving the biochemical oxygen demand (mg/l).

## Source

Bates, D.M. and Watts, D.G. (1988), *Nonlinear Regression Analysis and Its Applications*, Wiley, Appendix A1.4.

Originally from Marske (1967), *Biochemical Oxygen Demand Data Interpretation Using Sum of Squares Surface* M.Sc. Thesis, University of Wisconsin – Madison.

## Examples

```
require(stats)
# simplest form of fitting a first-order model to these data
fm1 <- nls(demand ~ A*(1-exp(-exp(lrc)*Time)), data = BOD,
  start = c(A = 20, lrc = log(.35)))
coef(fm1)
print(fm1)
# using the plinear algorithm
fm2 <- nls(demand ~ (1-exp(-exp(lrc)*Time)), data = BOD,
  start = c(lrc = log(.35)), algorithm = "plinear", trace = TRUE)
# using a self-starting model
fm3 <- nls(demand ~ SSasympOrig(Time, A, lrc), data = BOD)
summary( fm3 )
```

cars

*Speed and Stopping Distances of Cars***Description**

The data give the speed of cars and the distances taken to stop. Note that the data were recorded in the 1920s.

**Usage**

```
cars
```

**Format**

A data frame with 50 observations on 2 variables.

```
[,1] speed  numeric  Speed (mph)
[,2] dist   numeric  Stopping distance (ft)
```

**Source**

Ezekiel, M. (1930) *Methods of Correlation Analysis*. Wiley.

**References**

McNeil, D. R. (1977) *Interactive Data Analysis*. Wiley.

**Examples**

```
require(stats); require(graphics)
plot(cars, xlab = "Speed (mph)", ylab = "Stopping distance (ft)",
     las = 1)
lines(lowess(cars$speed, cars$dist, f = 2/3, iter = 3), col = "red")
title(main = "cars data")
plot(cars, xlab = "Speed (mph)", ylab = "Stopping distance (ft)",
     las = 1, log = "xy")
title(main = "cars data (logarithmic scales)")
lines(lowess(cars$speed, cars$dist, f = 2/3, iter = 3), col = "red")
summary(fm1 <- lm(log(dist) ~ log(speed), data = cars))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
           mar = c(4.1, 4.1, 2.1, 1.1))
plot(fm1)
par(opar)

## An example of polynomial regression
plot(cars, xlab = "Speed (mph)", ylab = "Stopping distance (ft)",
     las = 1, xlim = c(0, 25))
d <- seq(0, 25, length.out = 200)
for(degree in 1:4) {
  fm <- lm(dist ~ poly(speed, degree), data = cars)
  assign(paste("cars", degree, sep="."), fm)
  lines(d, predict(fm, data.frame(speed=d)), col = degree)
}
anova(cars.1, cars.2, cars.3, cars.4)
```



ChickWeight

*Weight versus age of chicks on different diets***Description**

The `ChickWeight` data frame has 578 rows and 4 columns from an experiment on the effect of diet on early growth of chicks.

**Usage**

```
ChickWeight
```

**Format**

This data frame contains the following columns:

**weight** a numeric vector giving the body weight of the chick (gm).

**Time** a numeric vector giving the number of days since birth when the measurement was made.

**Chick** an ordered factor with levels 18 < ... < 48 giving a unique identifier for the chick. The ordering of the levels groups chicks on the same diet together and orders them according to their final weight (lightest to heaviest) within diet.

**Diet** a factor with levels 1, ..., 4 indicating which experimental diet the chick received.

**Details**

The body weights of the chicks were measured at birth and every second day thereafter until day 20. They were also measured on day 21. There were four groups on chicks on different protein diets.

**Source**

Crowder, M. and Hand, D. (1990), *Analysis of Repeated Measures*, Chapman and Hall (example 5.3)

Hand, D. and Crowder, M. (1996), *Practical Longitudinal Data Analysis*, Chapman and Hall (table A.2)

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer.

**Examples**

```
require(stats); require(graphics)
coplot(weight ~ Time | Chick, data = ChickWeight,
        type = "b", show.given = FALSE)
## fit a representative chick
fm1 <- nls(weight ~ SSlogis( Time, Asym, xmid, scal ),
           data = ChickWeight, subset = Chick == 1)
summary( fm1 )
```

---

`chickwts`*Chicken Weights by Feed Type*

---

### Description

An experiment was conducted to measure and compare the effectiveness of various feed supplements on the growth rate of chickens.

### Usage

```
chickwts
```

### Format

A data frame with 71 observations on 2 variables.

**weight** a numeric variable giving the chick weight.

**feed** a factor giving the feed type.

### Details

Newly hatched chicks were randomly allocated into six groups, and each group was given a different feed supplement. Their weights in grams after six weeks are given along with feed types.

### Source

Anonymous (1948) *Biometrika*, **35**, 214.

### References

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

### Examples

```
require(stats); require(graphics)
boxplot(weight ~ feed, data = chickwts, col = "lightgray",
        varwidth = TRUE, notch = TRUE, main = "chickwt data",
        ylab = "Weight at six weeks (gm)")
anova(fm1 <- lm(weight ~ feed, data = chickwts))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
           mar = c(4.1, 4.1, 2.1, 1.1))
plot(fm1)
par(opar)
```

**Description**

The CO2 data frame has 84 rows and 5 columns of data from an experiment on the cold tolerance of the grass species *Echinochloa crus-galli*.

**Usage**

```
CO2
```

**Format**

This data frame contains the following columns:

**Plant** an ordered factor with levels Qn1 < Qn2 < Qn3 < ... < Mc1 giving a unique identifier for each plant.

**Type** a factor with levels Quebec Mississippi giving the origin of the plant

**Treatment** a factor with levels nonchilled chilled

**conc** a numeric vector of ambient carbon dioxide concentrations (mL/L).

**uptake** a numeric vector of carbon dioxide uptake rates ( $\mu\text{mol}/\text{m}^2 \text{ sec}$ ).

**Details**

The  $\text{CO}_2$  uptake of six plants from Quebec and six plants from Mississippi was measured at several levels of ambient  $\text{CO}_2$  concentration. Half the plants of each type were chilled overnight before the experiment was conducted.

**Source**

Potvin, C., Lechowicz, M. J. and Tardif, S. (1990) "The statistical analysis of ecophysiological response curves obtained from experiments involving repeated measures", *Ecology*, **71**, 1389–1400.

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer.

**Examples**

```
require(stats); require(graphics)
coplot(uptake ~ conc | Plant, data = CO2, show.given = FALSE, type = "b")
## fit the data for the first plant
fml <- nls(uptake ~ SSasymp(conc, Asym, lrc, c0),
  data = CO2, subset = Plant == 'Qn1')
summary(fml)
## fit each plant separately
fmlist <- list()
for (pp in levels(CO2$Plant)) {
  fmlist[[pp]] <- nls(uptake ~ SSasymp(conc, Asym, lrc, c0),
    data = CO2, subset = Plant == pp)
}
## check the coefficients by plant
sapply(fmlist, coef)
```

---

`co2`*Mauna Loa Atmospheric CO2 Concentration*

---

**Description**

Atmospheric concentrations of CO<sub>2</sub> are expressed in parts per million (ppm) and reported in the preliminary 1997 SIO manometric mole fraction scale.

**Usage**`co2`**Format**

A time series of 468 observations; monthly from 1959 to 1997.

**Details**

The values for February, March and April of 1964 were missing and have been obtained by interpolating linearly between the values for January and May of 1964.

**Source**

Keeling, C. D. and Whorf, T. P., Scripps Institution of Oceanography (SIO), University of California, La Jolla, California USA 92093-0220.

<ftp://cdiac.esd.ornl.gov/pub/maunaloa-co2/maunaloa.co2>.

**References**

Cleveland, W. S. (1993) *Visualizing Data*. New Jersey: Summit Press.

**Examples**

```
require(graphics)
plot(co2, ylab = expression("Atmospheric concentration of CO"[2]),
     las = 1)
title(main = "co2 data set")
```

---

`crimtab`*Student's 3000 Criminals Data*

---

**Description**

Data of 3000 male criminals over 20 years old undergoing their sentences in the chief prisons of England and Wales.

**Usage**`crimtab`

## Format

A `table` object of `integer` counts, of dimension  $42 \times 22$  with a total count, `sum(crimtab)` of 3000.

The 42 `rownames` ("9.4", "9.5", ...) correspond to midpoints of intervals of finger lengths whereas the 22 column names (`colnames`) ("142.24", "144.78", ...) correspond to (body) heights of 3000 criminals, see also below.

## Details

Student is the pseudonym of William Sealy Gosset. In his 1908 paper he wrote (on page 13) at the beginning of section VI entitled *Practical Test of the forgoing Equations*:

“Before I had succeeded in solving my problem analytically, I had endeavoured to do so empirically. The material used was a correlation table containing the height and left middle finger measurements of 3000 criminals, from a paper by W. R. MacDonell (*Biometrika*, Vol. I., p. 219). The measurements were written out on 3000 pieces of cardboard, which were then very thoroughly shuffled and drawn at random. As each card was drawn its numbers were written down in a book, which thus contains the measurements of 3000 criminals in a random order. Finally, each consecutive set of 4 was taken as a sample—750 in all—and the mean, standard deviation, and correlation of each sample determined. The difference between the mean of each sample and the mean of the population was then divided by the standard deviation of the sample, giving us the  $z$  of Section III.”

The table is in fact page 216 and not page 219 in MacDonell(1902). In the MacDonell table, the middle finger lengths were given in mm and the heights in feet/inches intervals, they are both converted into cm here. The midpoints of intervals were used, e.g., where MacDonell has  $4'7''9/16 - 8''9/16$ , we have 142.24 which is  $2.54 * 56 = 2.54 * (4'8'')$ .

MacDonell credited the source of data (page 178) as follows: *The data on which the memoir is based were obtained, through the kindness of Dr Garson, from the Central Metric Office, New Scotland Yard...* He pointed out on page 179 that : *The forms were drawn at random from the mass on the office shelves; we are therefore dealing with a random sampling.*

## Source

<http://pbil.univ-lyon1.fr/R/donnees/criminals1902.txt> thanks to Jean R. Lobry and Anne-Béatrice Dufour.

## References

Garson, J.G. (1900) The metric system of identification of criminals, as used in in Great Britain and Ireland. *The Journal of the Anthropological Institute of Great Britain and Ireland* **30**, 161–198.

MacDonell, W.R. (1902) On criminal anthropometry and the identification of criminals. *Biometrika* **1**, 2, 177–227.

Student (1908) The probable error of a mean. *Biometrika* **6**, 1–25.

## Examples

```
require(stats)
dim(crimtab)
utils::str(crimtab)
## for nicer printing:
local({cT <- crimtab
      colnames(cT) <- substring(colnames(cT), 2, 3)
      print(cT, zero.print = " ")
})
```

```

## Repeat Student's experiment:

# 1) Reconstitute 3000 raw data for heights in inches and rounded to
#     nearest integer as in Student's paper:

(heIn <- round(as.numeric(colnames(crimtab)) / 2.54))
d.hei <- data.frame(height = rep(heIn, colSums(crimtab)))

# 2) shuffle the data:

set.seed(1)
d.hei <- d.hei[sample(1:3000), , drop = FALSE]

# 3) Make 750 samples each of size 4:

d.hei$sample <- as.factor(rep(1:750, each = 4))

# 4) Compute the means and standard deviations (n) for the 750 samples:

h.mean <- with(d.hei, tapply(height, sample, FUN = mean))
h.sd    <- with(d.hei, tapply(height, sample, FUN = sd)) * sqrt(3/4)

# 5) Compute the difference between the mean of each sample and
#     the mean of the population and then divide by the
#     standard deviation of the sample:

zobs <- (h.mean - mean(d.hei[, "height"])) / h.sd

# 6) Replace infinite values by +/- 6 as in Student's paper:

zobs[infZ <- is.infinite(zobs)] # 3 of them
zobs[infZ] <- 6 * sign(zobs[infZ])

# 7) Plot the distribution:

require(grDevices); require(graphics)
hist(x = zobs, probability = TRUE, xlab = "Student's z",
     col = grey(0.8), border = grey(0.5),
     main = "Distribution of Student's z score for 'crimtab' data")

```

---

discoveries

*Yearly Numbers of Important Discoveries*


---

### Description

The numbers of “great” inventions and scientific discoveries in each year from 1860 to 1959.

### Usage

```
discoveries
```

### Format

A time series of 100 values.

**Source**

The World Almanac and Book of Facts, 1975 Edition, pages 315–318.

**References**

McNeil, D. R. (1977) *Interactive Data Analysis*. Wiley.

**Examples**

```
require(graphics)
plot(discoveries, ylab = "Number of important discoveries",
     las = 1)
title(main = "discoveries data set")
```

---

 DNase

*Elisa assay of DNase*


---

**Description**

The DNase data frame has 176 rows and 3 columns of data obtained during development of an ELISA assay for the recombinant protein DNase in rat serum.

**Usage**

```
DNase
```

**Format**

This data frame contains the following columns:

**Run** an ordered factor with levels 10 < ... < 3 indicating the assay run.

**conc** a numeric vector giving the known concentration of the protein.

**density** a numeric vector giving the measured optical density (dimensionless) in the assay. Duplicate optical density measurements were obtained.

**Source**

Davidian, M. and Giltinan, D. M. (1995) *Nonlinear Models for Repeated Measurement Data*, Chapman & Hall (section 5.2.4, p. 134)

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer.

**Examples**

```
require(stats); require(graphics)
coplot(density ~ conc | Run, data = DNase,
      show.given = FALSE, type = "b")
coplot(density ~ log(conc) | Run, data = DNase,
      show.given = FALSE, type = "b")
## fit a representative run
fm1 <- nls(density ~ SSlogis( log(conc), Asym, xmid, scal ),
      data = DNase, subset = Run == 1)
## compare with a four-parameter logistic
```

```
fm2 <- nls(density ~ SSfpl( log(conc), A, B, xmid, scal ),
  data = DNase, subset = Run == 1)
summary(fm2)
anova(fm1, fm2)
```

---

 esoph

*Smoking, Alcohol and (O)esophageal Cancer*


---

### Description

Data from a case-control study of (o)esophageal cancer in Ile-et-Vilaine, France.

### Usage

```
esoph
```

### Format

A data frame with records for 88 age/alcohol/tobacco combinations.

[,1]	"agegp"	Age group	1 25–34 years 2 35–44 3 45–54 4 55–64 5 65–74 6 75+
[,2]	"alcgp"	Alcohol consumption	1 0–39 gm/day 2 40–79 3 80–119 4 120+
[,3]	"tobgp"	Tobacco consumption	1 0– 9 gm/day 2 10–19 3 20–29 4 30+
[,4]	"ncases"	Number of cases	
[,5]	"ncontrols"	Number of controls	

### Author(s)

Thomas Lumley

### Source

Breslow, N. E. and Day, N. E. (1980) *Statistical Methods in Cancer Research. 1: The Analysis of Case-Control Studies*. IARC Lyon / Oxford University Press.

### Examples

```
require(stats)
require(graphics) # for mosaicplot
summary(esoph)
## effects of alcohol, tobacco and interaction, age-adjusted
```



```

modell1 <- glm(cbind(ncases, ncontrols) ~ agegp + tobgp * alcgp,
              data = esoph, family = binomial())
anova(modell1)
## Try a linear effect of alcohol and tobacco
modell2 <- glm(cbind(ncases, ncontrols) ~ agegp + unclass(tobgp)
              + unclass(alcgp),
              data = esoph, family = binomial())
summary(modell2)
## Re-arrange data for a mosaic plot
ttt <- table(esoph$agegp, esoph$alcgp, esoph$tobgp)
ttt[ttt == 1] <- esoph$ncases
ttl <- table(esoph$agegp, esoph$alcgp, esoph$tobgp)
ttl[ttl == 1] <- esoph$ncontrols
tt <- array(c(ttt, ttl), c(dim(ttt),2),
            c(dimnames(ttt), list(c("Cancer", "control"))))
mosaicplot(tt, main = "esoph data set", color = TRUE)

```

euro

*Conversion Rates of Euro Currencies***Description**

Conversion rates between the various Euro currencies.

**Usage**

```
euro
euro.cross
```

**Format**

`euro` is a named vector of length 11, `euro.cross` a matrix of size 11 by 11, with `dimnames`.

**Details**

The data set `euro` contains the value of 1 Euro in all currencies participating in the European monetary union (Austrian Schilling ATS, Belgian Franc BEF, German Mark DEM, Spanish Peseta ESP, Finnish Markka FIM, French Franc FRF, Irish Punt IEP, Italian Lira ITL, Luxembourg Franc LUF, Dutch Guilder NLG and Portuguese Escudo PTE). These conversion rates were fixed by the European Union on December 31, 1998. To convert old prices to Euro prices, divide by the respective rate and round to 2 digits.

The data set `euro.cross` contains conversion rates between the various Euro currencies, i.e., the result of `outer(1 / euro, euro)`.

**Examples**

```

cbind(euro)

## These relations hold:
euro == signif(euro,6) # [6 digit precision in Euro's definition]
all(euro.cross == outer(1/euro, euro))

## Convert 20 Euro to Belgian Franc

```

```

20 * euro["BEF"]
## Convert 20 Austrian Schilling to Euro
20 / euro["ATS"]
## Convert 20 Spanish Pesetas to Italian Lira
20 * euro.cross["ESP", "ITL"]

require(graphics)
dotchart(euro,
         main = "euro data: 1 Euro in currency unit")
dotchart(1/euro,
         main = "euro data: 1 currency unit in Euros")
dotchart(log(euro, 10),
         main = "euro data: log10(1 Euro in currency unit)")

```

---

eurodist

*Distances Between European Cities*


---

### Description

The data give the road distances (in km) between 21 cities in Europe. The data are taken from a table in *The Cambridge Encyclopaedia*.

### Usage

```
eurodist
```

### Format

A `dist` object based on 21 objects. (You must have the **stats** package loaded to have the methods for this kind of object available).

### Source

Crystal, D. Ed. (1990) *The Cambridge Encyclopaedia*. Cambridge: Cambridge University Press,

---

EuStockMarkets

*Daily Closing Prices of Major European Stock Indices, 1991–1998*


---

### Description

Contains the daily closing prices of major European stock indices: Germany DAX (Ibis), Switzerland SMI, France CAC, and UK FTSE. The data are sampled in business time, i.e., weekends and holidays are omitted.

### Usage

```
EuStockMarkets
```

### Format

A multivariate time series with 1860 observations on 4 variables. The object is of class `"mts"`.

**Source**

The data were kindly provided by Erste Bank AG, Vienna, Austria.

---

faithful

*Old Faithful Geysier Data*

---

**Description**

Waiting time between eruptions and the duration of the eruption for the Old Faithful geyser in Yellowstone National Park, Wyoming, USA.

**Usage**

```
faithful
```

**Format**

A data frame with 272 observations on 2 variables.

[,1]	eruptions	numeric	Eruption time in mins
[,2]	waiting	numeric	Waiting time to next eruption (in mins)

**Details**

A closer look at `faithful$eruptions` reveals that these are heavily rounded times originally in seconds, where multiples of 5 are more frequent than expected under non-human measurement. For a better version of the eruption times, see the example below.

There are many versions of this dataset around: Azzalini and Bowman (1990) use a more complete version.

**Source**

W. Härdle.

**References**

Härdle, W. (1991) *Smoothing Techniques with Implementation in S*. New York: Springer.

Azzalini, A. and Bowman, A. W. (1990). A look at some data on the Old Faithful geyser. *Applied Statistics* **39**, 357–365.

**See Also**

`geyser` in package **MASS** for the Azzalini–Bowman version.

**Examples**

```
require(stats); require(graphics)
f.tit <- "faithful data: Eruptions of Old Faithful"

ne60 <- round(e60 <- 60 * faithful$eruptions)
```

```

all.equal(e60, ne60)           # relative diff. ~ 1/10000
table(zapsmall(abs(e60 - ne60))) # 0, 0.02 or 0.04
faithful$better.eruptions <- ne60 / 60
te <- table(ne60)
te[te >= 4]                   # (too) many multiples of 5 !
plot(names(te), te, type="h", main = f.tit, xlab = "Eruption time (sec)")

plot(faithful[, -3], main = f.tit,
     xlab = "Eruption time (min)",
     ylab = "Waiting time to next eruption (min)")
lines(lowess(faithful$eruptions, faithful$waiting, f = 2/3, iter = 3),
      col = "red")

```

---

Formaldehyde

*Determination of Formaldehyde*


---

### Description

These data are from a chemical experiment to prepare a standard curve for the determination of formaldehyde by the addition of chromotropic acid and concentrated sulphuric acid and the reading of the resulting purple color on a spectrophotometer.

### Usage

Formaldehyde

### Format

A data frame with 6 observations on 2 variables.

```

[ ,1] carb    numeric Carbohydrate (ml)
[ ,2] optden  numeric Optical Density

```

### Source

Bennett, N. A. and N. L. Franklin (1954) *Statistical Analysis in Chemistry and the Chemical Industry*. New York: Wiley.

### References

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

### Examples

```

require(stats); require(graphics)
plot(optden ~ carb, data = Formaldehyde,
     xlab = "Carbohydrate (ml)", ylab = "Optical Density",
     main = "Formaldehyde data", col = 4, las = 1)
abline(fm1 <- lm(optden ~ carb, data = Formaldehyde))
summary(fm1)
opar <- par(mfrow = c(2,2), oma = c(0, 0, 1.1, 0))
plot(fm1)
par(opar)

```

---

`freeny`*Freeny's Revenue Data*

---

**Description**

Freeny's data on quarterly revenue and explanatory variables.

**Usage**

```
freeny
freeny.x
freeny.y
```

**Format**

There are three 'freeny' data sets.

`freeny.y` is a time series with 39 observations on quarterly revenue from (1962,2Q) to (1971,4Q).

`freeny.x` is a matrix of explanatory variables. The columns are `freeny.y` lagged 1 quarter, price index, income level, and market potential.

Finally, `freeny` is a data frame with variables `y`, `lag.quarterly.revenue`, `price.index`, `income.level`, and `market.potential` obtained from the above two data objects.

**Source**

A. E. Freeny (1977) *A Portable Linear Regression Package with Test Programs*. Bell Laboratories memorandum.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**Examples**

```
require(stats); require(graphics)
summary(freeny)
pairs(freeny, main = "freeny data")
# gives warning: freeny$y has class "ts"

summary(fm1 <- lm(y ~ ., data = freeny))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
            mar = c(4.1, 4.1, 2.1, 1.1))

plot(fm1)
par(opar)
```

---

`HairEyeColor`*Hair and Eye Color of Statistics Students*

---

**Description**

Distribution of hair and eye color and sex in 592 statistics students.

**Usage**`HairEyeColor`**Format**

A 3-dimensional array resulting from cross-tabulating 592 observations on 3 variables. The variables and their levels are as follows:

No	Name	Levels
1	Hair	Black, Brown, Red, Blond
2	Eye	Brown, Blue, Hazel, Green
3	Sex	Male, Female

**Details**

The Hair  $\times$  Eye table comes from a survey of students at the University of Delaware reported by Snee (1974). The split by Sex was added by Friendly (1992a) for didactic purposes.

This data set is useful for illustrating various techniques for the analysis of contingency tables, such as the standard chi-squared test or, more generally, log-linear modelling, and graphical methods such as mosaic plots, sieve diagrams or association plots.

**Source**

<http://euclid.psych.yorku.ca/ftp/sas/vcd/catdata/haireye.sas>

Snee (1974) gives the two-way table aggregated over Sex. The Sex split of the ‘Brown hair, Brown eye’ cell was changed in R 2.6.0 to agree with that used by Friendly (2000).

**References**

Snee, R. D. (1974) Graphical display of two-way contingency tables. *The American Statistician*, **28**, 9–12.

Friendly, M. (1992a) Graphical methods for categorical data. *SAS User Group International Conference Proceedings*, **17**, 190–200. <http://www.math.yorku.ca/SCS/sugi/sugi17-paper.html>

Friendly, M. (1992b) Mosaic displays for loglinear models. *Proceedings of the Statistical Graphics Section*, American Statistical Association, pp. 61–68. <http://www.math.yorku.ca/SCS/Papers/asa92.html>

Friendly, M. (2000) *Visualizing Categorical Data*. SAS Institute, ISBN 1-58025-660-0.

**See Also**

[chisq.test](#), [loglin](#), [mosaicplot](#)

**Examples**

```
require(graphics)
## Full mosaic
mosaicplot(HairEyeColor)
## Aggregate over sex (as in Snee's original data)
x <- apply(HairEyeColor, c(1, 2), sum)
x
mosaicplot(x, main = "Relation between hair and eye color")
```

---

Harman23.cor

*Harman Example 2.3*


---

**Description**

A correlation matrix of eight physical measurements on 305 girls between ages seven and seventeen.

**Usage**

```
Harman23.cor
```

**Source**

Harman, H. H. (1976) *Modern Factor Analysis*, Third Edition Revised, University of Chicago Press, Table 2.3.

**Examples**

```
require(stats)
(Harman23.FA <- factanal(factors = 1, covmat = Harman23.cor))
for(factors in 2:4) print(update(Harman23.FA, factors = factors))
```

---

Harman74.cor

*Harman Example 7.4*


---

**Description**

A correlation matrix of 24 psychological tests given to 145 seventh and eight-grade children in a Chicago suburb by Holzinger and Swineford.

**Usage**

```
Harman74.cor
```

**Source**

Harman, H. H. (1976) *Modern Factor Analysis*, Third Edition Revised, University of Chicago Press, Table 7.4.

**Examples**

```
require(stats)
(Harman74.FA <- factanal(factors = 1, covmat = Harman74.cor))
for(factors in 2:5) print(update(Harman74.FA, factors = factors))
Harman74.FA <- factanal(factors = 5, covmat = Harman74.cor,
                      rotation="promax")
print(Harman74.FA$loadings, sort = TRUE)
```

Indometh

*Pharmacokinetics of Indomethicin***Description**

The `Indometh` data frame has 66 rows and 3 columns of data on the pharmacokinetics of indomethicin.

**Usage**

```
Indometh
```

**Format**

This data frame contains the following columns:

**Subject** an ordered factor with containing the subject codes. The ordering is according to increasing maximum response.

**time** a numeric vector of times at which blood samples were drawn (hr).

**conc** a numeric vector of plasma concentrations of indomethicin (mcg/ml).

**Details**

Each of the six subjects were given an intravenous injection of indomethicin.

**Source**

Kwan, Breault, Umbenhauer, McMahon and Duggan (1976), Kinetics of Indomethicin absorption, elimination, and enterohepatic circulation in man. *Journal of Pharmacokinetics and Biopharmaceutics*, **4**, 255–280.

Davidian, M. and Giltinan, D. M. (1995) *Nonlinear Models for Repeated Measurement Data*, Chapman & Hall (section 5.2.4, p. 134)

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer.

**Examples**

```
require(stats)
fm1 <- nls(conc ~ SSbiexp(time, A1, lrc1, A2, lrc2),
          data = Indometh, subset = Subject == 1)
summary(fm1)
```



infert

*Infertility after Spontaneous and Induced Abortion***Description**

This is a matched case-control study dating from before the availability of conditional logistic regression.

**Usage**

infert

**Format**

1. Education	0 = 0-5 years 1 = 6-11 years 2 = 12+ years
2. age	age in years of case
3. parity	count
4. number of prior induced abortions	0 = 0 1 = 1 2 = 2 or more
5. case status	1 = case 0 = control
6. number of prior spontaneous abortions	0 = 0 1 = 1 2 = 2 or more
7. matched set number	1-83
8. stratum number	1-63

**Note**

One case with two prior spontaneous abortions and two prior induced abortions is omitted.

**Source**

Trichopoulos et al. (1976) *Br. J. of Obst. and Gynaec.* **83**, 645–650.

**Examples**

```
require(stats)
modell1 <- glm(case ~ spontaneous+induced, data=infert, family=binomial())
summary(modell1)
## adjusted for other potential confounders:
summary(model2 <- glm(case ~ age+parity+education+spontaneous+induced,
                      data=infert, family=binomial()))
## Really should be analysed by conditional logistic regression
## which is in the survival package
if(require(survival)){
```

```

model3 <- clogit(case~spontaneous+induced+strata(stratum), data=infert)
print(summary(model3))
detach()# survival (conflicts)
}

```

---

InsectSprays                      *Effectiveness of Insect Sprays*

---

### Description

The counts of insects in agricultural experimental units treated with different insecticides.

### Usage

```
InsectSprays
```

### Format

A data frame with 72 observations on 2 variables.

[,1]	count	numeric	Insect count
[,2]	spray	factor	The type of spray

### Source

Beall, G., (1942) The Transformation of data from entomological field experiments, *Biometrika*, **29**, 243–262.

### References

McNeil, D. (1977) *Interactive Data Analysis*. New York: Wiley.

### Examples

```

require(stats); require(graphics)
boxplot(count ~ spray, data = InsectSprays,
        xlab = "Type of spray", ylab = "Insect count",
        main = "InsectSprays data", varwidth = TRUE, col = "lightgray")
fm1 <- aov(count ~ spray, data = InsectSprays)
summary(fm1)
opar <- par(mfrow = c(2,2), oma = c(0, 0, 1.1, 0))
plot(fm1)
fm2 <- aov(sqrt(count) ~ spray, data = InsectSprays)
summary(fm2)
plot(fm2)
par(opar)

```

---

iris                                      *Edgar Anderson's Iris Data*

---

## Description

This famous (Fisher's or Anderson's) iris data set gives the measurements in centimeters of the variables sepal length and width and petal length and width, respectively, for 50 flowers from each of 3 species of iris. The species are *Iris setosa*, *versicolor*, and *virginica*.

## Usage

```
iris
iris3
```

## Format

`iris` is a data frame with 150 cases (rows) and 5 variables (columns) named `Sepal.Length`, `Sepal.Width`, `Petal.Length`, `Petal.Width`, and `Species`.

`iris3` gives the same data arranged as a 3-dimensional array of size 50 by 4 by 3, as represented by S-PLUS. The first dimension gives the case number within the species subsample, the second the measurements with names `Sepal L.`, `Sepal W.`, `Petal L.`, and `Petal W.`, and the third the species.

## Source

Fisher, R. A. (1936) The use of multiple measurements in taxonomic problems. *Annals of Eugenics*, 7, Part II, 179–188.

The data were collected by Anderson, Edgar (1935). The irises of the Gaspé Peninsula, *Bulletin of the American Iris Society*, 59, 2–5.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (has `iris3` as `iris`.)

## See Also

[matplot](#) some examples of which use `iris`.

## Examples

```
dni3 <- dimnames(iris3)
ii <- data.frame(matrix(aperm(iris3, c(1,3,2)), ncol=4,
                        dimnames = list(NULL, sub(" L.", ".Length",
                                                sub(" W.", ".Width", dni3[[2]]))),
                  Species = gl(3, 50, labels=sub("S", "s", sub("V", "v", dni3[[3]]))))
all.equal(ii, iris) # TRUE
```

---

 islands

*Areas of the World's Major Landmasses*


---

**Description**

The areas in thousands of square miles of the landmasses which exceed 10,000 square miles.

**Usage**

```
islands
```

**Format**

A named vector of length 48.

**Source**

The World Almanac and Book of Facts, 1975, page 406.

**References**

McNeil, D. R. (1977) *Interactive Data Analysis*. Wiley.

**Examples**

```
require(graphics)
dotchart(log(islands, 10),
  main = "islands data: log10(area) (log10(sq. miles))")
dotchart(log(islands[order(islands)], 10),
  main = "islands data: log10(area) (log10(sq. miles))")
```

---

 JohnsonJohnson

*Quarterly Earnings per Johnson & Johnson Share*


---

**Description**

Quarterly earnings (dollars) per Johnson & Johnson share 1960–80.

**Usage**

```
JohnsonJohnson
```

**Format**

A quarterly time series

**Source**

Shumway, R. H. and Stoffer, D. S. (2000) *Time Series Analysis and its Applications*. Second Edition. Springer. Example 1.1.

**Examples**

```
require(stats); require(graphics)
JJ <- log10(JohnsonJohnson)
plot(JJ)
(fit <- StructTS(JJ, type="BSM"))
tsdiag(fit)
sm <- tsSmooth(fit)
plot(cbind(JJ, sm[, 1], sm[, 3]-0.5), plot.type = "single",
      col = c("black", "green", "blue"))
abline(h = -0.5, col = "grey60")

monthplot(fit)
```

---

LakeHuron

*Level of Lake Huron 1875–1972*


---

**Description**

Annual measurements of the level, in feet, of Lake Huron 1875–1972.

**Usage**

LakeHuron

**Format**

A time series of length 98.

**Source**

Brockwell, P. J. and Davis, R. A. (1991). *Time Series and Forecasting Methods*. Second edition. Springer, New York. Series A, page 555.

Brockwell, P. J. and Davis, R. A. (1996). *Introduction to Time Series and Forecasting*. Springer, New York. Sections 5.1 and 7.6.

---

lh

*Luteinizing Hormone in Blood Samples*


---

**Description**

A regular time series giving the luteinizing hormone in blood samples at 10 mins intervals from a human female, 48 samples.

**Usage**

lh

**Source**

P.J. Diggle (1990) *Time Series: A Biostatistical Introduction*. Oxford, table A.1, series 3

---

LifeCycleSavings     *Intercountry Life-Cycle Savings Data*

---

### Description

Data on the savings ratio 1960–1970.

### Usage

LifeCycleSavings

### Format

A data frame with 50 observations on 5 variables.

[,1]	sr	numeric	aggregate personal savings
[,2]	pop15	numeric	% of population under 15
[,3]	pop75	numeric	% of population over 75
[,4]	dpi	numeric	real per-capita disposable income
[,5]	ddpi	numeric	% growth rate of dpi

### Details

Under the life-cycle savings hypothesis as developed by Franco Modigliani, the savings ratio (aggregate personal saving divided by disposable income) is explained by per-capita disposable income, the percentage rate of change in per-capita disposable income, and two demographic variables: the percentage of population less than 15 years old and the percentage of the population over 75 years old. The data are averaged over the decade 1960–1970 to remove the business cycle or other short-term fluctuations.

### Source

The data were obtained from Belsley, Kuh and Welsch (1980). They in turn obtained the data from Sterling (1977).

### References

- Sterling, Arnie (1977) Unpublished BS Thesis. Massachusetts Institute of Technology.
- Belsley, D. A., Kuh, E. and Welsch, R. E. (1980) *Regression Diagnostics*. New York: Wiley.

### Examples

```
require(stats); require(graphics)
pairs(LifeCycleSavings, panel = panel.smooth,
      main = "LifeCycleSavings data")
fml <- lm(sr ~ pop15 + pop75 + dpi + ddpi, data = LifeCycleSavings)
summary(fml)
```

---

Loblolly

*Growth of Loblolly pine trees*


---

**Description**

The `Loblolly` data frame has 84 rows and 3 columns of records of the growth of Loblolly pine trees.

**Usage**

```
Loblolly
```

**Format**

This data frame contains the following columns:

**height** a numeric vector of tree heights (ft).

**age** a numeric vector of tree ages (yr).

**Seed** an ordered factor indicating the seed source for the tree. The ordering is according to increasing maximum height.

**Source**

Kung, F. H. (1986), Fitting logistic growth curve with predetermined carrying capacity, in *Proceedings of the Statistical Computing Section, American Statistical Association*, 340–343.

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer.

**Examples**

```
require(stats); require(graphics)
plot(height ~ age, data = Loblolly, subset = Seed == 329,
      xlab = "Tree age (yr)", las = 1,
      ylab = "Tree height (ft)",
      main = "Loblolly data and fitted curve (Seed 329 only)")
fm1 <- nls(height ~ SSasymp(age, Asym, R0, lrc),
          data = Loblolly, subset = Seed == 329)
summary(fm1)
age <- seq(0, 30, length.out = 101)
lines(age, predict(fm1, list(age = age)))
```

---

longley

*Longley's Economic Regression Data*


---

**Description**

A macroeconomic data set which provides a well-known example for a highly collinear regression.

**Usage**

```
longley
```

**Format**

A data frame with 7 economical variables, observed yearly from 1947 to 1962 ( $n = 16$ ).

**GNP.deflator:** GNP implicit price deflator (1954 = 100)

**GNP:** Gross National Product.

**Unemployed:** number of unemployed.

**Armed.Forces:** number of people in the armed forces.

**Population:** 'noninstitutionalized' population  $\geq 14$  years of age.

**Year:** the year (time).

**Employed:** number of people employed.

The regression `lm(Employed ~ .)` is known to be highly collinear.

**Source**

J. W. Longley (1967) An appraisal of least-squares programs from the point of view of the user. *Journal of the American Statistical Association*, **62**, 819–841.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**Examples**

```
require(stats); require(graphics)
## give the data set in the form it is used in S-PLUS:
longley.x <- data.matrix(longley[, 1:6])
longley.y <- longley[, "Employed"]
pairs(longley, main = "longley data")
summary(fm1 <- lm(Employed ~ ., data = longley))
opar <- par(mfrow = c(2, 2), oma = c(0, 0, 1.1, 0),
           mar = c(4.1, 4.1, 2.1, 1.1))
plot(fm1)
par(opar)
```

---

lynx

*Annual Canadian Lynx trappings 1821–1934*


---

**Description**

Annual numbers of lynx trappings for 1821–1934 in Canada. Taken from Brockwell & Davis (1991), this appears to be the series considered by Campbell & Walker (1977).

**Usage**

```
lynx
```

**Source**

Brockwell, P. J. and Davis, R. A. (1991) *Time Series and Forecasting Methods*. Second edition. Springer. Series G (page 557).



## References

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- Campbell, M. J. and A. M. Walker (1977). A Survey of statistical work on the Mackenzie River series of annual Canadian lynx trappings for the years 1821–1934 and a new analysis. *Journal of the Royal Statistical Society series A*, **140**, 411–431.

---

morley

*Michaelson-Morley Speed of Light Data*

---

## Description

The classical data of Michaelson and Morley on the speed of light. The data consists of five experiments, each consisting of 20 consecutive ‘runs’. The response is the speed of light measurement, suitably coded.

## Usage

morley

## Format

A data frame contains the following components:

- Expt The experiment number, from 1 to 5.
- Run The run number within each experiment.
- Speed Speed-of-light measurement.

## Details

The data is here viewed as a randomized block experiment with ‘experiment’ and ‘run’ as the factors. ‘run’ may also be considered a quantitative variate to account for linear (or polynomial) changes in the measurement over the course of a single experiment.

## Source

A. J. Weekes (1986) *A Genstat Primer*. London: Edward Arnold.

## Examples

```
require(stats); require(graphics)
morley$Expt <- factor(morley$Expt)
morley$Run <- factor(morley$Run)

xtabs(~ Expt + Run, data = morley)# 5 x 20 balanced (two-way)
plot(Speed ~ Expt, data = morley,
     main = "Speed of Light Data", xlab = "Experiment No.")
fm <- aov(Speed ~ Run + Expt, data = morley)
summary(fm)
fm0 <- update(fm, . ~ . - Run)
anova(fm0, fm)
```

mtcars

*Motor Trend Car Road Tests***Description**

The data was extracted from the 1974 *Motor Trend* US magazine, and comprises fuel consumption and 10 aspects of automobile design and performance for 32 automobiles (1973–74 models).

**Usage**

```
mtcars
```

**Format**

A data frame with 32 observations on 11 variables.

[, 1]	mpg	Miles/(US) gallon
[, 2]	cyl	Number of cylinders
[, 3]	disp	Displacement (cu.in.)
[, 4]	hp	Gross horsepower
[, 5]	drat	Rear axle ratio
[, 6]	wt	Weight (lb/1000)
[, 7]	qsec	1/4 mile time
[, 8]	vs	V/S
[, 9]	am	Transmission (0 = automatic, 1 = manual)
[,10]	gear	Number of forward gears
[,11]	carb	Number of carburetors

**Source**

Henderson and Velleman (1981), Building multiple regression models interactively. *Biometrics*, **37**, 391–411.

**Examples**

```
require(graphics)
pairs(mtcars, main = "mtcars data")
coplot(mpg ~ disp | as.factor(cyl), data = mtcars,
       panel = panel.smooth, rows = 1)
```

nhtemp

*Average Yearly Temperatures in New Haven***Description**

The mean annual temperature in degrees Fahrenheit in New Haven, Connecticut, from 1912 to 1971.

**Usage**

```
nhtemp
```

**Format**

A time series of 60 observations.

**Source**

Vaux, J. E. and Brinker, N. B. (1972) *Cycles*, **1972**, 117–121.

**References**

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

**Examples**

```
require(stats); require(graphics)
plot(nhtemp, main = "nhtemp data",
     ylab = "Mean annual temperature in New Haven, CT (deg. F)")
```

---

Nile

*Flow of the River Nile*

---

**Description**

Measurements of the annual flow of the river Nile at Ashwan 1871–1970.

**Usage**

Nile

**Format**

A time series of length 100.

**Source**

Durbin, J. and Koopman, S. J. (2001) *Time Series Analysis by State Space Methods*. Oxford University Press. <http://www.ssfpack.com/DKbook.html>

**References**

Balke, N. S. (1993) Detecting level shifts in time series. *Journal of Business and Economic Statistics* **11**, 81–92.

Cobb, G. W. (1978) The problem of the Nile: conditional solution to a change-point problem. *Biometrika* **65**, 243–51.

**Examples**

```

require(stats); require(graphics)
par(mfrow = c(2,2))
plot(Nile)
acf(Nile)
pacf(Nile)
ar(Nile) # selects order 2
cpgram(ar(Nile)$resid)
par(mfrow = c(1,1))
arima(Nile, c(2, 0, 0))

## Now consider missing values, following Durbin & Koopman
NileNA <- Nile
NileNA[c(21:40, 61:80)] <- NA
arima(NileNA, c(2, 0, 0))
plot(NileNA)
pred <-
  predict(arima(window(NileNA, 1871, 1890), c(2,0,0)), n.ahead = 20)
lines(pred$pred, lty = 3, col = "red")
lines(pred$pred + 2*pred$se, lty=2, col="blue")
lines(pred$pred - 2*pred$se, lty=2, col="blue")
pred <-
  predict(arima(window(NileNA, 1871, 1930), c(2,0,0)), n.ahead = 20)
lines(pred$pred, lty = 3, col = "red")
lines(pred$pred + 2*pred$se, lty=2, col="blue")
lines(pred$pred - 2*pred$se, lty=2, col="blue")

## Structural time series models
par(mfrow = c(3, 1))
plot(Nile)
## local level model
(fit <- StructTS(Nile, type = "level"))
lines(fitted(fit), lty = 2) # contemporaneous smoothing
lines(tsSmooth(fit), lty = 2, col = 4) # fixed-interval smoothing
plot(residuals(fit)); abline(h = 0, lty = 3)
## local trend model
(fit2 <- StructTS(Nile, type = "trend")) ## constant trend fitted
pred <- predict(fit, n.ahead = 30)
## with 50% confidence interval
ts.plot(Nile, pred$pred,
        pred$pred + 0.67*pred$se, pred$pred - 0.67*pred$se)

## Now consider missing values
plot(NileNA)
(fit3 <- StructTS(NileNA, type = "level"))
lines(fitted(fit3), lty = 2)
lines(tsSmooth(fit3), lty = 3)
plot(residuals(fit3)); abline(h = 0, lty = 3)

```

**Description**

A time series object containing average air temperatures at Nottingham Castle in degrees Fahrenheit for 20 years.

**Usage**

```
nottem
```

**Source**

Anderson, O. D. (1976) *Time Series Analysis and Forecasting: The Box-Jenkins approach*. Butterworths. Series R.

**Examples**

```
## Not run: require(stats); require(graphics)
nott <- window(nottem, end=c(1936,12))
fit <- arima(nott,order=c(1,0,0), list(order=c(2,1,0), period=12))
nott.fore <- predict(fit, n.ahead=36)
ts.plot(nott, nott.fore$pred, nott.fore$pred+2*nott.fore$se,
        nott.fore$pred-2*nott.fore$se, gpars=list(col=c(1,1,4,4)))

## End(Not run)
```

---

occupationalStatus *Occupational Status of Fathers and their Sons*

---

**Description**

Cross-classification of a sample of British males according to each subject's occupational status and his father's occupational status.

**Usage**

```
occupationalStatus
```

**Format**

A `table` of counts, with classifying factors `origin` (father's occupational status; levels 1:8) and `destination` (son's occupational status; levels 1:8).

**Source**

Goodman, L. A. (1979) Simple Models for the Analysis of Association in Cross-Classifications having Ordered Categories. *J. Am. Stat. Assoc.*, **74** (367), 537–552.

The data set has been in package `gnm` and been provided by the package authors.

**Examples**

```
require(stats); require(graphics)

plot(occupationalStatus)

## Fit a uniform association model separating diagonal effects
Diag <- as.factor(diag(1:8))
Rscore <- scale(as.numeric(row(occupationalStatus)), scale = FALSE)
Cscore <- scale(as.numeric(col(occupationalStatus)), scale = FALSE)
modUnif <- glm(Freq ~ origin + destination + Diag + Rscore:Cscore,
              family = poisson, data = occupationalStatus)

summary(modUnif)
plot(modUnif) # 4 plots, with warning about h_ii ~= 1
```

Orange

*Growth of Orange Trees***Description**

The Orange data frame has 35 rows and 3 columns of records of the growth of orange trees.

**Usage**

```
Orange
```

**Format**

This data frame contains the following columns:

**Tree** an ordered factor indicating the tree on which the measurement is made. The ordering is according to increasing maximum diameter.

**age** a numeric vector giving the age of the tree (days since 1968/12/31)

**circumference** a numeric vector of trunk circumferences (mm). This is probably “circumference at breast height”, a standard measurement in forestry.

**Source**

Draper, N. R. and Smith, H. (1998), *Applied Regression Analysis (3rd ed)*, Wiley (exercise 24.N).

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer.

**Examples**

```
require(stats); require(graphics)
coplot(circumference ~ age | Tree, data = Orange, show.given = FALSE)
fml <- nls(circumference ~ SSlogis(age, Asym, xmid, scal),
          data = Orange, subset = Tree == 3)
plot(circumference ~ age, data = Orange, subset = Tree == 3,
     xlab = "Tree age (days since 1968/12/31)",
     ylab = "Tree circumference (mm)", las = 1,
     main = "Orange tree data and fitted model (Tree 3 only)")
age <- seq(0, 1600, length.out = 101)
lines(age, predict(fml, list(age = age)))
```

OrchardSprays

*Potency of Orchard Sprays***Description**

An experiment was conducted to assess the potency of various constituents of orchard sprays in repelling honeybees, using a Latin square design.

**Usage**

OrchardSprays

**Format**

A data frame with 64 observations on 4 variables.

[,1]	rowpos	numeric	Row of the design
[,2]	colpos	numeric	Column of the design
[,3]	treatment	factor	Treatment level
[,4]	decrease	numeric	Response

**Details**

Individual cells of dry comb were filled with measured amounts of lime sulphur emulsion in sucrose solution. Seven different concentrations of lime sulphur ranging from a concentration of 1/100 to 1/1,562,500 in successive factors of 1/5 were used as well as a solution containing no lime sulphur.

The responses for the different solutions were obtained by releasing 100 bees into the chamber for two hours, and then measuring the decrease in volume of the solutions in the various cells.

An  $8 \times 8$  Latin square design was used and the treatments were coded as follows:

A	highest level of lime sulphur
B	next highest level of lime sulphur
.	
.	
.	
G	lowest level of lime sulphur
H	no lime sulphur

**Source**

Finney, D. J. (1947) *Probit Analysis*. Cambridge.

**References**

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

**Examples**

```
require(graphics)
pairs(OrchardSprays, main = "OrchardSprays data")
```

---

 PlantGrowth

*Results from an Experiment on Plant Growth*


---

**Description**

Results from an experiment to compare yields (as measured by dried weight of plants) obtained under a control and two different treatment conditions.

**Usage**

```
PlantGrowth
```

**Format**

A data frame of 30 cases on 2 variables.

[, 1]	weight	numeric
[, 2]	group	factor

The levels of group are 'ctrl', 'trt1', and 'trt2'.

**Source**

Dobson, A. J. (1983) *An Introduction to Statistical Modelling*. London: Chapman and Hall.

**Examples**

```
## One factor ANOVA example from Dobson's book, cf. Table 7.4:
require(stats); require(graphics)
boxplot(weight ~ group, data = PlantGrowth, main = "PlantGrowth data",
        ylab = "Dried weight of plants", col = "lightgray",
        notch = TRUE, varwidth = TRUE)
anova(lm(weight ~ group, data = PlantGrowth))
```

---

 precip

*Annual Precipitation in US Cities*


---

**Description**

The average amount of precipitation (rainfall) in inches for each of 70 United States (and Puerto Rico) cities.

**Usage**

```
precip
```

**Format**

A named vector of length 70.



**Source**

Statistical Abstracts of the United States, 1975.

**References**

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

**Examples**

```
require(graphics)
dotchart(precip[order(precip)], main = "precip data")
title(sub = "Average annual precipitation (in.)")
```

---

presidents

*Quarterly Approval Ratings of US Presidents*

---

**Description**

The (approximately) quarterly approval rating for the President of the United states from the first quarter of 1945 to the last quarter of 1974.

**Usage**

```
presidents
```

**Format**

A time series of 120 values.

**Details**

The data are actually a fudged version of the approval ratings. See McNeil's book for details.

**Source**

The Gallup Organisation.

**References**

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

**Examples**

```
require(stats); require(graphics)
plot(presidents, las = 1, ylab = "Approval rating (%)",
     main = "presidents data")
```

---

 pressure

*Vapor Pressure of Mercury as a Function of Temperature*


---

**Description**

Data on the relation between temperature in degrees Celsius and vapor pressure of mercury in millimeters (of mercury).

**Usage**

```
pressure
```

**Format**

A data frame with 19 observations on 2 variables.

[, 1]	temperature	numeric	temperature (deg C)
[, 2]	pressure	numeric	pressure (mm)

**Source**

Weast, R. C., ed. (1973) *Handbook of Chemistry and Physics*. CRC Press.

**References**

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

**Examples**

```
require(graphics)
plot(pressure, xlab = "Temperature (deg C)",
     ylab = "Pressure (mm of Hg)",
     main = "pressure data: Vapor Pressure of Mercury")
plot(pressure, xlab = "Temperature (deg C)", log = "y",
     ylab = "Pressure (mm of Hg)",
     main = "pressure data: Vapor Pressure of Mercury")
```

---

 Puromycin

*Reaction Velocity of an Enzymatic Reaction*


---

**Description**

The `Puromycin` data frame has 23 rows and 3 columns of the reaction velocity versus substrate concentration in an enzymatic reaction involving untreated cells or cells treated with Puromycin.

**Usage**

```
Puromycin
```

**Format**

This data frame contains the following columns:

**conc** a numeric vector of substrate concentrations (ppm)

**rate** a numeric vector of instantaneous reaction rates (counts/min/min)

**state** a factor with levels `treated` `untreated`

**Details**

Data on the velocity of an enzymatic reaction were obtained by Treloar (1974). The number of counts per minute of radioactive product from the reaction was measured as a function of substrate concentration in parts per million (ppm) and from these counts the initial rate (or velocity) of the reaction was calculated (counts/min/min). The experiment was conducted once with the enzyme treated with Puromycin, and once with the enzyme untreated.

**Source**

Bates, D.M. and Watts, D.G. (1988), *Nonlinear Regression Analysis and Its Applications*, Wiley, Appendix A1.3.

Treloar, M. A. (1974), *Effects of Puromycin on Galactosyltransferase in Golgi Membranes*, M.Sc. Thesis, U. of Toronto.

**Examples**

```
require(stats); require(graphics)
plot(rate ~ conc, data = Puromycin, las = 1,
      xlab = "Substrate concentration (ppm)",
      ylab = "Reaction velocity (counts/min/min)",
      pch = as.integer(Puromycin$state),
      col = as.integer(Puromycin$state),
      main = "Puromycin data and fitted Michaelis-Menten curves")
## simplest form of fitting the Michaelis-Menten model to these data
fm1 <- nls(rate ~ Vm * conc / (K + conc), data = Puromycin,
           subset = state == "treated",
           start = c(Vm = 200, K = 0.05), trace = TRUE)
fm2 <- nls(rate ~ Vm * conc / (K + conc), data = Puromycin,
           subset = state == "untreated",
           start = c(Vm = 160, K = 0.05), trace = TRUE)
summary(fm1)
summary(fm2)
## using partial linearity
fm3 <- nls(rate ~ conc / (K + conc), data = Puromycin,
           subset = state == "treated", start = c(K = 0.05),
           algorithm = "plinear", trace = TRUE)
## using a self-starting model
fm4 <- nls(rate ~ SSmicmen(conc, Vm, K), data = Puromycin,
           subset = state == "treated")
summary(fm4)
## add fitted lines to the plot
conc <- seq(0, 1.2, length.out = 101)
lines(conc, predict(fm1, list(conc = conc)), lty = 1, col = 1)
lines(conc, predict(fm2, list(conc = conc)), lty = 2, col = 2)
legend(0.8, 120, levels(Puromycin$state),
      col = 1:2, lty = 1:2, pch = 1:2)
```

---

 quakes

*Locations of Earthquakes off Fiji*


---

**Description**

The data set give the locations of 1000 seismic events of MB > 4.0. The events occurred in a cube near Fiji since 1964.

**Usage**

quakes

**Format**

A data frame with 1000 observations on 5 variables.

[,1]	lat	numeric	Latitude of event
[,2]	long	numeric	Longitude
[,3]	depth	numeric	Depth (km)
[,4]	mag	numeric	Richter Magnitude
[,5]	stations	numeric	Number of stations reporting

**Details**

There are two clear planes of seismic activity. One is a major plate junction; the other is the Tonga trench off New Zealand. These data constitute a subsample from a larger dataset of containing 5000 observations.

**Source**

This is one of the Harvard PRIM-H project data sets. They in turn obtained it from Dr. John Woodhouse, Dept. of Geophysics, Harvard University.

**Examples**

```
require(graphics)
pairs(quakes, main = "Fiji Earthquakes, N = 1000", cex.main=1.2, pch=".")
```

---

 randu

*Random Numbers from Congruential Generator RANDU*


---

**Description**

400 triples of successive random numbers were taken from the VAX FORTRAN function RANDU running under VMS 1.5.

**Usage**

randu

**Format**

A data frame with 400 observations on 3 variables named  $x$ ,  $y$  and  $z$  which give the first, second and third random number in the triple.

**Details**

In three dimensional displays it is evident that the triples fall on 15 parallel planes in 3-space. This can be shown theoretically to be true for all triples from the RANDU generator.

These particular 400 triples start 5 apart in the sequence, that is they are  $(U[5i+1], U[5i+2], U[5i+3])$ ,  $i = 0, \dots, 399$ , and they are rounded to 6 decimal places.

Under VMS versions 2.0 and higher, this problem has been fixed.

**Source**

David Donoho

**Examples**

```
## Not run: ## We could re-generate the dataset by the following R code
seed <- as.double(1)
RANDU <- function() {
  seed <<- ((2^16 + 3) * seed) %% (2^31)
  seed/(2^31)
}
for(i in 1:400) {
  U <- c(RANDU(), RANDU(), RANDU(), RANDU(), RANDU())
  print(round(U[1:3], 6))
}
## End(Not run)
```

---

rivers

*Lengths of Major North American Rivers*

---

**Description**

This data set gives the lengths (in miles) of 141 “major” rivers in North America, as compiled by the US Geological Survey.

**Usage**

```
rivers
```

**Format**

A vector containing 141 observations.

**Source**

World Almanac and Book of Facts, 1975, page 406.

**References**

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

---

 rock

*Measurements on Petroleum Rock Samples*


---

**Description**

Measurements on 48 rock samples from a petroleum reservoir.

**Usage**

rock

**Format**

A data frame with 48 rows and 4 numeric columns.

[,1]	area	area of pores space, in pixels out of 256 by 256
[,2]	peri	perimeter in pixels
[,3]	shape	perimeter/sqrt(area)
[,4]	perm	permeability in milli-Darcies

**Details**

Twelve core samples from petroleum reservoirs were sampled by 4 cross-sections. Each core sample was measured for permeability, and each cross-section has total area of pores, total perimeter of pores, and shape.

**Source**

Data from BP Research, image analysis by Ronit Katz, U. Oxford.

---

 sleep

*Student's Sleep Data*


---

**Description**

Data which show the effect of two soporific drugs (increase in hours of sleep compared to control) on 10 patients.

**Usage**

sleep

**Format**

A data frame with 20 observations on 2 variables.

[, 1]	extra	numeric	increase in hours of sleep
[, 2]	group	factor	drug given

**Source**

Cushny, A. R. and Peebles, A. R. (1905) The action of optical isomers: II hyoscines. *The Journal of Physiology* **32**, 501–510.

Student (1908) The probable error of the mean. *Biometrika*, **6**, 20.

**References**

Scheffé, Henry (1959) *The Analysis of Variance*. New York, NY: Wiley.

**Examples**

```
require(stats)
## Student's paired t-test
t.test(extra ~ group, data = sleep, paired = TRUE)
```

---

stackloss

*Brownlee's Stack Loss Plant Data*

---

**Description**

Operational data of a plant for the oxidation of ammonia to nitric acid.

**Usage**

```
stackloss

stack.x
stack.loss
```

**Format**

stackloss is a data frame with 21 observations on 4 variables.

[,1]	Air Flow	Flow of cooling air
[,2]	Water Temp	Cooling Water Inlet Temperature
[,3]	Acid Conc.	Concentration of acid [per 1000, minus 500]
[,4]	stack.loss	Stack loss

For compatibility with S-PLUS, the data sets `stack.x`, a matrix with the first three (independent) variables of the data frame, and `stack.loss`, the numeric vector giving the fourth (dependent) variable, are provided as well.

**Details**

“Obtained from 21 days of operation of a plant for the oxidation of ammonia (NH<sub>3</sub>) to nitric acid (HNO<sub>3</sub>). The nitric oxides produced are absorbed in a countercurrent absorption tower”. (Brownlee, cited by Dodge, slightly reformatted by MM.)

Air Flow represents the rate of operation of the plant. Water Temp is the temperature of cooling water circulated through coils in the absorption tower. Acid Conc. is the concentration of the acid circulating, minus 50, times 10: that is, 89 corresponds to 58.9 per cent acid. stack.loss

(the dependent variable) is 10 times the percentage of the ingoing ammonia to the plant that escapes from the absorption column unabsorbed; that is, an (inverse) measure of the over-all efficiency of the plant.

### Source

Brownlee, K. A. (1960, 2nd ed. 1965) *Statistical Theory and Methodology in Science and Engineering*. New York: Wiley. pp. 491–500.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Dodge, Y. (1996) The guinea pig of multiple regression. In: *Robust Statistics, Data Analysis, and Computer Intensive Methods; In Honor of Peter Huber's 60th Birthday, 1996, Lecture Notes in Statistics* **109**, Springer-Verlag, New York.

### Examples

```
require(stats)
summary(lm.stack <- lm(stack.loss ~ stack.x))
```

---

state

*US State Facts and Figures*

---

### Description

Data sets related to the 50 states of the United States of America.

### Usage

```
state.abb
state.area
state.center
state.division
state.name
state.region
state.x77
```

### Details

R currently contains the following “state” data sets. Note that all data are arranged according to alphabetical order of the state names.

`state.abb`: character vector of 2-letter abbreviations for the state names.

`state.area`: numeric vector of state areas (in square miles).

`state.center`: list with components named `x` and `y` giving the approximate geographic center of each state in negative longitude and latitude. Alaska and Hawaii are placed just off the West Coast.

`state.division`: factor giving state divisions (New England, Middle Atlantic, South Atlantic, East South Central, West South Central, East North Central, West North Central, Mountain, and Pacific).



`state.name`: character vector giving the full state names.  
`state.region`: factor giving the region (Northeast, South, North Central, West) that each state belongs to.  
`state.x77`: matrix with 50 rows and 8 columns giving the following statistics in the respective columns.  
   `Population`: population estimate as of July 1, 1975  
   `Income`: per capita income (1974)  
   `Illiteracy`: illiteracy (1970, percent of population)  
   `Life Exp`: life expectancy in years (1969–71)  
   `Murder`: murder and non-negligent manslaughter rate per 100,000 population (1976)  
   `HS Grad`: percent high-school graduates (1970)  
   `Frost`: mean number of days with minimum temperature below freezing (1931–1960) in capital or large city  
   `Area`: land area in square miles

### Source

U.S. Department of Commerce, Bureau of the Census (1977) *Statistical Abstract of the United States*.  
 U.S. Department of Commerce, Bureau of the Census (1977) *County and City Data Book*.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

---

sunspot.month      *Monthly Sunspot Data, 1749–1997*

---

### Description

Monthly numbers of sunspots.

### Usage

`sunspot.month`

### Format

The univariate time series `sunspot.year` and `sunspot.month` contain 289 and 2988 observations, respectively. The objects are of class "ts".

### Source

World Data Center-C1 For Sunspot Index Royal Observatory of Belgium, Av. Circulaire, 3, B-1180 BRUSSELS [http://www.oma.be/KSB-ORB/SIDC/sidc\\_txt.html](http://www.oma.be/KSB-ORB/SIDC/sidc_txt.html)

### See Also

`sunspot.month` is a longer version of `sunspots` that runs until 1988 rather than 1983.

**Examples**

```

require(stats); require(graphics)
## Compare the monthly series
plot (sunspot.month, main = "sunspot.month [stats]", col = 2)
lines(sunspots) # "very barely" see something

## Now look at the difference :
all(tsp(sunspots)      [c(1,3)] ==
     tsp(sunspot.month)[c(1,3)]) ## Start & Periodicity are the same
n1 <- length(sunspots)
table(eq <- sunspots == sunspot.month[1:n1]) #> 132 are different !
i <- which(!eq)
rug(time(eq)[i])
s1 <- sunspots[i] ; s2 <- sunspot.month[i]
cbind(i = i, sunspots = s1, ss.month = s2,
      perc.diff = round(100*2*abs(s1-s2)/(s1+s2), 1))

```

---

sunspot.year	<i>Yearly Sunspot Data, 1700–1988</i>
--------------	---------------------------------------

---

**Description**

Yearly numbers of sunspots.

**Usage**

```
sunspot.year
```

**Format**

The univariate time series `sunspot.year` contains 289 observations, and is of class "ts".

**Source**

H. Tong (1996) *Non-Linear Time Series*. Clarendon Press, Oxford, p. 471.

---

sunspots	<i>Monthly Sunspot Numbers, 1749–1983</i>
----------	---

---

**Description**

Monthly mean relative sunspot numbers from 1749 to 1983. Collected at Swiss Federal Observatory, Zurich until 1960, then Tokyo Astronomical Observatory.

**Usage**

```
sunspots
```

**Format**

A time series of monthly data from 1749 to 1983.

**Source**

Andrews, D. F. and Herzberg, A. M. (1985) *Data: A Collection of Problems from Many Fields for the Student and Research Worker*. New York: Springer-Verlag.

**See Also**

`sunspot.month` has a longer (and a bit different) series.

**Examples**

```
require(graphics)
plot(sunspots, main = "sunspots data", xlab = "Year",
     ylab = "Monthly sunspot numbers")
```

---

swiss

*Swiss Fertility and Socioeconomic Indicators (1888) Data*


---

**Description**

Standardized fertility measure and socio-economic indicators for each of 47 French-speaking provinces of Switzerland at about 1888.

**Usage**

```
swiss
```

**Format**

A data frame with 47 observations on 6 variables, *each* of which is in percent, i.e., in [0, 100].

[,1]	Fertility	$I_g$ , ‘common standardized fertility measure’
[,2]	Agriculture	% of males involved in agriculture as occupation
[,3]	Examination	% draftees receiving highest mark on army examination
[,4]	Education	% education beyond primary school for draftees.
[,5]	Catholic	% ‘catholic’ (as opposed to ‘protestant’).
[,6]	Infant.Mortality	live births who live less than 1 year.

All variables but ‘Fertility’ give proportions of the population.

**Details**

(paraphrasing Mosteller and Tukey):

Switzerland, in 1888, was entering a period known as the *demographic transition*; i.e., its fertility was beginning to fall from the high level typical of underdeveloped countries.

The data collected are for 47 French-speaking “provinces” at about 1888.

Here, all variables are scaled to [0, 100], where in the original, all but "Catholic" were scaled to [0, 1].

**Note**

Files for all 182 districts in 1888 and other years have been available at <http://opr.princeton.edu/archive/eufert/switz.html> or <http://opr.princeton.edu/archive/pefp/switz.asp>.

They state that variables Examination and Education are averages for 1887, 1888 and 1889.

**Source**

Project “16P5”, pages 549–551 in

Mosteller, F. and Tukey, J. W. (1977) *Data Analysis and Regression: A Second Course in Statistics*. Addison-Wesley, Reading Mass.

indicating their source as “Data used by permission of Franice van de Walle. Office of Population Research, Princeton University, 1976. Unpublished data assembled under NICHD contract number No 1-HD-O-2077.”

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**Examples**

```
require(stats); require(graphics)
pairs(swiss, panel = panel.smooth, main = "swiss data",
      col = 3 + (swiss$Catholic > 50))
summary(lm(Fertility ~ . , data = swiss))
```

---

Theoph

*Pharmacokinetics of Theophylline*


---

**Description**

The Theoph data frame has 132 rows and 5 columns of data from an experiment on the pharmacokinetics of theophylline.

**Usage**

Theoph

**Format**

This data frame contains the following columns:

**Subject** an ordered factor with levels 1, ..., 12 identifying the subject on whom the observation was made. The ordering is by increasing maximum concentration of theophylline observed.

**Wt** weight of the subject (kg).

**Dose** dose of theophylline administered orally to the subject (mg/kg).

**Time** time since drug administration when the sample was drawn (hr).

**conc** theophylline concentration in the sample (mg/L).

**Details**

Boeckmann, Sheiner and Beal (1994) report data from a study by Dr. Robert Upton of the kinetics of the anti-asthmatic drug theophylline. Twelve subjects were given oral doses of theophylline then serum concentrations were measured at 11 time points over the next 25 hours.

These data are analyzed in Davidian and Giltinan (1995) and Pinheiro and Bates (2000) using a two-compartment open pharmacokinetic model, for which a self-starting model function, `SSfol`, is available.

**Source**

Boeckmann, A. J., Sheiner, L. B. and Beal, S. L. (1994), *NONMEM Users Guide: Part V*, NONMEM Project Group, University of California, San Francisco.

Davidian, M. and Giltinan, D. M. (1995) *Nonlinear Models for Repeated Measurement Data*, Chapman & Hall (section 5.5, p. 145 and section 6.6, p. 176)

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer (Appendix A.29)

**See Also**

[SSfol](#)

**Examples**

```
require(stats); require(graphics)
coplot(conc ~ Time | Subject, data = Theoph, show.given = FALSE)
Theoph.4 <- subset(Theoph, Subject == 4)
fml <- nls(conc ~ SSfol(Dose, Time, lKe, lKa, lCl),
           data = Theoph.4)
summary(fml)
plot(conc ~ Time, data = Theoph.4,
     xlab = "Time since drug administration (hr)",
     ylab = "Theophylline concentration (mg/L)",
     main = "Observed concentrations and fitted model",
     sub = "Theophylline data - Subject 4 only",
     las = 1, col = 4)
xvals <- seq(0, par("usr")[2], length.out = 55)
lines(xvals, predict(fml, newdata = list(Time = xvals)),
      col = 4)
```

---

Titanic

*Survival of passengers on the Titanic*

---

**Description**

This data set provides information on the fate of passengers on the fatal maiden voyage of the ocean liner 'Titanic', summarized according to economic status (class), sex, age and survival.

**Usage**

Titanic

**Format**

A 4-dimensional array resulting from cross-tabulating 2201 observations on 4 variables. The variables and their levels are as follows:

No	Name	Levels
1	Class	1st, 2nd, 3rd, Crew
2	Sex	Male, Female
3	Age	Child, Adult
4	Survived	No, Yes

**Details**

The sinking of the Titanic is a famous event, and new books are still being published about it. Many well-known facts—from the proportions of first-class passengers to the ‘women and children first’ policy, and the fact that that policy was not entirely successful in saving the women and children in the third class—are reflected in the survival rates for various classes of passenger.

These data were originally collected by the British Board of Trade in their investigation of the sinking. Note that there is not complete agreement among primary sources as to the exact numbers on board, rescued, or lost.

Due in particular to the very successful film ‘Titanic’, the last years saw a rise in public interest in the Titanic. Very detailed data about the passengers is now available on the Internet, at sites such as *Encyclopedia Titanica* (<http://www.rmplc.co.uk/eduweb/sites/phind>).

**Source**

Dawson, Robert J. MacG. (1995), The ‘Unusual Episode’ Data Revisited. *Journal of Statistics Education*, **3**. <http://www.amstat.org/publications/jse/v3n3/datasets.dawson.html>

The source provides a data set recording class, sex, age, and survival status for each person on board of the Titanic, and is based on data originally collected by the British Board of Trade and reprinted in:

British Board of Trade (1990), *Report on the Loss of the ‘Titanic’ (S.S.)*. British Board of Trade Inquiry Report (reprint). Gloucester, UK: Allan Sutton Publishing.

**Examples**

```
require(graphics)
mosaicplot(Titanic, main = "Survival on the Titanic")
## Higher survival rates in children?
apply(Titanic, c(3, 4), sum)
## Higher survival rates in females?
apply(Titanic, c(2, 4), sum)
## Use loglm() in package 'MASS' for further analysis ...
```

**Description**

The response is the length of odontoblasts (teeth) in each of 10 guinea pigs at each of three dose levels of Vitamin C (0.5, 1, and 2 mg) with each of two delivery methods (orange juice or ascorbic acid).

**Usage**

```
ToothGrowth
```

**Format**

A data frame with 60 observations on 3 variables.

[,1]	len	numeric	Tooth length
[,2]	supp	factor	Supplement type (VC or OJ).
[,3]	dose	numeric	Dose in milligrams.

**Source**

C. I. Bliss (1952) *The Statistics of Bioassay*. Academic Press.

**References**

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

**Examples**

```
require(graphics)
coplot(len ~ dose | supp, data = ToothGrowth, panel = panel.smooth,
       xlab = "ToothGrowth data: length vs dose, given type of supplement")
```

---

treering

*Yearly Treering Data, -6000–1979*

---

**Description**

Contains normalized tree-ring widths in dimensionless units.

**Usage**

```
treering
```

**Format**

A univariate time series with 7981 observations. The object is of class "ts".

Each tree ring corresponds to one year.

**Details**

The data were recorded by Donald A. Graybill, 1980, from Gt Basin Bristlecone Pine 2805M, 3726-11810 in Methuselah Walk, California.

**Source**

Time Series Data Library: <http://www-personal.buseco.monash.edu.au/~hyndman/TSDL/>, series 'CA535.DAT'

**References**

For background on Bristlecone pines and Methuselah Walk, see <http://www.sonic.net/bristlecone/>; for some photos see <http://www.ltrr.arizona.edu/~hallman/sitephotos/meth.html>

trees

*Girth, Height and Volume for Black Cherry Trees***Description**

This data set provides measurements of the girth, height and volume of timber in 31 felled black cherry trees. Note that girth is the diameter of the tree (in inches) measured at 4 ft 6 in above the ground.

**Usage**

trees

**Format**

A data frame with 31 observations on 3 variables.

[,1]	Girth	numeric	Tree diameter in inches
[,2]	Height	numeric	Height in ft
[,3]	Volume	numeric	Volume of timber in cubic ft

**Source**

Ryan, T. A., Joiner, B. L. and Ryan, B. F. (1976) *The Minitab Student Handbook*. Duxbury Press.

**References**

Atkinson, A. C. (1985) *Plots, Transformations and Regression*. Oxford University Press.

**Examples**

```
require(stats); require(graphics)
pairs(trees, panel = panel.smooth, main = "trees data")
plot(Volume ~ Girth, data = trees, log = "xy")
coplot(log(Volume) ~ log(Girth) | Height, data = trees,
       panel = panel.smooth)
summary(fm1 <- lm(log(Volume) ~ log(Girth), data = trees))
summary(fm2 <- update(fm1, ~ . + log(Height), data = trees))
step(fm2)
## i.e., Volume ~ c * Height * Girth^2 seems reasonable
```



UCBAdmissions

*Student Admissions at UC Berkeley***Description**

Aggregate data on applicants to graduate school at Berkeley for the six largest departments in 1973 classified by admission and sex.

**Usage**

```
UCBAdmissions
```

**Format**

A 3-dimensional array resulting from cross-tabulating 4526 observations on 3 variables. The variables and their levels are as follows:

No	Name	Levels
1	Admit	Admitted, Rejected
2	Gender	Male, Female
3	Dept	A, B, C, D, E, F

**Details**

This data set is frequently used for illustrating Simpson's paradox, see Bickel et al. (1975). At issue is whether the data show evidence of sex bias in admission practices. There were 2691 male applicants, of whom 1198 (44.5%) were admitted, compared with 1835 female applicants of whom 557 (30.4%) were admitted. This gives a sample odds ratio of 1.83, indicating that males were almost twice as likely to be admitted. In fact, graphical methods (as in the example below) or log-linear modelling show that the apparent association between admission and sex stems from differences in the tendency of males and females to apply to the individual departments (females used to apply *more* to departments with higher rejection rates).

This data set can also be used for illustrating methods for graphical display of categorical data, such as the general-purpose mosaic plot or the fourfold display for 2-by-2-by-*k* tables. See the home page of Michael Friendly (<http://www.math.yorku.ca/SCS/friendly.html>) for further information.

**References**

Bickel, P. J., Hammel, E. A., and O'Connell, J. W. (1975) Sex bias in graduate admissions: Data from Berkeley. *Science*, **187**, 398–403.

**Examples**

```
require(graphics)
## Data aggregated over departments
apply(UCBAdmissions, c(1, 2), sum)
mosaicplot(apply(UCBAdmissions, c(1, 2), sum),
           main = "Student admissions at UC Berkeley")
## Data for individual departments
opar <- par(mfrow = c(2, 3), oma = c(0, 0, 2, 0))
for(i in 1:6)
```

```

mosaicplot(UCBAdmissions[, , i],
           xlab = "Admit", ylab = "Sex",
           main = paste("Department", LETTERS[i]))
mtext(expression(bold("Student admissions at UC Berkeley")),
       outer = TRUE, cex = 1.5)
par(opar)

```

---

UKDriverDeaths

*Road Casualties in Great Britain 1969–84*


---

### Description

UKDriverDeaths is a time series giving the monthly totals of car drivers in Great Britain killed or seriously injured Jan 1969 to Dec 1984. Compulsory wearing of seat belts was introduced on 31 Jan 1983.

Seatbelts is more information on the same problem.

### Usage

```

UKDriverDeaths
Seatbelts

```

### Format

Seatbelts is a multiple time series, with columns

DriversKilled car drivers killed.

drivers same as UKDriverDeaths.

front front-seat passengers killed or seriously injured.

rear rear-seat passengers killed or seriously injured.

kms distance driven.

PetrolPrice petrol price.

VanKilled number of van ('light goods vehicle') drivers.

law 0/1: was the law in effect that month?

### Source

Harvey, A.C. (1989) *Forecasting, Structural Time Series Models and the Kalman Filter*. Cambridge University Press, pp. 519–523.

Durbin, J. and Koopman, S. J. (2001) *Time Series Analysis by State Space Methods*. Oxford University Press. <http://www.ssfpack.com/dkbook/>

### References

Harvey, A. C. and Durbin, J. (1986) The effects of seat belt legislation on British road casualties: A case study in structural time series modelling. *Journal of the Royal Statistical Society series B*, **149**, 187–227.

**Examples**

```

require(stats); require(graphics)
## work with pre-seatbelt period to identify a model, use logs
work <- window(log10(UKDriverDeaths), end = 1982+11/12)
par(mfrow = c(3,1))
plot(work); acf(work); pacf(work)
par(mfrow = c(1,1))
(fit <- arima(work, c(1,0,0), seasonal = list(order= c(1,0,0))))
z <- predict(fit, n.ahead = 24)
ts.plot(log10(UKDriverDeaths), z$pred, z$pred+2*z$se, z$pred-2*z$se,
        lty = c(1,3,2,2), col = c("black", "red", "blue", "blue"))

## now see the effect of the explanatory variables
X <- Seatbelts[, c("kms", "PetrolPrice", "law")]
X[, 1] <- log10(X[, 1]) - 4
arima(log10(Seatbelts[, "drivers"]), c(1,0,0),
      seasonal = list(order= c(1,0,0)), xreg = X)

```

---

 UKgas

*UK Quarterly Gas Consumption*


---

**Description**

Quarterly UK gas consumption from 1960Q1 to 1986Q4, in millions of therms.

**Usage**

UKgas

**Format**

A quarterly time series of length 108.

**Source**

Durbin, J. and Koopman, S. J. (2001) *Time Series Analysis by State Space Methods*. Oxford University Press. <http://www.ssfpack.com/dkbook/>

**Examples**

```
## maybe str(UKgas) ; plot(UKgas) ...
```

UKLungDeaths

*Monthly Deaths from Lung Diseases in the UK***Description**

Three time series giving the monthly deaths from bronchitis, emphysema and asthma in the UK, 1974–1979, both sexes (`ldeaths`), males (`mdeaths`) and females (`fdeaths`).

**Usage**

```
ldeaths
fdeaths
mdeaths
```

**Source**

P. J. Diggle (1990) *Time Series: A Biostatistical Introduction*. Oxford, table A.3

**Examples**

```
require(stats); require(graphics) # for time
plot(ldeaths)
plot(mdeaths, fdeaths)
## Better labels:
yr <- floor(tt <- time(mdeaths))
plot(mdeaths, fdeaths,
      xy.labels = paste(month.abb[12*(tt - yr)], yr-1900, sep=""))
```

USAccDeaths

*Accidental Deaths in the US 1973–1978***Description**

A time series giving the monthly totals of accidental deaths in the USA. The values for the first six months of 1979 are 7798 7406 8363 8460 9217 9316.

**Usage**

```
USAccDeaths
```

**Source**

P. J. Brockwell and R. A. Davis (1991) *Time Series: Theory and Methods*. Springer, New York.

---

 USArrests

*Violent Crime Rates by US State*


---

**Description**

This data set contains statistics, in arrests per 100,000 residents for assault, murder, and rape in each of the 50 US states in 1973. Also given is the percent of the population living in urban areas.

**Usage**

USArrests

**Format**

A data frame with 50 observations on 4 variables.

[,1]	Murder	numeric	Murder arrests (per 100,000)
[,2]	Assault	numeric	Assault arrests (per 100,000)
[,3]	UrbanPop	numeric	Percent urban population
[,4]	Rape	numeric	Rape arrests (per 100,000)

**Source**

World Almanac and Book of facts 1975. (Crime rates).

Statistical Abstracts of the United States 1975. (Urban rates).

**References**

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

**See Also**

The [state](#) data sets.

**Examples**

```
require(graphics)
pairs(USArrests, panel = panel.smooth, main = "USArrests data")
```

---

 USJudgeRatings

*Lawyers' Ratings of State Judges in the US Superior Court*


---

**Description**

Lawyers' ratings of state judges in the US Superior Court.

**Usage**

USJudgeRatings

**Format**

A data frame containing 43 observations on 12 numeric variables.

[,1]	CONT	Number of contacts of lawyer with judge.
[,2]	INTG	Judicial integrity.
[,3]	DMNR	Demeanor.
[,4]	DILG	Diligence.
[,5]	CFMG	Case flow managing.
[,6]	DECI	Prompt decisions.
[,7]	PREP	Preparation for trial.
[,8]	FAMI	Familiarity with law.
[,9]	ORAL	Sound oral rulings.
[,10]	WRIT	Sound written rulings.
[,11]	PHYS	Physical ability.
[,12]	RTEN	Worthy of retention.

**Source**

New Haven Register, 14 January, 1977 (from John Hartigan).

**Examples**

```
require(graphics)
pairs(USJudgeRatings, main = "USJudgeRatings data")
```

---

USPersonalExpenditure  
*Personal Expenditure Data*

---

**Description**

This data set consists of United States personal expenditures (in billions of dollars) in the categories; food and tobacco, household operation, medical and health, personal care, and private education for the years 1940, 1945, 1950, 1955 and 1960.

**Usage**

```
USPersonalExpenditure
```

**Format**

A matrix with 5 rows and 5 columns.

**Source**

The World Almanac and Book of Facts, 1962, page 756.

**References**

Tukey, J. W. (1977) *Exploratory Data Analysis*. Addison-Wesley.  
McNeil, D. R. (1977) *Interactive Data Analysis*. Wiley.

**Examples**

```
require(stats) # for medpolish
USPersonalExpenditure
medpolish(log10(USPersonalExpenditure))
```

---

 uspop

*Populations Recorded by the US Census*


---

**Description**

This data set gives the population of the United States (in millions) as recorded by the decennial census for the period 1790–1970.

**Usage**

```
uspop
```

**Format**

A time series of 19 values.

**Source**

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

**Examples**

```
require(graphics)
plot(uspop, log = "y", main = "uspop data", xlab = "Year",
     ylab = "U.S. Population (millions)")
```

---

 VADeaths

*Death Rates in Virginia (1940)*


---

**Description**

Death rates per 1000 in Virginia in 1940.

**Usage**

```
VADeaths
```

**Format**

A matrix with 5 rows and 4 columns.

**Details**

The death rates are measured per 1000 population per year. They are cross-classified by age group (rows) and population group (columns). The age groups are: 50–54, 55–59, 60–64, 65–69, 70–74 and the population groups are Rural/Male, Rural/Female, Urban/Male and Urban/Female.

This provides a rather nice 3-way analysis of variance example.

**Source**

Molyneaux, L., Gilliam, S. K., and Florant, L. C. (1947) Differences in Virginia death rates by color, sex, age, and rural or urban residence. *American Sociological Review*, **12**, 525–535.

**References**

McNeil, D. R. (1977) *Interactive Data Analysis*. Wiley.

**Examples**

```
require(stats); require(graphics)
n <- length(dr <- c(VADeaths))
nam <- names(VADeaths)
d.VAD <- data.frame(
  Drate = dr,
  age = rep(ordered(rownames(VADeaths)), length.out=n),
  gender= gl(2,5,n, labels= c("M", "F")),
  site = gl(2,10, labels= c("rural", "urban")))
coplot(Drate ~ as.numeric(age) | gender * site, data = d.VAD,
       panel = panel.smooth, xlab = "VADeaths data - Given: gender")
summary(aov.VAD <- aov(Drate ~ .^2, data = d.VAD))
opar <- par(mfrow = c(2,2), oma = c(0, 0, 1.1, 0))
plot(aov.VAD)
par(opar)
```

---

volcano

*Topographic Information on Auckland's Maunga Whau Volcano*


---

**Description**

Maunga Whau (Mt Eden) is one of about 50 volcanos in the Auckland volcanic field. This data set gives topographic information for Maunga Whau on a 10m by 10m grid.

**Usage**

```
volcano
```

**Format**

A matrix with 87 rows and 61 columns, rows corresponding to grid lines running east to west and columns to grid lines running south to north.

**Source**

Digitized from a topographic map by Ross Ihaka. These data should not be regarded as accurate.

**See Also**

[filled.contour](#) for a nice plot.



**Examples**

```
require(grDevices); require(graphics)
filled.contour(volcano, color.palette = terrain.colors, asp = 1)
title(main = "volcano data: filled contour map")
```

warpbreaks

*The Number of Breaks in Yarn during Weaving***Description**

This data set gives the number of warp breaks per loom, where a loom corresponds to a fixed length of yarn.

**Usage**

```
warpbreaks
```

**Format**

A data frame with 54 observations on 3 variables.

[,1]	breaks	numeric	The number of breaks
[,2]	wool	factor	The type of wool (A or B)
[,3]	tension	factor	The level of tension (L, M, H)

There are measurements on 9 looms for each of the six types of warp (AL, AM, AH, BL, BM, BH).

**Source**

Tippett, L. H. C. (1950) *Technological Applications of Statistics*. Wiley. Page 106.

**References**

Tukey, J. W. (1977) *Exploratory Data Analysis*. Addison-Wesley.

McNeil, D. R. (1977) *Interactive Data Analysis*. Wiley.

**See Also**

[xtabs](#) for ways to display these data as a table.

**Examples**

```
require(stats); require(graphics)
summary(warpbreaks)
opar <- par(mfrow = c(1,2), oma = c(0, 0, 1.1, 0))
plot(breaks ~ tension, data = warpbreaks, col = "lightgray",
     varwidth = TRUE, subset = wool == "A", main = "Wool A")
plot(breaks ~ tension, data = warpbreaks, col = "lightgray",
     varwidth = TRUE, subset = wool == "B", main = "Wool B")
mtext("warpbreaks data", side = 3, outer = TRUE)
par(opar)
summary(fm1 <- lm(breaks ~ wool*tension, data = warpbreaks))
```

```
anova (fm1)
```

---

women

*Average Heights and Weights for American Women*

---

### Description

This data set gives the average heights and weights for American women aged 30–39.

### Usage

```
women
```

### Format

A data frame with 15 observations on 2 variables.

[, 1]	height	numeric	Height (in)
[, 2]	weight	numeric	Weight (lbs)

### Details

The data set appears to have been taken from the American Society of Actuaries *Build and Blood Pressure Study* for some (unknown to us) earlier year.

The World Almanac notes: “The figures represent weights in ordinary indoor clothing and shoes, and heights with shoes”.

### Source

The World Almanac and Book of Facts, 1975.

### References

McNeil, D. R. (1977) *Interactive Data Analysis*. Wiley.

### Examples

```
require(graphics)
plot(women, xlab = "Height (in)", ylab = "Weight (lb)",
     main = "women data: American women aged 30-39")
```

---

WorldPhones

*The World's Telephones*

---

### Description

The number of telephones in various regions of the world (in thousands).

### Usage

```
WorldPhones
```

**Format**

A matrix with 7 rows and 8 columns. The columns of the matrix give the figures for a given region, and the rows the figures for a year.

The regions are: North America, Europe, Asia, South America, Oceania, Africa, Central America.

The years are: 1951, 1956, 1957, 1958, 1959, 1960, 1961.

**Source**

AT&T (1961) *The World's Telephones*.

**References**

McNeil, D. R. (1977) *Interactive Data Analysis*. New York: Wiley.

**Examples**

```
require(graphics)
matplot(rownames(WorldPhones), WorldPhones, type = "b", log = "y",
        xlab = "Year", ylab = "Number of telephones (1000's)")
legend(1951.5, 80000, colnames(WorldPhones), col = 1:6, lty = 1:5,
       pch = rep(21, 7))
title(main = "World phones data: log scale for response")
```

---

WWWusage

*Internet Usage per Minute*

---

**Description**

A time series of the numbers of users connected to the Internet through a server every minute.

**Usage**

WWWusage

**Format**

A time series of length 100.

**Source**

Durbin, J. and Koopman, S. J. (2001) *Time Series Analysis by State Space Methods*. Oxford University Press. <http://www.ssfpack.com/dkbook/>

**References**

Makridakis, S., Wheelwright, S. C. and Hyndman, R. J. (1998) *Forecasting: Methods and Applications*. Wiley.

**Examples**

```
require(graphics)
work <- diff(WWWusage)
par(mfrow = c(2,1)); plot(WWWusage); plot(work)
## Not run:
require(stats)
aics <- matrix(, 6, 6, dimnames=list(p=0:5, q=0:5))
for(q in 1:5) aics[1, 1+q] <- arima(WWWusage, c(0,1,q),
  optim.control = list(maxit = 500))$aic
for(p in 1:5)
  for(q in 0:5) aics[1+p, 1+q] <- arima(WWWusage, c(p,1,q),
    optim.control = list(maxit = 500))$aic
round(aics - min(aics, na.rm=TRUE), 2)

## End(Not run)
```



## Chapter 3

# The grDevices package

---

grDevices-package *The R Graphics Devices and Support for Colours and Fonts*

---

### Description

Graphics devices and support for base and grid graphics

### Details

This package contains functions which support both [base](#) and [grid](#) graphics.

For a complete list of functions, use `library(help="grDevices")`.

### Author(s)

R Development Core Team and contributors worldwide

Maintainer: R Core Team <R-core@r-project.org>

---

as.graphicsAnnot *Coerce an Object for Graphics Annotation*

---

### Description

Coerce an R object into a form suitable for graphics annotation.

### Usage

```
as.graphicsAnnot(x)
```

### Arguments

x                    an R object

## Details

Expressions, calls and names (as used by `plotmath`) are passed through unchanged. All other objects with an S3 class (as determined by `is.object`) are coerced by `as.character` to character vectors.

All the **graphics** and **grid** functions which use this coerce calls and names to expressions internally.

## Value

A language object or a character vector.

---

<code>as.raster</code>	<i>Create a Raster Object</i>
------------------------	-------------------------------

---

## Description

Functions to create a raster object (representing a bitmap image) and coerce other objects to a raster object.

## Usage

```
is.raster(x)
as.raster(x, ...)

## S3 method for class 'logical':
as.raster(x, max=1, ...)
## S3 method for class 'numeric':
as.raster(x, max=1, ...)
## S3 method for class 'character':
as.raster(x, max=1, ...)
## S3 method for class 'matrix':
as.raster(x, max=1, ...)
## S3 method for class 'array':
as.raster(x, max=1, ...)
```

## Arguments

<code>x</code>	Any R object.
<code>max</code>	number giving the maximum of the color values range.
<code>...</code>	further arguments passed to or from other methods.

## Details

It is not expected that the user will call these functions directly; functions to render bitmap images in graphics packages will make use of the `as.raster()` function to automatically generate a raster object from their input.

The `as.raster()` function is generic so methods can be written to convert other R objects to a raster object.

**Value**

For `as.raster()`, a raster object.

For `is.raster()`, a logical indicating whether `x` is a raster object.

**Examples**

```
# A red gradient
as.raster(matrix(hcl(0, 80, seq(50, 80, 10)),
                nrow=4, ncol=5))

# Vectors are 1-column matrices ...
# character vectors are color names ...
as.raster(hcl(0, 80, seq(50, 80, 10)))
# numeric vectors are greyscale ...
as.raster(1:5, max=5)
# logical vectors are black and white ...
as.raster(1:10 %% 2 == 0)

# ... unless nrow/ncol are supplied ...
as.raster(1:10 %% 2 == 0, nrow=1)

# Matrix can also be logical or numeric ...
as.raster(matrix(c(TRUE, FALSE), nrow=3, ncol=2))
as.raster(matrix(1:3/4, nrow=3, ncol=4))

# An array can be 3-plane numeric (R, G, B planes) ...
as.raster(array(c(0:1, rep(0.5, 4)), c(2, 1, 3)))

# ... or 4-plane numeric (R, G, B, A planes)
as.raster(array(c(0:1, rep(0.5, 6)), c(2, 1, 4)))
```

---

 boxplot.stats

*Box Plot Statistics*


---

**Description**

This function is typically called by another function to gather the statistics necessary for producing box plots, but may be invoked separately.

**Usage**

```
boxplot.stats(x, coef = 1.5, do.conf = TRUE, do.out = TRUE)
```

**Arguments**

<code>x</code>	a numeric vector for which the boxplot will be constructed (NAs and NaNs are allowed and omitted).
<code>coef</code>	this determines how far the plot ‘whiskers’ extend out from the box. If <code>coef</code> is positive, the whiskers extend to the most extreme data point which is no more than <code>coef</code> times the length of the box away from the box. A value of zero causes the whiskers to extend to the data extremes (and no outliers be returned).



`do.conf, do.out`

logicals; if `FALSE`, the `conf` or `out` component respectively will be empty in the result.

### Details

The two ‘hinges’ are versions of the first and third quartile, i.e., close to `quantile(x, c(1, 3)/4)`. The hinges equal the quartiles for odd  $n$  (where  $n <- \text{length}(x)$ ) and differ for even  $n$ . Whereas the quartiles only equal observations for  $n \%\% 4 == 1$  ( $n \equiv 1 \pmod{4}$ ), the hinges do so *additionally* for  $n \%\% 4 == 2$  ( $n \equiv 2 \pmod{4}$ ), and are in the middle of two observations otherwise.

The notches (if requested) extend to  $\pm 1.58 \text{ IQR}/\sqrt{n}$ . This seems to be based on the same calculations as the formula with 1.57 in Chambers *et al.* (1983, p. 62), given in McGill *et al.* (1978, p. 16). They are based on asymptotic normality of the median and roughly equal sample sizes for the two medians being compared, and are said to be rather insensitive to the underlying distributions of the samples. The idea appears to be to give roughly a 95% confidence interval for the difference in two medians.

### Value

List with named components as follows:

<code>stats</code>	a vector of length 5, containing the extreme of the lower whisker, the lower ‘hinge’, the median, the upper ‘hinge’ and the extreme of the upper whisker.
<code>n</code>	the number of non-NA observations in the sample.
<code>conf</code>	the lower and upper extremes of the ‘notch’ (if <code>do.conf</code> ). See the details.
<code>out</code>	the values of any data points which lie beyond the extremes of the whiskers (if <code>do.out</code> ).

Note that `$stats` and `$conf` are sorted in *increasing* order, unlike `S`, and that `$n` and `$out` include any  $\pm \text{Inf}$  values.

### References

- Tukey, J. W. (1977) *Exploratory Data Analysis*. Section 2C.
- McGill, R., Tukey, J. W. and Larsen, W. A. (1978) Variations of box plots. *The American Statistician* **32**, 12–16.
- Velleman, P. F. and Hoaglin, D. C. (1981) *Applications, Basics and Computing of Exploratory Data Analysis*. Duxbury Press.
- Emerson, J. D and Strenio, J. (1983). Boxplots and batch comparison. Chapter 3 of *Understanding Robust and Exploratory Data Analysis*, eds. D. C. Hoaglin, F. Mosteller and J. W. Tukey. Wiley.
- Chambers, J. M., Cleveland, W. S., Kleiner, B. and Tukey, P. A. (1983) *Graphical Methods for Data Analysis*. Wadsworth & Brooks/Cole.

### See Also

`fivenum`, `boxplot`, `bxp`.

**Examples**

```

require(stats)
x <- c(1:100, 1000)
(b1 <- boxplot.stats(x))
(b2 <- boxplot.stats(x, do.conf=FALSE, do.out=FALSE))
stopifnot(b1 $ stats == b2 $ stats) # do.out=F is still robust
boxplot.stats(x, coef = 3, do.conf=FALSE)
## no outlier treatment:
boxplot.stats(x, coef = 0)

boxplot.stats(c(x, NA)) # slight change : n is 101
(r <- boxplot.stats(c(x, -1:1/0)))
stopifnot(r$out == c(1000, -Inf, Inf))

```

---

 cairo

*Cairo-based SVG, PDF and PostScript Graphics Devices*


---

**Description**

Graphics devices for SVG, PDF and PostScript graphics files.

**Usage**

```

svg(filename = if(onefile) "Rplots.svg" else "Rplot%03d.svg",
     width = 7, height = 7, pointsize = 12,
     onefile = FALSE, bg = "white",
     antialias = c("default", "none", "gray", "subpixel"))

cairo_pdf(filename = if(onefile) "Rplots.pdf" else "Rplot%03d.pdf",
           width = 7, height = 7, pointsize = 12,
           onefile = FALSE, bg = "white",
           antialias = c("default", "none", "gray", "subpixel"))

cairo_ps(filename = if(onefile) "Rplots.ps" else "Rplot%03d.ps",
          width = 7, height = 7, pointsize = 12,
          onefile = FALSE, bg = "white",
          antialias = c("default", "none", "gray", "subpixel"))

```

**Arguments**

filename	the name of the output file. The page number is substituted if a C integer format is included in the character string, as in the default. (The result must be less than <code>PATH_MAX</code> characters long, and may be truncated if not. See <a href="#">postscript</a> for further details.) Tilde expansion is performed where supported by the platform.
width	the width of the device in inches.
height	the height of the device in inches.
pointsize	the default pointsize of plotted text (in big points).

<code>onefile</code>	should all plots appear in one file or in separate files?
<code>bg</code>	the initial background colour: can be overridden by setting <code>par("bg")</code> .
<code>antialias</code>	string, the type of anti-aliasing (if any) to be used; defaults to "default", see <a href="#">X11</a> .

### Details

SVG (Scalar Vector Graphics) is a W3C standard for vector graphics. See <http://www.w3.org/Graphics/SVG/>. The output is SVG version 1.1 for `onefile = FALSE` (the default), otherwise SVG 1.2. (Very few SVG viewers are capable of displaying multi-page SVG files.)

Note that unlike `postscript` and `pdf`, `cairo_pdf` and `cairo_ps` sometimes record *bitmaps* and not vector graphics: a resolution of 72dpi is used. On the other hand, they can (on suitable platforms) include a much wider range of UTF-8 glyphs, and embed the fonts used. They are somewhat experimental.

R can be compiled without support for any of these devices: this will be reported if you attempt to use them on a system where they are not supported. They all require cairo version 1.2 or later.

If you plot more than one page on one of these devices and do not include something like `%d` for the sequence number in `file` (or set `onefile=TRUE`) the file will contain the last page plotted.

The `cairo_ps` output is not yet encapsulated (that is coming in cairo 1.6).

There is full support of transparency, but using this is one of the things liable to trigger bitmap output (and will always do so for `cairo_ps`).

### Value

A plot device is opened: nothing is returned to the R interpreter.

### Conventions

This section describes the implementation of the conventions for graphics devices set out in the “R Internals Manual”.

- The default device size is in pixels (`svg`) or inches.
- Font sizes are in big points.
- The default font family is Helvetica.
- Line widths are multiples of 1/96 inch.
- Circle radii have a minimum of 1/72 inch.
- Colours are interpreted by the viewing application.

### See Also

[Devices](#), [dev.print](#), [pdf](#), [postscript capabilities](#) to see if cairo is supported.

---

check.options      *Set Options with Consistency Checks*

---

### Description

Utility function for setting options with some consistency checks. The `attributes` of the new settings in `new` are checked for consistency with the `model` (often default) list in `name.opt`.

### Usage

```
check.options(new, name.opt, reset = FALSE, assign.opt = FALSE,
              envir = .GlobalEnv,
              check.attributes = c("mode", "length"),
              override.check = FALSE)
```

### Arguments

<code>new</code>	a <i>named</i> list
<code>name.opt</code>	character with the name of R object containing the default list.
<code>reset</code>	logical; if TRUE, reset the options from <code>name.opt</code> . If there is more than one R object with name <code>name.opt</code> , remove the first one in the <code>search()</code> path.
<code>assign.opt</code>	logical; if TRUE, assign the ...
<code>envir</code>	the <i>environment</i> used for <code>get</code> and <code>assign</code> .
<code>check.attributes</code>	character containing the attributes which <code>check.options</code> should check.
<code>override.check</code>	logical vector of length <code>length(new)</code> (or 1 which entails recycling). For those <code>new[i]</code> where <code>override.check[i] == TRUE</code> , the checks are overridden and the changes made anyway.

### Value

A list of components with the same names as the one called `name.opt`. The values of the components are changed from the `new` list, as long as these pass the checks (when these are not overridden according to `override.check`).

### Note

Option "names" is exempt from all the checks or warnings, as in the application it can be NULL or a variable-length character vector.

### Author(s)

Martin Maechler

### See Also

`ps.options` and `pdf.options`, which use `check.options`.

**Examples**

```
(L1 <- list(a=1:3, b=pi, ch="CH"))
check.options(list(a=0:2), name.opt = "L1")
check.options(NULL, reset = TRUE, name.opt = "L1")
```

---

`chull`*Compute Convex Hull of a Set of Points*

---

**Description**

Computes the subset of points which lie on the convex hull of the set of points specified.

**Usage**

```
chull(x, y = NULL)
```

**Arguments**

`x`, `y` coordinate vectors of points. This can be specified as two vectors `x` and `y`, a 2-column matrix `x`, a list `x` with two components, etc, see [xy.coords](#).

**Details**

[xy.coords](#) is used to interpret the specification of the points. The algorithm is that given by Eddy (1977).

‘Peeling’ as used in the S function `chull` can be implemented by calling `chull` recursively.

**Value**

An integer vector giving the indices of the points lying on the convex hull, in clockwise order.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Eddy, W. F. (1977) A new convex hull algorithm for planar sets. *ACM Transactions on Mathematical Software*, **3**, 398–403.

Eddy, W. F. (1977) Algorithm 523. CONVEX, A new convex hull algorithm for planar sets[Z]. *ACM Transactions on Mathematical Software*, **3**, 411–412.

**See Also**

[xy.coords](#), [polygon](#)

**Examples**

```
require(stats)
X <- matrix(rnorm(2000), ncol = 2)
chull(X)
## Not run:
# Example usage from graphics package
plot(X, cex = 0.5)
hpts <- chull(X)
hpts <- c(hpts, hpts[1])
lines(X[hpts, ])

## End(Not run)
```

---

cm

*Unit Transformation*

---

**Description**

Translates from inches to cm (centimeters).

**Usage**

```
cm(x)
```

**Arguments**

x                    numeric vector

**Examples**

```
cm(1) # = 2.54

## Translate *from* cm *to* inches:
10 / cm(1) # -> 10cm are 3.937 inches
```

---

col2rgb

*Color to RGB Conversion*

---

**Description**

R color to RGB (red/green/blue) conversion.

**Usage**

```
col2rgb(col, alpha = FALSE)
```

**Arguments**

`col` vector of any of the three kind of R colors, i.e., either a color name (an element of `colors()`), a hexadecimal string of the form "#rrggbb", or an integer `i` meaning `palette()[i]`. Non-string values are coerced to integer.

`alpha` logical value indicating whether alpha channel values should be returned.

**Details**

For integer colors, 0 is shorthand for the current `par("bg")` (and hence is only relevant to base graphics), and `NA` means transparent.

For character colors, "NA" is equivalent to `NA` above.

**Value**

an integer matrix with three or four rows and number of columns the length (and names if any) as `col`.

**Author(s)**

Martin Maechler

**See Also**

[rgb](#), [colors](#), [palette](#), etc.

**Examples**

```
col2rgb("peachpuff")
col2rgb(c(blu = "royalblue", reddish = "tomato")) # names kept

col2rgb(1:8) # the ones from the palette() :

col2rgb(paste("gold", 1:4, sep=""))

col2rgb("#08a0ff")
## all three kind of colors mixed :
col2rgb(c(red="red", palette= 1:3, hex="#abcdef"))

##-- NON-INTRODUCTORY examples --

grC <- col2rgb(paste("gray", 0:100, sep=""))
table(print(diff(grC["red", ]))) # '2' or '3': almost equidistant
## The 'named' grays are in between {"slate gray" is not gray, strictly}
col2rgb(c(g66="gray66", darkg= "dark gray", g67="gray67",
          g74="gray74", gray = "gray", g75="gray75",
          g82="gray82", light="light gray", g83="gray83"))

crgb <- col2rgb(cc <- colors())
colnames(crgb) <- cc
t(crgb) ## The whole table

ccodes <- c(256^(2:0) %*% crgb) ## = internal codes
## How many names are 'aliases' of each other:
table(tcc <- table(ccodes))
length(uc <- unique(sort(ccodes))) # 502
```

```
## All the multiply named colors:
mult <- uc[tcc >= 2]
cl <- lapply(mult, function(m) cc[ccodes == m])
names(cl) <- apply(col2rgb(sapply(cl, function(x)x[1])),
                  2, function(n)paste(n, collapse=","))
utils::str(cl)
## Not run:
if(require(xgobi)) { ## Look at the color cube dynamically :
  tc <- t(crgb[, !duplicated(ccodes)])
  table(is.gray <- tc[,1] == tc[,2] & tc[,2] == tc[,3])# (397, 105)
  xgobi(tc, color = c("gold", "gray")[1 + is.gray])
}

## End(Not run)
```

---

colorRamp

*Color interpolation*


---

## Description

These functions return functions that interpolate a set of given colors to create new color palettes (like [topo.colors](#)) and color ramps, functions that map the interval  $[0, 1]$  to colors (like [grey](#)).

## Usage

```
colorRamp(colors, bias = 1, space = c("rgb", "Lab"),
          interpolate = c("linear", "spline"))
colorRampPalette(colors, ...)
```

## Arguments

colors	Colors to interpolate
bias	A positive number. Higher values give more widely spaced colors at the high end.
space	Interpolation in RGB or CIE Lab color spaces
interpolate	Use spline or linear interpolation.
...	arguments to pass to <code>colorRamp</code> .

## Details

The CIE Lab color space is approximately perceptually uniform, and so gives smoother and more uniform color ramps. On the other hand, palettes that vary from one hue to another via white may have a more symmetrical appearance in RGB space.

The conversion formulas in this function do not appear to be completely accurate and the color ramp may not reach the extreme values in Lab space. Future changes in the R color model may change the colors produced with `space="Lab"`.

## Value

`colorRamp` returns a function that maps values between 0 and 1 to colors. `colorRampPalette` returns a function that takes an integer argument and returns that number of colors interpolating the given sequence (similar to [heat.colors](#) or [terrain.colors](#)).



**See Also**

Good starting points for interpolation are the "sequential" and "diverging" ColorBrewer palettes in the RColorBrewer package

**Examples**

```
require(graphics)

## Here space="rgb" gives palettes that vary only in saturation,
## as intended.
## With space="Lab" the steps are more uniform, but the hues
## are slightly purple.
filled.contour(volcano,
               color.palette =
                 colorRampPalette(c("red", "white", "blue")),
               asp = 1)
filled.contour(volcano,
               color.palette =
                 colorRampPalette(c("red", "white", "blue"),
                                 space = "Lab"),
               asp = 1)

## Interpolating a 'sequential' ColorBrewer palette
YlOrBr <- c("#FFFFD4", "#FED98E", "#FE9929", "#D95F0E", "#993404")
filled.contour(volcano,
               color.palette = colorRampPalette(YlOrBr, space = "Lab"),
               asp = 1)
filled.contour(volcano,
               color.palette = colorRampPalette(YlOrBr, space = "Lab",
                                                bias = 0.5),
               asp = 1)

## 'jet.colors' is "as in Matlab"
## (and hurting the eyes by over-saturation)
jet.colors <-
  colorRampPalette(c("#00007F", "blue", "#007FFF", "cyan",
                    "#7FFF7F", "yellow", "#FF7F00", "red", "#7F0000"))
filled.contour(volcano, color = jet.colors, asp = 1)

## space="Lab" helps when colors don't form a natural sequence
m <- outer(1:20, 1:20, function(x, y) sin(sqrt(x*y)/3))
rgb.palette <- colorRampPalette(c("red", "orange", "blue"),
                               space = "rgb")
Lab.palette <- colorRampPalette(c("red", "orange", "blue"),
                               space = "Lab")
filled.contour(m, col = rgb.palette(20))
filled.contour(m, col = Lab.palette(20))
```

---

 colors

*Color Names*


---

**Description**

Returns the built-in color names which R knows about.

**Usage**

```
colors()
colours()
```

**Details**

These color names can be used with a `col=` specification in graphics functions.

An even wider variety of colors can be created with primitives `rgb` and `hsv` or the derived `rainbow`, `heat.colors`, etc.

**Value**

A character vector containing all the built-in color names.

**See Also**

`palette` for setting the ‘palette’ of colors for `par(col=<num>)`; `rgb`, `hsv`, `hcl`, `gray`; `rainbow` for a nice example; and `heat.colors`, `topo.colors` for images.

`col2rgb` for translating to RGB numbers and extended examples.

**Examples**

```
cl <- colors()
length(cl); cl[1:20]
```

---

contourLines	<i>Calculate Contour Lines</i>
--------------	--------------------------------

---

**Description**

Calculate contour lines for a given set of data.

**Usage**

```
contourLines(x = seq(0, 1, length.out = nrow(z)),
             y = seq(0, 1, length.out = ncol(z)),
             z, nlevels = 10,
             levels = pretty(range(z, na.rm=TRUE), nlevels))
```

**Arguments**

<code>x, y</code>	locations of grid lines at which the values in <code>z</code> are measured. These must be in ascending order. By default, equally spaced values from 0 to 1 are used. If <code>x</code> is a list, its components <code>x\$x</code> and <code>x\$y</code> are used for <code>x</code> and <code>y</code> , respectively. If the list has component <code>z</code> this is used for <code>z</code> .
<code>z</code>	a matrix containing the values to be plotted (NAs are allowed). Note that <code>x</code> can be used instead of <code>z</code> for convenience.
<code>nlevels</code>	number of contour levels desired <b>iff</b> <code>levels</code> is not supplied.
<code>levels</code>	numeric vector of levels at which to draw contour lines.

**Details**

`contourLines` draws nothing, but returns a set of contour lines.

There is currently no documentation about the algorithm. The source code is in '[R\\_HOME/src/main/plot3d.c](#)'.

**Value**

A list of contours. Each contour is a list with elements:

<code>level</code>	The contour level.
<code>x</code>	The x-coordinates of the contour.
<code>y</code>	The y-coordinates of the contour.

**See Also**

`options("max.contour.segments")` for the maximal complexity of a single contour line.  
[contour](#).

**Examples**

```
x <- 10*1:nrow(volcano)
y <- 10*1:ncol(volcano)
contourLines(x, y, volcano)
```

---

<code>convertColor</code>	<i>Convert between colour spaces</i>
---------------------------	--------------------------------------

---

**Description**

Convert colours between standard colour space representations. This function is experimental.

**Usage**

```
convertColor(color, from, to, from.ref.white, to.ref.white,
             scale.in=1, scale.out=1, clip=TRUE)
```

**Arguments**

<code>color</code>	A matrix whose rows specify colors.
<code>from,to</code>	Input and output color spaces. See 'Details' below.
<code>from.ref.white,to.ref.white</code>	Reference whites or NULL if these are built in to the definition, as for RGB spaces. D65 is the default, see 'Details' for others.
<code>scale.in, scale.out</code>	Input is divided by <code>scale.in</code> , output is multiplied by <code>scale.out</code> . Use NULL to suppress scaling when input or output is not numeric.
<code>clip</code>	If TRUE, truncate RGB output to [0,1], FALSE return out-of-range RGB, NA set out of range colors to NaN.

## Details

Color spaces are specified by objects of class `colorConverter`, created by `colorConverter` or `make.rgb`. Built-in color spaces may be referenced by strings: "XYZ", "sRGB", "Apple RGB", "CIE RGB", "Lab", "Luv". The converters for these colour spaces are in the object `colorspaces`.

The "sRGB" color space is that used by standard PC monitors. "Apple RGB" is used by Apple monitors. "Lab" and "Luv" are approximately perceptually uniform spaces standardized by the Commission Internationale d'Eclairage. XYZ is a 1931 CIE standard capable of representing all visible colors (and then some), but not in a perceptually uniform way.

The Lab and Luv spaces describe colors of objects, and so require the specification of a reference 'white light' color. Illuminant D65 is a standard indirect daylight, Illuminant D50 is close to direct sunlight, and Illuminant A is the light from a standard incandescent bulb. Other standard CIE illuminants supported are B, C, E and D55. RGB colour spaces are defined relative to a particular reference white, and can be only approximately translated to other reference whites. The Bradford chromatic adaptation algorithm is used for this.

The RGB color spaces are specific to a particular class of display. An RGB space cannot represent all colors, and the `clip` option controls what is done to out-of-range colors.

## Value

A 3-row matrix whose columns specify the colors.

## References

For all the conversion equations <http://www.brucelindbloom.com/>

For the white points <http://www.efg2.com/Lab/Graphics/Colors/Chromaticity.htm>

## See Also

`col2rgb` and `colors` for ways to specify colors in graphics.

`make.rgb` for specifying other colour spaces.

## Examples

```
require(graphics); require(stats) # for na.omit
par(mfrow=c(2,2))
## The displayable colors from four planes of Lab space
ab <- expand.grid(a=(-10:15)*10,b=(-15:10)*10)

Lab <- cbind(L=20,ab)
srgb <- convertColor(Lab,from="Lab",to="sRGB",clip=NA)
clipped <- attr(na.omit(srgb),"na.action")
srgb[clipped,] <- 0
cols <- rgb(srgb[,1],srgb[,2],srgb[,3])
image((-10:15)*10,(-15:10)*10,matrix(1:(26*26),ncol=26),col=cols,
      xlab="a",ylab="b",main="Lab: L=20")

Lab <- cbind(L=40,ab)
srgb <- convertColor(Lab,from="Lab",to="sRGB",clip=NA)
clipped <- attr(na.omit(srgb),"na.action")
srgb[clipped,] <- 0
cols <- rgb(srgb[,1],srgb[,2],srgb[,3])
```

```

image((-10:15)*10, (-15:10)*10, matrix(1:(26*26), ncol=26), col=cols,
      xlab="a", ylab="b", main="Lab: L=40")

Lab <- cbind(L=60, ab)
srgb <- convertColor(Lab, from="Lab", to="sRGB", clip=NA)
clipped <- attr(na.omit(srgb), "na.action")
srgb[clipped,] <- 0
cols <- rgb(srgb[,1], srgb[,2], srgb[,3])
image((-10:15)*10, (-15:10)*10, matrix(1:(26*26), ncol=26), col=cols,
      xlab="a", ylab="b", main="Lab: L=60")

Lab <- cbind(L=80, ab)
srgb <- convertColor(Lab, from="Lab", to="sRGB", clip=NA)
clipped <- attr(na.omit(srgb), "na.action")
srgb[clipped,] <- 0
cols <- rgb(srgb[,1], srgb[,2], srgb[,3])
image((-10:15)*10, (-15:10)*10, matrix(1:(26*26), ncol=26), col=cols,
      xlab="a", ylab="b", main="Lab: L=80")

(cols <- t(col2rgb(palette()))
 (lab <- convertColor(cols, from="sRGB", to="Lab", scale.in=255))
 round(convertColor(lab, from="Lab", to="sRGB", scale.out=255)))

```

densCols

*Colors for Smooth Density Plots*

## Description

`densCols` produces a vector containing colors which encode the local densities at each point in a scatterplot.

## Usage

```

densCols(x, y = NULL, nbin = 128, bandwidth,
         colramp = colorRampPalette(blues9[-(1:3)]))
blues9

```

## Arguments

<code>x</code> , <code>y</code>	the <code>x</code> and <code>y</code> arguments provide the <code>x</code> and <code>y</code> coordinates of the points. Any reasonable way of defining the coordinates is acceptable. See the function <a href="#">xy.coords</a> for details. If supplied separately, they must be of the same length.
<code>nbin</code>	numeric vector of length one (for both directions) or two (for <code>x</code> and <code>y</code> separately) specifying the number of equally spaced grid points for the density estimation; directly used as <code>gridsize</code> in <a href="#">bkde2D()</a> .
<code>bandwidth</code>	numeric vector (length 1 or 2) of smoothing bandwidth(s). If missing, a more or less useful default is used. <code>bandwidth</code> is subsequently passed to function <a href="#">bkde2D</a> .
<code>colramp</code>	function accepting an integer <code>n</code> as an argument and returning <code>n</code> colors.

## Details

`densCols` computes and returns the set of colors that will be used in plotting.

`blues9` is a set of 9 color shades of blue used as the default in plotting.

## Value

`densCols` returns a vector of length `nrow(x)` that contains colors to be used in a subsequent scatterplot. Each color represents the local density around the corresponding point.

## Author(s)

Florian Hahne at FHCRC, originally

## See Also

`bkde2D` from package **KernSmooth**, and `smoothScatter()` which builds on the same computations as `densCols`.

## Examples

```
x1 <- matrix(rnorm(1e3), ncol=2)
x2 <- matrix(rnorm(1e3, mean=3, sd=1.5), ncol=2)
x <- rbind(x1,x2)

dcols <- densCols(x)
graphics::plot(x, col = dcols, pch=20, main = "n = 1000")
```

---

dev

*Control Multiple Devices*

---

## Description

These functions provide control over multiple graphics devices.

## Usage

```
dev.cur()
dev.list()
dev.next(which = dev.cur())
dev.prev(which = dev.cur())
dev.off(which = dev.cur())
dev.set(which = dev.next())
dev.new(...)
graphics.off()
```

## Arguments

`which` An integer specifying a device number.  
`...` arguments to be passed to the device selected.

## Details

Only one device is the ‘active’ device: this is the device in which all graphics operations occur. There is a "null device" which is always open but is really a placeholder: any attempt to use it will open a new device specified by `getOption("device")`.

Devices are associated with a name (e.g., "X11" or "postscript") and a number in the range 1 to 63; the "null device" is always device 1. Once a device has been opened the null device is not considered as a possible active device. There is a list of open devices, and this is considered as a circular list not including the null device. `dev.next` and `dev.prev` select the next open device in the appropriate direction, unless no device is open.

`dev.off` shuts down the specified (by default the current) device. If the current device is shut down and any other devices are open, the next open device is made current. It is an error to attempt to shut down device 1. `graphics.off()` shuts down all open graphics devices. Normal termination of a session runs the internal equivalent of `graphics.off()`.

`dev.set` makes the specified device the active device. If there is no device with that number, it is equivalent to `dev.next`. If `which = 1` it opens a new device and selects that.

`dev.new` opens a new device. Normally R will open a new device automatically when needed, but this enables you to open further devices in a platform-independent way. (For which device is used see `getOption("device")`.) Note that care is needed with file-based devices such as `pdf` and `postscript` and in that case file names such as ‘Rplots.pdf’, ‘Rplots1.pdf’, ..., ‘Rplots999.pdf’ are tried in turn. Only named arguments are passed to the device, and then only if they match the argument list of the device. Even so, care is needed with the interpretation of e.g. `width`, and for the standard bitmap devices `units="in"`, `res=72` is forced if neither is supplied but both `width` and `height` are.

## Value

`dev.cur` returns a length-one named integer vector giving the number and name of the active device, or 1, the null device, if none is active.

`dev.list` returns the numbers of all open devices, except device 1, the null device. This is a numeric vector with a `names` attribute giving the device names, or `NULL` if there is no open device.

`dev.next` and `dev.prev` return the number and name of the next / previous device in the list of devices. This will be the null device if and only if there are no open devices.

`dev.off` returns the number and name of the new active device (after the specified device has been shut down).

`dev.set` returns the number and name of the new active device.

`dev.new` returns the return value of the device opened, usually invisible `NULL`.

## See Also

[Devices](#), such as `postscript`, etc.

[layout](#) and its links for setting up plotting regions on the current device.

## Examples

```
## Not run: ## Unix-specific example
x11()
plot(1:10)
x11()
plot(rnorm(10))
```

```

dev.set(dev.prev())
abline(0,1)# through the 1:10 points
dev.set(dev.next())
abline(h=0, col="gray")# for the residual plot
dev.set(dev.prev())
dev.off(); dev.off()#- close the two X devices

## End(Not run)

```

---

dev.interactive      *Is the Current Graphics Device Interactive?*

---

### Description

Test if the current graphics device (or that which would be opened) is interactive.

### Usage

```

dev.interactive(orElse = FALSE)

deviceIsInteractive(name = NULL)

```

### Arguments

orElse	logical; if TRUE, the function also returns TRUE when <code>.Device == "null device"</code> and <code>getOption("device")</code> is among the known interactive devices.
name	one or more device names as a character vector, or NULL to give the existing list.

### Details

The X11 (Unix), windows (Windows) and quartz (Mac OS X, on-screen types only) are regarded as interactive, together with JavaGD (from the package of the same name) and CairoWin and CairoX11 (from package **Cairo**). Packages can add their devices to the list by calling `deviceIsInteractive`.

### Value

`dev.interactive()` returns a logical, TRUE if and only if an interactive (screen) device is in use.

`deviceIsInteractive` returns the updated list of known interactive devices, invisibly unless `name = NULL`.

### See Also

[Devices](#) for the available devices on your platform.

### Examples

```

dev.interactive()
print(deviceIsInteractive(NULL))

```



---

 dev.size

*Find Size of Device Surface*


---

### Description

Find the dimensions of the device surface of the current device.

### Usage

```
dev.size(units = c("in", "cm", "px"))
```

### Arguments

`units` the units in which to return the value – inches, cm, or pixels (device units).

### Value

A two-element numeric vector giving width and height of the current device; a new device is opened if there is none, similarly to `dev.new()`.

### See Also

The size information in inches can be obtained by `par("din")`, but this provides a way to access it independent of the graphics sub-system in use.

### Examples

```
dev.size("cm")
```

---

 dev2

*Copy Graphics Between Multiple Devices*


---

### Description

`dev.copy` copies the graphics contents of the current device to the device specified by `which` or to a new device which has been created by the function specified by `device` (it is an error to specify both `which` and `device`). (If recording is off on the current device, there are no contents to copy: this will result in no plot or an empty plot.) The device copied to becomes the current device.

`dev.print` copies the graphics contents of the current device to a new device which has been created by the function specified by `device` and then shuts the new device.

`dev.copy2eps` is similar to `dev.print` but produces an EPSF output file in portrait orientation (`horizontal = FALSE`). `dev.copy2pdf` is the analogue for PDF output.

`dev.control` allows the user to control the recording of graphics operations in a device. If `displaylist` is "inhibit" ("enable") then recording is turned off (on). It is only safe to change this at the beginning of a plot (just before or just after a new page). Initially recording is on for screen devices, and off for print devices.

## Usage

```
dev.copy(device, ..., which = dev.next())
dev.print(device = postscript, ...)
dev.copy2eps(...)
dev.copy2pdf(..., out.type = "pdf")
dev.control(displaylist = c("inhibit", "enable"))
```

## Arguments

<code>device</code>	A device function (e.g., <code>x11</code> , <code>postscript</code> , ...)
<code>...</code>	Arguments to the device function above: for <code>dev.copy2eps</code> arguments to <code>postscript</code> and for <code>dev.copy2pdf</code> , arguments to <code>pdf</code> . For <code>dev.print</code> , this includes <code>which</code> and by default any <code>postscript</code> arguments.
<code>which</code>	A device number specifying the device to copy to.
<code>out.type</code>	The name of the output device: can be "pdf", or "quartz" (some Mac OS X builds) or "cairo" (some Unix-alikes, see <code>cairo_pdf</code> ).
<code>displaylist</code>	A character string: the only valid values are "inhibit" and "enable".

## Details

Note that these functions copy the *device region* and not a plot: the background colour of the device surface is part of what is copied. Most screen devices default to a transparent background, which is probably not what is needed when copying to a device such as `png`.

For `dev.copy2eps` and `dev.copy2pdf`, `width` and `height` are taken from the current device unless otherwise specified. If just one of `width` and `height` is specified, the other is adjusted to preserve the aspect ratio of the device being copied. The default file name is `Rplot.eps` or `Rplot.pdf`, and can be overridden by specifying a `file` argument.

Copying to devices such as `postscript` and `pdf` which need font families pre-specified needs extra care – R is unaware of which families were used in a plot and so they will need to manually specified by the `fonts` argument passed as part of `...`. Similarly, if the device to be copied from was opened with a `family` argument, a suitable `family` argument will need to be included in `...`

The default for `dev.print` is to produce and print a postscript copy, if `options("printcmd")` is set suitably.

`dev.print` is most useful for producing a postscript print (its default) when the following applies. Unless `file` is specified, the plot will be printed. Unless `width`, `height` and `pointsize` are specified the plot dimensions will be taken from the current device, shrunk if necessary to fit on the paper. (`pointsize` is rescaled if the plot is shrunk.) If `horizontal` is not specified and the plot can be printed at full size by switching its value this is done instead of shrinking the plot region.

If `dev.print` is used with a specified device (even `postscript`) it sets the `width` and `height` in the same way as `dev.copy2eps`. This will not be appropriate unless the device specifies dimensions in inches, in particular not for `png`, `jpeg`, `tiff` and `bmp` unless `units="inches"` is specified.

## Value

`dev.copy` returns the name and number of the device which has been copied to.

`dev.print`, `dev.copy2eps` and `dev.copy2pdf` return the name and number of the device which has been copied from.

**Note**

Most devices (including all screen devices) have a display list which records all of the graphics operations that occur in the device. `dev.copy` copies graphics contents by copying the display list from one device to another device. Also, automatic redrawing of graphics contents following the resizing of a device depends on the contents of the display list.

After the command `dev.control("inhibit")`, graphics operations are not recorded in the display list so that `dev.copy` and `dev.print` will not copy anything and the contents of a device will not be redrawn automatically if the device is resized.

The recording of graphics operations is relatively expensive in terms of memory so the command `dev.control("inhibit")` can be useful if memory usage is an issue.

**See Also**

`dev.cur` and other `dev.xxx` functions.

**Examples**

```
## Not run:
x11()
plot(rnorm(10), main="Plot 1")
dev.copy(device=x11)
mtext("Copy 1", 3)
dev.print(width=6, height=6, horizontal=FALSE) # prints it
dev.off(dev.prev())
dev.off()

## End(Not run)
```

---

dev2bitmap

*Graphics Device for Bitmap Files via GhostScript*


---

**Description**

`bitmap` generates a graphics file. `dev2bitmap` copies the current graphics device to a file in a graphics format.

**Usage**

```
bitmap(file, type = "png16m", height = 7, width = 7, res = 72,
       units = "in", pointsize, taa = NA, gaa = NA, ...)

dev2bitmap(file, type = "png16m", height = 7, width = 7, res = 72,
          units = "in", pointsize, ...,
          method = c("postscript", "pdf"), taa = NA, gaa = NA)
```

**Arguments**

`file`                   The output file name, with an appropriate extension.

`type`                   The type of bitmap. the default is "png256".

`width, height`           Dimensions of the display region.

res	Resolution, in dots per inch.
units	The units in which height and width are given. Can be in (inches), px (pixels), cm or mm.
pointsize	The pointsize to be used for text: defaults to something reasonable given the width and height
...	Other parameters passed to <a href="#">postscript</a> or <a href="#">pdf</a> .
method	Should the plot be done by <a href="#">postscript</a> or <a href="#">pdf</a> ?
taa, gaa	Number of bits of antialiasing for text and for graphics respectively. Usually 4 (for best effect) or 2. Not supported on all types.

### Details

dev2bitmap works by copying the current device to a [postscript](#) or [pdf](#) device, and post-processing the output file using `ghostscript`. `bitmap` works in the same way using a `postscript` device and post-processing the output as ‘printing’.

You will need `ghostscript`: the full path to the executable can be set by the environment variable `R_GSCMD`. (If this is unset the command `gs` is used, which will work if it is in your path.)

The types available will depend on the version of `ghostscript`, but are likely to include `"pcxmono"`, `"pcxgray"`, `"pcx16"`, `"pcx256"`, `"pcx24b"`, `"pcxcmyk"`, `"pbm"`, `"pbmraw"`, `"pgm"`, `"pgmraw"`, `"pgnm"`, `"pgnmraw"`, `"pnm"`, `"pnmraw"`, `"ppm"`, `"ppmraw"`, `"pkm"`, `"pkmraw"`, `"tiffcrl"`, `"tiffg3"`, `"tiffg32d"`, `"tiffg4"`, `"tiffllzw"`, `"tiffpack"`, `"tiff12nc"`, `"tiff24nc"`, `"psmono"`, `"psgray"`, `"psrgb"`, `"bit"`, `"bitrgb"`, `"bitcmyk"`, `"pngmono"`, `"pnggray"`, `"pngalpha"`, `"png16"`, `"png256"`, `"png16m"`, `"png48"`, `"jpeg"`, `"jpeggray"`, `"pdfwrite"`.

The default type, `"png16m"` supports 24-bit colour and anti-aliasing. Versions of R prior to 2.7.0 defaulted to `"png256"`, which uses a palette of 256 colours and could be a more compact representation. Monochrome graphs can use `"pngmono"`, or `"pnggray"` if anti-aliasing is desired.

Note that for a colour TIFF image you probably want `"tiff24nc"`, which is 8-bit per channel RGB (the most common TIFF format). None of the listed TIFF types support transparency.

For formats which contain a single image, a file specification like `Rplots%03d.png` can be used: this is interpreted by GhostScript.

For `dev2bitmap` if just one of `width` and `height` is specified, the other is chosen to preserve aspect ratio of the device being copied. The main reason to prefer `method = "pdf"` over the default would be to allow semi-transparent colours to be used.

For graphics parameters such as `"cra"` that need to work in pixels, the default resolution of 72dpi is always used.

### Value

None.

### Conventions

This section describes the implementation of the conventions for graphics devices set out in the “R Internals Manual”. These devices follow the underlying device, so when viewed at the stated `res`:

- The default device size is 7 inches square.
- Font sizes are in big points.
- The default font family is (for the standard GhostScript setup) URW Nimbus Sans.

- Line widths are as a multiple of 1/96 inch, with no minimum.
- Circle of any radius are allowed.
- Colours are interpreted by the viewing/printing application.

### Note

Although using `type = "pdfwrite"` will work for simple plots, it is not recommended. Either use `pdf` to produce PDF directly, or call `ps2pdf -dAutoRotatePages=/None` on the output of `postscript`: that command is optimized to do the conversion to PDF in ways that these functions are not.

### See Also

`savePlot`, which for windows and X11 (`type = "Cairo"`) provides a simple way to record a PNG record of the current plot.

`postscript`, `pdf`, `png`, `jpeg`, `tiff` and `bmp`.

To display an array of data, see `image`.

---

devAskNewPage

*Prompt before New Page*

---

### Description

This function can be used to control (for the current device) whether the user is prompted before starting a new page of output.

### Usage

```
devAskNewPage(ask = NULL)
```

### Arguments

<code>ask</code>	NULL or a logical value. If TRUE, the user is prompted before a new page of output is started.
------------------	--

### Details

If the current device is the null device, this will open a graphics device.

The default argument just returns the current setting and does not change it.

The default value when a device is opened is taken from the setting of `options("device.ask.default")`.

The precise circumstances when the user will be asked to confirm a new page depend on the graphics subsystem. Obviously this needs to be an interactive session. In addition 'recording' needs to be in operation, so only when the display list is enabled (see `dev.control`) which it usually is only on a screen device.

### Value

The current prompt setting *before* any new setting is applied.

**See Also**

[plot.new](#), [grid.newpage](#)

---

Devices

*List of Graphical Devices*

---

**Description**

The following graphics devices are currently available:

- [postscript](#) Writes PostScript graphics commands to a file
- [pdf](#) Write PDF graphics commands to a file
- [pictex](#) Writes LaTeX/PicTeX graphics commands to a file
- [png](#) PNG bitmap device
- [jpeg](#) JPEG bitmap device
- [bmp](#) BMP bitmap device
- [tiff](#) TIFF bitmap device
- [xfig](#) Device for XFIG graphics file format
- [bitmap](#) bitmap pseudo-device via GhostScript (if available).

The following devices will be functional if R was compiled to use them (they exist but will return with a warning on other systems):

- [X11](#) The graphics device for the X11 Window system
- [cairo\\_pdf](#), [cairo\\_ps](#) PDF and PostScript devices based on cairo graphics.
- [quartz](#) The graphics device for the Mac OS X native Quartz 2d graphics system. (This is only functional on Mac OS X where it can be used from the R.app GUI and from the command line: but it will display on the local screen even for a remote session.)

**Details**

If no device is open, using a high-level graphics function will cause a device to be opened. Which device is given by `options("device")` which is initially set as the most appropriate for each platform: a screen device for most interactive use and `pdf` (or the setting of `R_DEFAULT_DEVICE`) otherwise. The exception is interactive use under Unix if no screen device is known to be available, when `pdf()` is used.

**See Also**

The individual help files for further information on any of the devices listed here; [X11.options](#), [quartz.options](#), [ps.options](#) and [pdf.options](#) for how to customize devices. [dev.interactive](#), [dev.cur](#), [dev.print](#), [graphics.off](#), [image](#), [dev2bitmap.capabilities](#) to see if [X11](#), [jpeg](#) [png](#) and [quartz](#) are available.

**Examples**

```
## Not run:
## open the default screen device on this platform if no device is
## open
if(dev.cur() == 1) dev.new()

## End(Not run)
```

---

`embedFonts`*Embed Fonts in PostScript and PDF*

---

### Description

Runs Ghostscript to process a PDF or PostScript file and embed all fonts in the file.

### Usage

```
embedFonts(file, format, outfile = file, fontpaths = "",
           options = "")
```

### Arguments

<code>file</code>	a character string giving the name of the original file.
<code>format</code>	either "pswrite" or "pdfwrite". If not specified, it is guessed from the suffix of <code>file</code> .
<code>outfile</code>	the name of the new file (with fonts embedded).
<code>fontpaths</code>	a character vector giving directories that Ghostscript will search for fonts.
<code>options</code>	a character string containing further options to Ghostscript.

### Details

This function is not necessary if you just use the standard default fonts for PostScript and PDF output.

If you use a special font, this function is useful for embedding that font in your PostScript or PDF document so that it can be shared with others without them having to install your special font (provided the font licence allows this).

If the special font is not installed for Ghostscript, you will need to tell Ghostscript where the font is, using something like `options="-sFONTPATH=path/to/font"`.

This function relies on a suitable Ghostscript executable being in your path, or the environment variable `R_GSCMD` (the same as `bitmap`) being set as the full path to the Ghostscript executable. This defaults to "gs".

Note that Ghostscript may do font substitution, so the font embedded may differ from that specified in the original file.

### Value

The shell command used to invoke Ghostscript is returned invisibly. This may be useful for debugging purposes as you can run the command by hand in a shell to look for problems.

### See Also

[postscriptFonts, Devices](#).

Paul Murrell and Brian Ripley (2006) Non-standard fonts in PostScript and PDF graphics. *R News*, 6(2):41–47. [http://cran.r-project.org/doc/Rnews/Rnews\\_2006-2.pdf](http://cran.r-project.org/doc/Rnews/Rnews_2006-2.pdf).

---

extendrange	<i>Extend a Numerical Range by a Small Percentage</i>
-------------	---

---

**Description**

Extends a numerical range by a small percentage, i.e., fraction, *on both sides*.

**Usage**

```
extendrange(x, r = range(x, na.rm = TRUE), f = 0.05)
```

**Arguments**

<code>x</code>	numeric vector; not used if <code>r</code> is specified.
<code>r</code>	numeric vector of length 2; defaults to the <a href="#">range</a> of <code>x</code> .
<code>f</code>	number specifying the fraction by which the range should be extended.

**Value**

A numeric vector of length 2,  $r + c(-f, f) * \text{diff}(r)$ .

**See Also**

[range](#); [pretty](#) which can be considered a sophisticated extension of `extendrange`.

**Examples**

```
x <- 1:5
(r <- range(x))           # 1     5
extendrange(x)           # 0.8   5.2
extendrange(x, f= 0.01) # 0.96  5.04
## Use 'r' if you have it already:
stopifnot(identical(extendrange(r=r),
                    extendrange(x)))
```

---

getGraphicsEvent	<i>Wait for a mouse or keyboard event from a graphics window</i>
------------------	--

---

**Description**

This function waits for input from a graphics window in the form of a mouse or keyboard event.

**Usage**

```
getGraphicsEvent(prompt = "Waiting for input",
                 onMouseDown = NULL, onMouseMove = NULL,
                 onMouseUp = NULL, onKeybd = NULL)
```



**Arguments**

<code>prompt</code>	prompt to be displayed to the user
<code>onMouseDown</code>	a function to respond to mouse clicks
<code>onMouseMove</code>	a function to respond to mouse movement
<code>onMouseUp</code>	a function to respond to mouse button releases
<code>onKeybd</code>	a function to respond to key presses

**Details**

This function allows user input from some graphics devices (currently only the Windows screen display). When called, event handlers may be installed to respond to events involving the mouse or keyboard.

The mouse event handlers should be functions with header `function(buttons, x, y)`. The coordinates `x` and `y` will be passed to mouse event handlers in device independent coordinates (i.e. the lower left corner of the window is  $(0, 0)$ , the upper right is  $(1, 1)$ ). The `buttons` argument will be a vector listing the buttons that are pressed at the time of the event, with 0 for left, 1 for middle, and 2 for right.

The keyboard event handler should be a function with header `function(key)`. A single element character vector will be passed to this handler, corresponding to the key press. Shift and other modifier keys will have been processed, so `shift-a` will be passed as "A". The following special keys may also be passed to the handler:

- Control keys, passed as "Ctrl-A", etc.
- Navigation keys, passed as one of "Left", "Up", "Right", "Down", "PgUp", "PgDn", "End", "Home"
- Edit keys, passed as one of "Ins", "Del"
- Function keys, passed as one of "F1", "F2", ...

The event handlers are standard R functions, and will be executed in an environment as though they had been called directly from `getGraphicsEvent`.

Events will be processed until

- one of the event handlers returns a non-NULL value which will be returned as the value of `getGraphicsEvent`, or
- the user interrupts the function from the console.

**Value**

A non-NULL value returned from one of the event handlers.

**Author(s)**

Duncan Murdoch

**Examples**

```
## Not run:
mousedown <- function(buttons, x, y) {
  plx <- grconvertX(x, "ndc", "user")
  ply <- grconvertY(y, "ndc", "user")
  cat("Buttons ", paste(buttons, collapse=" "), " at ndc",
```

```

        x, y, "user", plx, ply, "\n")
    points(plx, ply, col="red", pch=19, cex=2)
    if (x > 0.85 && y > 0.85) "Done"
    else NULL
}

mousemove <- function(buttons, x, y) {
  plx <- grconvertX(x, "ndc", "user")
  ply <- grconvertY(y, "ndc", "user")
  points(plx, ply)
  NULL
}

keybd <- function(key) {
  cat("Key <", key, ">\n", sep = "")
}

plot(0:1, 0:1, type='n')
getGraphicsEvent("Click on upper right to quit",
  onMouseDown = mousedown,
  onMouseMove = mousemove,
  onKeybd = keybd)

## End(Not run)

```

---

gray

*Gray Level Specification*


---

## Description

Create a vector of colors from a vector of gray levels.

## Usage

```
gray(level)
grey(level)
```

## Arguments

`level` a vector of desired gray levels between 0 and 1; zero indicates "black" and one indicates "white".

## Details

The values returned by `gray` can be used with a `col=` specification in graphics functions or in [par](#).

`grey` is an alias for `gray`.

## Value

A vector of colors of the same length as `level`.

**See Also**

[rainbow](#), [hsv](#), [hcl](#), [rgb](#).

**Examples**

```
gray(0:8 / 8)
```

---

gray.colors

*Gray Color Palette*

---

**Description**

Create a vector of  $n$  gamma-corrected gray colors.

**Usage**

```
gray.colors(n, start = 0.3, end = 0.9, gamma = 2.2)
grey.colors(n, start = 0.3, end = 0.9, gamma = 2.2)
```

**Arguments**

<code>n</code>	the number of gray colors ( $\geq 1$ ) to be in the palette.
<code>start</code>	starting gray level in the palette (should be between 0 and 1 where zero indicates "black" and one indicates "white").
<code>end</code>	ending gray level in the palette.
<code>gamma</code>	the gamma correction.

**Details**

The function `gray.colors` chooses a series of  $n$  gamma-corrected gray levels between `start` and `end`: `seq(start^gamma, end^gamma, length = n)^(1/gamma)`. The returned palette contains the corresponding gray colors. This palette is used in `barplot.default`.

`grey.colors` is an alias for `gray.colors`.

**Value**

A vector of  $n$  gray colors.

**See Also**

[gray](#), [rainbow](#), [palette](#).

**Examples**

```
require(graphics)

pie(rep(1,12), col = gray.colors(12))
barplot(1:12, col = gray.colors(12))
```

---

**hcl** *HCL Color Specification*

---

**Description**

Create a vector of colors from vectors specifying hue, chroma and luminance.

**Usage**

```
hcl(h = 0, c = 35, l = 85, alpha, fixup = TRUE)
```

**Arguments**

<code>h</code>	The hue of the color specified as an angle in the range [0,360]. 0 yields red, 120 yields green 240 yields blue, etc.
<code>c</code>	The chroma of the color. The upper bound for chroma depends on hue and luminance.
<code>l</code>	A value in the range [0,100] giving the luminance of the colour. For a given combination of hue and chroma, only a subset of this range is possible.
<code>alpha</code>	numeric vector of values in the range [0, 1] for alpha transparency channel (0 means transparent and 1 means opaque).
<code>fixup</code>	a logical value which indicates whether the resulting RGB values should be corrected to ensure that a real color results. if <code>fixup</code> is <code>FALSE</code> RGB components lying outside the range [0,1] will result in an NA value.

**Details**

This function corresponds to polar coordinates in the CIE-LUV color space. Steps of equal size in this space correspond to approximately equal perceptual changes in color. Thus, `hcl` can be thought of as a perceptually based version of `hsv`.

The function is primarily intended as a way of computing colors for filling areas in plots where area corresponds to a numerical value (pie charts, bar charts, mosaic plots, histograms, etc). Choosing colors which have equal chroma and luminance provides a way of minimising the irradiation illusion which would otherwise produce a misleading impression of how large the areas are.

The default values of chroma and luminance make it possible to generate a full range of hues and have a relatively pleasant pastel appearance.

The RGB values produced by this function correspond to the sRGB color space used on most PC computer displays. There are other packages which provide more general color space facilities.

Semi-transparent colors ( $0 < \text{alpha} < 1$ ) are supported only on some devices: see [rgb](#).

**Value**

A vector of character strings which can be used as color specifications by R graphics functions.

**Note**

At present there is no guarantee that the colours rendered by R graphics devices will correspond to their sRGB description. It is planned to adopt sRGB as the standard R color description in future.

**Author(s)**

Ross Ihaka

**References**

Ihaka, R. (2003). Colour for Presentation Graphics, Proceedings of the 3rd International Workshop on Distributed Statistical Computing (DSC 2003), March 20-22, 2003, Technische Universität Wien, Vienna, Austria. <http://www.ci.tuwien.ac.at/Conferences/DSC-2003>.

**See Also**

[hsv](#), [rgb](#).

**Examples**

```
require(graphics)

# The Foley and Van Dam PhD Data.
csd <- matrix(c( 4,2,4,6, 4,3,1,4, 4,7,7,1,
                0,7,3,2, 4,5,3,2, 5,4,2,2,
                3,1,3,0, 4,4,6,7, 1,10,8,7,
                1,5,3,2, 1,5,2,1, 4,1,4,3,
                0,3,0,6, 2,1,5,5), nrow=4)

csphd <- function(colors)
  barplot(csd, col = colors, ylim = c(0,30),
          names = 72:85, xlab = "Year", ylab = "Students",
          legend = c("Winter", "Spring", "Summer", "Fall"),
          main = "Computer Science PhD Graduates", las = 1)

# The Original (Metaphorical) Colors (Ouch!)
csphd(c("blue", "green", "yellow", "orange"))

# A Color Tetrad (Maximal Color Differences)
csphd(hcl(h = c(30, 120, 210, 300)))

# Same, but lighter and less colorful
# Turn of automatic correction to make sure
# that we have defined real colors.
csphd(hcl(h = c(30, 120, 210, 300),
            c = 20, l = 90, fixup = FALSE))

# Analogous Colors
# Good for those with red/green color confusion
csphd(hcl(h = seq(60, 240, by = 60)))

# Metaphorical Colors
csphd(hcl(h = seq(210, 60, length = 4)))

# Cool Colors
csphd(hcl(h = seq(120, 0, length = 4) + 150))

# Warm Colors
csphd(hcl(h = seq(120, 0, length = 4) - 30))

# Single Color
```

```
hist(stats::rnorm(1000), col = hcl(240))
```

Hershey

*Hershey Vector Fonts in R***Description**

If the `family` graphical parameter (see [par](#)) has been set to one of the Hershey fonts (see ‘Details’) Hershey vector fonts are used to render text.

When using the `text` and `contour` functions Hershey fonts may be selected via the `vfont` argument, which is a character vector of length 2 (see ‘Details’ for valid values). This allows Cyrillic to be selected, which is not available via the font families.

**Usage**

```
Hershey
```

**Details**

The Hershey fonts have two advantages:

1. vector fonts describe each character in terms of a set of points; R renders the character by joining up the points with straight lines. This intimate knowledge of the outline of each character means that R can arbitrarily transform the characters, which can mean that the vector fonts look better for rotated text.
2. this implementation was adapted from the GNU libplot library which provides support for non-ASCII and non-English fonts. This means that it is possible, for example, to produce weird plotting symbols and Japanese characters.

Drawback:

You cannot use mathematical expressions ([plotmath](#)) with Hershey fonts.

The Hershey characters are organised into a set of fonts. A particular font is selected by specifying one of the following font families via `par(family)` and specifying the desired font face (plain, bold, italic, bold-italic) via `par(font)`.

family	faces available
"HersheySerif"	plain, bold, italic, bold-italic
"HersheySans"	plain, bold, italic, bold-italic
"HersheyScript"	plain, bold
"HersheyGothicEnglish"	plain
"HersheyGothicGerman"	plain
"HersheyGothicItalian"	plain
"HersheySymbol"	plain, bold, italic, bold-italic
"HersheySansSymbol"	plain, italic

In the `vfont` specification for the `text` and `contour` functions, the Hershey font is specified by a `typeface` (e.g., `serif` or `sans serif`) and a `fontindex` or ‘style’ (e.g., `plain` or `italic`). The first element of `vfont` specifies the typeface and the second element specifies the fontindex. The

first table produced by `demo (Hershey)` shows the character `a` produced by each of the different fonts.

The available `typeface` and `fontindex` values are available as list components of the variable `Hershey`. The allowed pairs for `(typeface, fontindex)` are:

serif	plain
serif	italic
serif	bold
serif	bold italic
serif	cyrillic
serif	oblique cyrillic
serif	EUC
sans serif	plain
sans serif	italic
sans serif	bold
sans serif	bold italic
script	plain
script	italic
script	bold
gothic english	plain
gothic german	plain
gothic italian	plain
serif symbol	plain
serif symbol	italic
serif symbol	bold
serif symbol	bold italic
sans serif symbol	plain
sans serif symbol	italic

and the indices of these are available as `Hershey$allowed`.

**Escape sequences:** The string to be drawn can include escape sequences, which all begin with a `'\'`. When `R` encounters a `'\'`, rather than drawing the `'\'`, it treats the subsequent character(s) as a coded description of what to draw.

One useful escape sequence (in the current context) is of the form: `'\123'`. The three digits following the `'\'` specify an octal code for a character. For example, the octal code for `p` is 160 so the strings `"p"` and `"\160"` are equivalent. This is useful for producing characters when there is not an appropriate key on your keyboard.

The other useful escape sequences all begin with `'\\'`. These are described below. Remember that backslashes have to be doubled in `R` character strings, so they need to be entered with *four* backslashes.

**Symbols:** an entire string of Greek symbols can be produced by selecting the `HersheySymbol` or `HersheySansSymbol` family or the `Serif Symbol` or `Sans Serif Symbol` typeface. To allow Greek symbols to be embedded in a string which uses a non-symbol typeface, there are a set of symbol escape sequences of the form `'\\*a'`. For example, the escape sequence `'\\*a'` produces a Greek alpha. The second table in `demo (Hershey)` shows all of the symbol escape sequences and the symbols that they produce.

**ISO Latin-1:** further escape sequences of the form `'\\*ab'` are provided for producing ISO Latin-1 characters. Another option is to use the appropriate octal code. The (non-ASCII) ISO Latin-1 characters are in the range 241...377. For example, `'\366'` produces the character `o` with an umlaut. The third table in `demo (Hershey)` shows all of the ISO Latin-1 escape sequences.

These characters can be used directly in a Latin-1 locale or on a system with MBCS support. (In the latter, characters not in Latin-1 are replaced by a dot.)

Several characters are missing, c-cedilla has no cedilla and ‘sharp s’ (‘U+00DF’, also known as ‘esszett’) is rendered as `ss`.

**Special Characters:** a set of characters are provided which do not fall into any standard font. These can only be accessed by escape sequence. For example, ‘`\\LI`’ produces the zodiac sign for Libra, and ‘`\\JU`’ produces the astronomical sign for Jupiter. The fourth table in `demo(Hershey)` shows all of the special character escape sequences.

**Cyrillic Characters:** cyrillic characters are implemented according to the K018-R encoding, and can be used directly in such a locale using the Serif typeface and Cyrillic (or Oblique Cyrillic) fontindex. Alternatively they can be specified via an octal code in the range 300 to 337 for lower case characters or 340 to 377 for upper case characters. The fifth table in `demo(Hershey)` shows the octal codes for the available Cyrillic characters.

Cyrillic has to be selected via a (“`serif`”, `fontindex`) pair rather than via a font family.

**Japanese Characters:** 83 Hiragana, 86 Katakana, and 603 Kanji characters are implemented according to the EUC-JP (Extended Unix Code) encoding. Each character is identified by a unique hexadecimal code. The Hiragana characters are in the range 0x2421 to 0x2473, Katakana are in the range 0x2521 to 0x2576, and Kanji are (scattered about) in the range 0x3021 to 0x6d55.

When using the Serif typeface and EUC fontindex, these characters can be produced by a *pair* of octal codes. Given the hexadecimal code (e.g., 0x2421), take the first two digits and add 0x80 and do the same to the second two digits (e.g., 0x21 and 0x24 become 0xa4 and 0xa1), then convert both to octal (e.g., 0xa4 and 0xa1 become 244 and 241). For example, the first Hiragana character is produced by ‘`\244\241`’.

It is also possible to use the hexadecimal code directly. This works for all non-EUC fonts by specifying an escape sequence of the form ‘`\#J1234`’. For example, the first Hiragana character is produced by ‘`\#J2421`’.

The Kanji characters may be specified in a third way, using the so-called "Nelson Index", by specifying an escape sequence of the form ‘`\#N1234`’. For example, the (obsolete) Kanji for ‘one’ is produced by ‘`\#N0001`’.

`demo(Japanese)` shows the available Japanese characters.

**Raw Hershey Glyphs:** all of the characters in the Hershey fonts are stored in a large array. Some characters are not accessible in any of the Hershey fonts. These characters can only be accessed via an escape sequence of the form ‘`\#H1234`’. For example, the fleur-de-lys is produced by ‘`\#H0746`’. The sixth and seventh tables of `demo(Hershey)` shows all of the available raw glyphs.

## References

<http://www.gnu.org/software/plotutils/plotutils.html>

## See Also

`demo(Hershey)`, [par](#), [text](#), [contour](#).

[Japanese](#) for the Japanese characters in the Hershey fonts.

## Examples

Hershey

## for tables of examples, see `demo(Hershey)`



hsv

*HSV Color Specification***Description**

Create a vector of colors from vectors specifying hue, saturation and value.

**Usage**

```
hsv(h = 1, s = 1, v = 1, gamma = 1, alpha)
```

**Arguments**

<code>h, s, v</code>	numeric vectors of values in the range $[0, 1]$ for ‘hue’, ‘saturation’ and ‘value’ to be combined to form a vector of colors. Values in shorter arguments are recycled.
<code>gamma</code>	a gamma-correction exponent, $\gamma$
<code>alpha</code>	numeric vector of values in the range $[0, 1]$ for alpha transparency channel (0 means transparent and 1 means opaque).

**Details**

Semi-transparent colors ( $0 < \text{alpha} < 1$ ) are supported only on some devices: see [rgb](#).

**Value**

This function creates a vector of colors corresponding to the given values in HSV space. The values returned by `hsv` can be used with a `col=` specification in graphics functions or in `par`.

**Gamma correction**

For each color,  $(r, g, b)$  in RGB space (with all values in  $[0, 1]$ ), the final color corresponds to  $(r^\gamma, g^\gamma, b^\gamma)$ .

**See Also**

[hcl](#) for a perceptually based version of `hsv()`, [rgb](#) and [rgb2hsv](#) for RGB to HSV conversion; [rainbow](#), [gray](#).

**Examples**

```
require(graphics)

hsv(.5, .5, .5)

## Look at gamma effect:
n <- 20; y <- -sin(3*pi*((1:n)-1/2)/n)
op <- par(mfrow=c(3,2),mar=rep(1.5,4))
for(gamma in c(.4, .6, .8, 1, 1.2, 1.5))
  plot(y, axes = FALSE, frame.plot = TRUE,
       xlab = "", ylab = "", pch = 21, cex = 30,
       bg = rainbow(n, start=.85, end=.1, gamma = gamma),
```

```

      main = paste("Red tones;  gamma=", format(gamma))
par(op)

```

Japanese

*Japanese characters in R***Description**

The implementation of Hershey vector fonts provides a large number of Japanese characters (Hiragana, Katakana, and Kanji).

**Details**

Without keyboard support for typing Japanese characters, the only way to produce these characters is to use special escape sequences: see [Hershey](#).

For example, the Hiragana character for the sound "ka" is produced by `'\#J242b'` and the Katakana character for this sound is produced by `'\#J252b'`. The Kanji ideograph for "one" is produced by `'\#J306c'` or `'\#N0001'`.

The output from `demo(Japanese)` shows tables of the escape sequences for the available Japanese characters.

**References**

<http://www.gnu.org/software/plotutils/plotutils.html>

**See Also**

`demo(Japanese)`, [Hershey](#), [text](#)

**Examples**

```

require(graphics)

plot(1:9, type="n", axes=FALSE, frame=TRUE, ylab="",
      main= "example(Japanese)", xlab= "using Hershey fonts")
par(cex=3)
Vf <- c("serif", "plain")

text(4, 2, "\#J2438\#J2421\#J2451\#J2473", vfont = Vf)
text(4, 4, "\#J2538\#J2521\#J2551\#J2573", vfont = Vf)
text(4, 6, "\#J467c\#J4b5c", vfont = Vf)
text(4, 8, "Japan", vfont = Vf)
par(cex=1)
text(8, 2, "Hiragana")
text(8, 4, "Katakana")
text(8, 6, "Kanji")
text(8, 8, "English")

```

---

 make.rgb

*Create colour spaces*


---

### Description

These functions specify colour spaces for use in `convertColor`.

### Usage

```
make.rgb(red, green, blue, name = NULL, white = "D65",
         gamma = 2.2)
```

```
colorConverter(toXYZ, fromXYZ, name, white=NULL)
```

### Arguments

<code>red, green, blue</code>	Chromaticity (xy or xyY) of RGB primaries
<code>name</code>	Name for the colour space
<code>white</code>	Character string specifying the reference white (see 'Details').
<code>gamma</code>	Display gamma (nonlinearity). A positive number or the string "sRGB"
<code>fromXYZ</code>	Function to convert from XYZ tristimulus coordinates to this space
<code>toXYZ</code>	Function to convert from this space to XYZ tristimulus coordinates.

### Details

An RGB colour space is defined by the chromaticities of the red, green and blue primaries. These are given as vectors of length 2 or 3 in xyY coordinates (the Y component is not used and may be omitted). The chromaticities are defined relative to a reference white, which must be one of the CIE standard illuminants: "A", "B", "C", "D50", "D55", "D60", "E" (usually "D65").

The display gamma is most commonly 2.2, though 1.8 is used for Apple RGB. The sRGB standard specifies a more complicated function that is close to a gamma of 2.2; `gamma="sRGB"` uses this function.

Colour spaces other than RGB can be specified directly by giving conversions to and from XYZ tristimulus coordinates. The functions should take two arguments. The first is a vector giving the coordinates for one colour. The second argument is the reference white. If a specific reference white is included in the definition of the colour space (as for the RGB spaces) this second argument should be ignored and may be . . .

### Value

An object of class `colorConverter`

### References

Conversion algorithms from <http://www.brucelindbloom.com>

### See Also

`convertColor`

**Examples**

```
(pal <- make.rgb(red= c(0.6400,0.3300),
                green=c(0.2900,0.6000),
                blue= c(0.1500,0.0600),
                name = "PAL/SECAM RGB"))

## converter for sRGB in #rrggbb format
hexcolor <- colorConverter(toXYZ = function(hex,...) {
  rgb <- t(col2rgb(hex))/255
  colorspace$sRGB$toXYZ(rgb,...) },
  fromXYZ = function(xyz,...) {
  rgb <- colorspace$sRGB$fromXYZ(xyz,..)
  rgb <- round(rgb,5)
  if (min(rgb) < 0 || max(rgb) > 1)
    as.character(NA)
  else
    rgb(rgb[1],rgb[2],rgb[3])},
  white = "D65", name = "#rrggbb")

(cols <- t(col2rgb(palette())))
(luv <- convertColor(cols,from="sRGB", to="Luv", scale.in=255))
(hex <- convertColor(luv, from="Luv", to=hexcolor, scale.out=NULL))

## must make hex a matrix before using it
(cc <- round(convertColor(as.matrix(hex), from= hexcolor, to= "sRGB",
                        scale.in=NULL, scale.out=255)))

stopifnot(cc == cols)
```

n2mfrow

*Compute Default mfrow From Number of Plots***Description**

Easy setup for plotting multiple figures (in a rectangular layout) on one page. This computes a sensible default for `par(mfrow)`.

**Usage**

```
n2mfrow(nr.plots)
```

**Arguments**

```
nr.plots      integer; the number of plot figures you'll want to draw.
```

**Value**

A length two integer vector `nr`, `nc` giving the number of rows and columns, fulfilling `nr >= nc >= 1` and `nr * nc >= nr.plots`.

**Author(s)**

Martin Maechler

**See Also**

[par](#), [layout](#).

**Examples**

```
require(graphics)

n2mfrow(8) # 3 x 3

n <- 5 ; x <- seq(-2,2, len=51)
## suppose now that 'n' is not known {inside function}
op <- par(mfrow = n2mfrow(n))
for (j in 1:n)
  plot(x, x^j, main = substitute(x^ exp, list(exp = j)), type = "l",
       col = "blue")

sapply(1:10, n2mfrow)
```

---

nclass

---

*Compute the Number of Classes for a Histogram*


---

**Description**

Compute the number of classes for a histogram.

**Usage**

```
nclass.Sturges(x)
nclass.scott(x)
nclass.FD(x)
```

**Arguments**

x                    A data vector.

**Details**

`nclass.Sturges` uses Sturges' formula, implicitly basing bin sizes on the range of the data.

`nclass.scott` uses Scott's choice for a normal distribution based on the estimate of the standard error, unless that is zero where it returns 1.

`nclass.FD` uses the Freedman-Diaconis choice based on the inter-quartile range ([IQR](#)) unless that's zero where it reverts to `mad(x, constant=2)` and when that is 0 as well, returns 1.

**Value**

The suggested number of classes.

## References

- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS*. Springer, page 112.
- Freedman, D. and Diaconis, P. (1981) On the histogram as a density estimator:  $L_2$  theory. *Zeitschrift für Wahrscheinlichkeitstheorie und verwandte Gebiete* **57**, 453–476.
- Scott, D. W. (1979) On optimal and data-based histograms. *Biometrika* **66**, 605–610.
- Scott, D. W. (1992) *Multivariate Density Estimation. Theory, Practice, and Visualization*. Wiley.
- Sturges, H. A. (1926) The choice of a class interval. *Journal of the American Statistical Association* **21**, 65–66.

## See Also

`hist` and `truehist` (package **MASS**); `dpih` (package **KernSmooth**) for a plugin bandwidth proposed by Wand(1995).

## Examples

```
set.seed(1)
x <- stats::rnorm(1111)
nclass.Sturges(x)

## Compare them:
NC <- function(x) c(Sturges = nclass.Sturges(x),
  Scott = nclass.scott(x), FD = nclass.FD(x))
NC(x)
onePt <- rep(1, 11)
NC(onePt) # no longer gives NaN
```

---

palette

*Set or View the Graphics Palette*

---

## Description

View or manipulate the color palette which is used when a `col=` has a numeric index.

## Usage

```
palette(value)
```

## Arguments

`value` an optional character vector.

## Details

If `value` has length 1, it is taken to be the name of a built in color palette. If `value` has length greater than 1 it is assumed to contain a description of the colors which are to make up the new palette (either by name or by RGB levels).

If `value` is omitted or has length 0, no change is made the current palette.

Currently, the only built-in palette is "default".

**Value**

The palette which *was* in effect. This is `invisible` unless the argument is omitted.

**See Also**

`colors` for the vector of built-in named colors; `hsv`, `gray`, `rainbow`, `terrain.colors`,... to construct colors.

`colorRamp` to interpolate colors, making custom palettes; `col2rgb` for translating colors to RGB 3-vectors.

**Examples**

```
require(graphics)

palette()           # obtain the current palette
palette(rainbow(6)) # six color rainbow

(palette(gray(seq(0,.9,len=25)))) # gray scales; print old palette
matplot(outer(1:100,1:30), type='l', lty=1,lwd=2, col=1:30,
        main = "Gray Scales Palette",
        sub = "palette(gray(seq(0,.9,len=25)))")
palette("default") # reset back to the default

## on a device where alpha-transparency is supported,
## use 'alpha = 0.3' transparency with the default palette :
opal <- col2rgb(palette(), alpha=TRUE)/255; opal["alpha",] <- 0.3
mycols <- do.call(rgb, as.list(as.data.frame(t(opal))))
opal <- palette(mycols)
x <- rnorm(1000); xy <- cbind(x, 3*x + rnorm(1000))
plot (xy, lwd=2,
      main = "Alpha-Transparency Palette\n alpha = 0.3")
xy[,1] <- -xy[,1]
points(xy, col=8, pch=16, cex = 1.5)
palette("default")
```

---

Palettes

*Color Palettes*

---

**Description**

Create a vector of  $n$  contiguous colors.

**Usage**

```
rainbow(n, s = 1, v = 1, start = 0, end = max(1, n - 1)/n,
        gamma = 1, alpha = 1)
heat.colors(n, alpha = 1)
terrain.colors(n, alpha = 1)
topo.colors(n, alpha = 1)
cm.colors(n, alpha = 1)
```

**Arguments**

<code>n</code>	the number of colors ( $\geq 1$ ) to be in the palette.
<code>s, v</code>	the ‘saturation’ and ‘value’ to be used to complete the HSV color descriptions.
<code>start</code>	the (corrected) hue in [0,1] at which the rainbow begins.
<code>end</code>	the (corrected) hue in [0,1] at which the rainbow ends.
<code>gamma</code>	the gamma correction, see argument <code>gamma</code> in <a href="#">hsv</a> .
<code>alpha</code>	the alpha transparency, a number in [0,1], see argument <code>alpha</code> in <a href="#">hsv</a> .

**Details**

Conceptually, all of these functions actually use (parts of) a line cut out of the 3-dimensional color space, parametrized by [hsv](#)(`h, s, v, gamma`), where `gamma=1` for the `foo.colors` function, and hence, equispaced hues in RGB space tend to cluster at the red, green and blue primaries.

Some applications such as contouring require a palette of colors which do not wrap around to give a final color close to the starting one.

With `rainbow`, the parameters `start` and `end` can be used to specify particular subranges of hues. The following values can be used when generating such a subrange: `red=0`, `yellow= $\frac{1}{6}$` , `green= $\frac{2}{6}$` , `cyan= $\frac{3}{6}$` , `blue= $\frac{4}{6}$`  and `magenta= $\frac{5}{6}$` .

**Value**

A character vector, `cv`, of color names. This can be used either to create a user-defined color palette for subsequent graphics by [palette](#)(`cv`), a `col=` specification in graphics functions or in [par](#).

**See Also**

[colors](#), [palette](#), [hsv](#), [hcl](#), [rgb](#), [gray](#) and [col2rgb](#) for translating to RGB numbers.

**Examples**

```
require(graphics)
# A Color Wheel
pie(rep(1,12), col=rainbow(12))

##----- Some palettes -----
demo.pal <-
  function(n, border = if (n<32) "light gray" else NA,
           main = paste("color palettes; n=",n),
           ch.col = c("rainbow(n, start=.7, end=.1)", "heat.colors(n)",
                     "terrain.colors(n)", "topo.colors(n)",
                     "cm.colors(n)"))
  {
    nt <- length(ch.col)
    i <- 1:n; j <- n / nt; d <- j/6; dy <- 2*d
    plot(i,i+d, type="n", yaxt="n", ylab="", main=main)
    for (k in 1:nt) {
      rect(i-.5, (k-1)*j+ dy, i+.4, k*j,
           col = eval(parse(text=ch.col[k])), border = border)
      text(2*j, k * j +dy/4, ch.col[k])
    }
  }
n <- if(.Device == "postscript") 64 else 16
# Since for screen, larger n may give color allocation problem
```



demo.pal(n)

---

pdf

*PDF Graphics Device*

---

## Description

pdf starts the graphics device driver for producing PDF graphics.

## Usage

```
pdf(file = ifelse(onefile, "Rplots.pdf", "Rplot%03d.pdf"),
     width, height, onefile, family, title, fonts, version,
     paper, encoding, bg, fg, pointsize, pagecentre, colormodel,
     useDingbats, useKerning, fillOddEven, maxRasters)
```

## Arguments

file	a character string giving the name of the file. For use with <code>onefile=FALSE</code> give a C integer format such as "Rplot%03d.pdf" (the default in that case). (See <a href="#">postscript</a> for further details.)
width, height	the width and height of the graphics region in inches. The default values are 7.
onefile	logical: if true (the default) allow multiple figures in one file. If false, generate a file with name containing the page number for each page. Defaults to TRUE.
family	the font family to be used, see <a href="#">postscript</a> . Defaults to "Helvetica".
title	title string to embed as the '/Title' field in the file. Defaults to "R Graphics Output".
fonts	a character vector specifying R graphics font family names for fonts which will be included in the PDF file. Defaults to NULL.
version	a string describing the PDF version that will be required to view the output. This is a minimum, and will be increased (with a warning) if necessary. Defaults to "1.4", but see 'Details'.
paper	the target paper size. The choices are "a4", "letter", "legal" (or "us") and "executive" (and these can be capitalized), or "a4r" and "USr" for rotated ('landscape'). The default is "special", which means that the width and height specify the paper size. A further choice is "default"; if this is selected, the papersize is taken from the option "papersize" if that is set and as "a4" if it is unset or empty. Defaults "special".
encoding	the name of an encoding file. See <a href="#">postscript</a> for details. Defaults to "default".
bg	the initial background color to be used. Defaults to "transparent".
fg	the initial foreground color to be used. Defaults to "black".
pointsize	the default point size to be used. Strictly speaking, in bp, that is 1/72 of an inch, but approximately in points. Defaults to 12.
pagecentre	logical: should the device region be centred on the page? – is only relevant for paper != "special". Defaults to true.

<code>colormodel</code>	a character string describing the color model: currently allowed values are "rgb", "gray" and "cmyk". Defaults to "rgb".
<code>useDingbats</code>	logical. Should small circles be rendered <i>via</i> the Dingbats font? Defaults to TRUE, which produces smaller and better output. Setting this to FALSE can work around font display problems in broken PDF viewers. See the ‘Note’ for a possible fix for such viewers.
<code>useKerning</code>	logical. Should kerning corrections be included in setting text and calculating string widths? Defaults to TRUE.
<code>fillOddEven</code>	logical controlling the polygon fill mode: see <a href="#">polygon</a> for details. Default FALSE.
<code>maxRasters</code>	integer. The maximum number of raster images that can be stored in this PDF document.

## Details

All arguments except `file` default to values given by `pdf.options()`. The ultimate defaults are quoted in the arguments section.

`pdf()` opens the file `file` and the PDF commands needed to plot any graphics requested are sent to that file.

The `file` argument is interpreted as a C integer format as used by `sprintf`, with integer argument the page number. The default gives files ‘Rplot001.pdf’, ..., ‘Rplot999.pdf’, ‘Rplot1000.pdf’, ...

The `family` argument can be used to specify a PDF-specific font family as the initial/default font for the device.

If a device-independent R graphics font family is specified (e.g., via `par(family=)` in the graphics package), the PDF device makes use of the PostScript font mappings to convert the R graphics font family to a PDF-specific font family description. (See the documentation for [pdfFonts](#).)

R does *not* embed fonts in the PDF file, so it is only straightforward to use mappings to the font families that can be assumed to be available in any PDF viewer: "Times" (equivalently "serif"), "Helvetica" (equivalently "sans") and "Courier" (equivalently "mono"). Other families may be specified, but it is the user’s responsibility to ensure that these fonts are available on the system and third-party software, e.g., Ghostscript, may be required to embed the fonts so that the PDF can be included in other documents (e.g., LaTeX): see [embedFonts](#). The URW-based families described for [postscript](#) can be used with viewers set up to use URW fonts, which is usual with those based on `xpdf` or Ghostscript. Since [embedFonts](#) makes use of Ghostscript, it should be able to embed the URW-based families for use with other viewers.

See [postscript](#) for details of encodings, as the internal code is shared between the drivers. The native PDF encoding is given in file ‘PDFDoc.enc’.

`pdf` writes uncompressed PDF. It is primarily intended for producing PDF graphics for inclusion in other documents, and PDF-includers such as `pdftex` are usually able to handle compression: there are a large number of PDF compression utilities such as ‘`pdftk`’.

The PDF produced is fairly simple, with each page being represented as a single stream. The R graphics model does not distinguish graphics objects at the level of the driver interface.

The `version` argument declares the version of PDF that gets produced. The version must be at least 1.4 for semi-transparent output to be understood, and at least 1.3 if CID fonts are to be used: if these features are used the version number will be increased (with a warning). Specifying a low version number is useful if you want to produce PDF output that can be viewed on older or non-Adobe PDF viewers. (PDF 1.4 requires Acrobat 5 or later.)

Line widths as controlled by `par(lwd=)` are in multiples of 1/96 inch. Multiples less than 1 are allowed. `pch="."` with `cex = 1` corresponds to a square of side 1/72 inch, which is also the 'pixel' size assumed for graphics parameters such as `"cra"`.

The `paper` argument sets the `'/MediaBox'` entry in the file, which defaults to `width` by `height`. If it is set to something other than `"special"`, a device region of the specified size is (by default) centred on the rectangle given by the paper size: if either `width` or `height` is less than 0.1 or too large to give a total margin of 0.5 inch, it is reset to the corresponding paper dimension minus 0.5. Thus if you want the default behaviour of `postscript` use `pdf(paper="a4r", width=0, height=0)` to centre the device region on a landscape A4 page with 0.25 inch margins.

When the background colour is fully transparent (as is the initial default value), the PDF produced does not paint the background. Almost all PDF viewers will use a white canvas so the visual effect is if the background were white. This will not be the case when printing onto coloured paper, though.

If you are planning to use a large number of raster images in your output, you may need to specify a larger value for `maxRasters`.

### Color models

The default color model is RGB, and model `"gray"` maps RGB colors to greyscale using perceived luminosity (biased towards green). `"cmyk"` outputs in CMYK colorspace. Nothing in R specifies the interpretation of the RGB or CMYK color spaces, and the simplest possible conversion to CMYK is used ([http://en.wikipedia.org/wiki/CMYK\\_color\\_model#Mapping\\_RGB\\_to\\_CMYK](http://en.wikipedia.org/wiki/CMYK_color_model#Mapping_RGB_to_CMYK)).

### Conventions

This section describes the implementation of the conventions for graphics devices set out in the "R Internals Manual".

- The default device size is 7 inches square.
- Font sizes are in big points.
- The default font family is Helvetica.
- Line widths are as a multiple of 1/96 inch, with no minimum.
- Circles of any radius are allowed. Unless `useDingbats = FALSE`, opaque circles of less than 10 big points radius are rendered using char 108 in the Dingbats font: all semi-transparent and larger circles using a Bézier curve for each quadrant.
- Colours are interpreted by the viewing/printing application.

### Note

If you see problems with PDF output, do remember that the problem is much more likely to be in your viewer than in R. Try another viewer if possible. Symptoms for which the viewer has been at fault are apparent grids on image plots (turn off graphics anti-aliasing in your viewer if you) and missing or incorrect glyphs in text (viewers silently doing font substitution).

Unfortunately the default viewers on most Linux and Mac OS X systems have these problems, and no obvious way to turn off graphics anti-aliasing.

Acrobat Reader does not use the fonts specified but rather emulates them from multiple-master fonts. This can be seen in imprecise centering of characters, for example the multiply and divide signs in Helvetica. This can be circumvented by embedding fonts where possible. Most other

viewers substitute fonts, e.g. URW fonts for the standard Helvetica and Times fonts, and these too often have different font metrics from the true fonts.

Acrobat Reader 5.x and later can be extended by support for Asian and (so-called) Central European fonts, and these will be needed for the full use of encodings other than Latin-1. See <http://www.adobe.com/products/acrobat/acrrasianfontpack.html> for Reader 6.x to 8.x, and <http://www.adobe.com/downloads/updates> for 9.x.

On some systems the default plotting character `pch = 1` is displayed in some PDF viewers incorrectly as a "q" character. (These seem to be viewers based on the 'poppler' PDF rendering library). This may be due to incorrect or incomplete mapping of font names to those used by the system. Adding the following lines to `~/.fonts.conf` or `/etc/fonts/local.conf` may circumvent this problem.

```
<alias binding="same">
  <family>ZapfDingbats</family>
  <accept><family>Dingbats</family></accept>
</alias>
```

### See Also

[pdfFonts](#), [pdf.options](#), [embedFonts](#), [Devices](#), [postscript](#). [cairo\\_pdf](#) and (on Mac OS X only) [quartz](#) for other devices that can produce PDF.

More details of font families and encodings and especially handling text in a non-Latin-1 encoding and embedding fonts can be found in

Paul Murrell and Brian Ripley (2006) Non-standard fonts in PostScript and PDF graphics. *R News*, 6(2):41–47. [http://cran.r-project.org/doc/Rnews/Rnews\\_2006-2.pdf](http://cran.r-project.org/doc/Rnews/Rnews_2006-2.pdf).

### Examples

```
## Not run:
## Test function for encodings
TestChars <- function(encoding="ISOLatin1", ...)
{
  pdf(encoding=encoding, ...)
  par(pty="s")
  plot(c(-1,16), c(-1,16), type="n", xlab="", ylab="",
        xaxs="i", yaxs="i")
  title(paste("Centred chars in encoding", encoding))
  grid(17, 17, lty=1)
  for(i in c(32:255)) {
    x <- i %% 16
    y <- i %/% 16
    points(x, y, pch=i)
  }
  dev.off()
}
## there will be many warnings.
TestChars("ISOLatin2")
## this does not view properly in older viewers.
TestChars("ISOLatin2", family="URWHelvetica")
## works well for viewing in gs-based viewers, and often in xpdf.

## End(Not run)
```

---

`pdf.options`*Auxiliary Function to Set/View Defaults for Arguments of pdf*

---

### Description

The auxiliary function `pdf.options` can be used to set or view (if called without arguments) the default values for some of the arguments to `pdf`.

`pdf.options` needs to be called before calling `pdf`, and the default values it sets can be overridden by supplying arguments to `pdf`.

### Usage

```
pdf.options(..., reset = FALSE)
```

### Arguments

<code>...</code>	arguments <code>width</code> , <code>height</code> , <code>onefile</code> , <code>family</code> , <code>title</code> , <code>fonts</code> , <code>paper</code> , <code>encoding</code> , <code>pointsize</code> , <code>bg</code> , <code>fg</code> , <code>pagecentre</code> , <code>useDingbats</code> , <code>colormodel</code> and <code>fillOddEven</code> can be supplied.
<code>reset</code>	logical: should the defaults be reset to their ‘factory-fresh’ values?

### Details

If both `reset = TRUE` and `...` are supplied the defaults are first reset to the ‘factory-fresh’ values and then the new values are applied.

### Value

A named list of all the defaults. If any arguments are supplied the return values are the old values and the result has the visibility flag turned off.

### See Also

[pdf](#), [ps.options](#).

### Examples

```
pdf.options(bg = "pink")
utils::str(pdf.options())
pdf.options(reset = TRUE) # back to factory-fresh
```

---

pictex

*A PicTeX Graphics Driver*

---

### Description

This function produces simple graphics suitable for inclusion in TeX and LaTeX documents. It dates from the very early days of R and is for historical interest only.

### Usage

```
pictex(file = "Rplots.tex", width = 5, height = 4, debug = FALSE,
       bg = "white", fg = "black")
```

### Arguments

file	the file where output will appear.
width	The width of the plot in inches.
height	the height of the plot in inches.
debug	should debugging information be printed.
bg	the background color for the plot. Ignored.
fg	the foreground color for the plot. Ignored.

### Details

This driver is much more basic than the other graphics drivers included in R. It does not have any font metric information, so the use of `plotmath` is not supported.

Line widths are ignored except when setting the spacing of line textures. `pch="."` corresponds to a square of side 1pt.

This device does not support colour (nor does the PicTeX package), and all colour settings are ignored.

Note that text is recorded in the file as-is, so annotations involving TeX special characters (such as ampersand and underscore) need to be quoted as they would be when entering TeX.

Multiple plots will be placed as separate environments in the output file.

### Conventions

This section describes the implementation of the conventions for graphics devices set out in the “R Internals Manual”.

- The default device size is 5 inches by 4 inches.
- There is no `pointsize` argument: the default size is interpreted as 10 point.
- The only font family is `cms10`.
- Line widths are only used when setting the spacing on line textures.
- Circle of any radius are allowed.
- Colour is not supported.

**Author(s)**

This driver was provided around 1996–7 by Valerio Aimale of the Department of Internal Medicine, University of Genoa, Italy.

**References**

Knuth, D. E. (1984) *The TeXbook*. Reading, MA: Addison-Wesley.

Lamport, L. (1994) *LATEX: A Document Preparation System*. Reading, MA: Addison-Wesley.

Goossens, M., Mittelbach, F. and Samarin, A. (1994) *The LATEX Companion*. Reading, MA: Addison-Wesley.

**See Also**

[postscript](#), [pdf](#), [Devices](#).

The `tikzDevice` in the CRAN package of that name for more modern LaTeX-based graphics (although including PDF figures is most common in LaTeX documents).

**Examples**

```
require(graphics)

pictex()
plot(1:11, (-5:5)^2, type='b', main="Simple Example Plot")
dev.off()
##-----
## Not run:
## LaTeX Example
\documentclass{article}
\usepackage{pictex}
\usepackage{graphics} % for \rotatebox
\begin{document}
%...
\begin{figure}[h]
  \centerline{\input{Rplots.tex}}
  \caption{}
\end{figure}
%...
\end{document}

## End(Not run)
##-----
unlink("Rplots.tex")
```

**Description**

If the `text` argument to one of the text-drawing functions (`text`, `mtext`, `axis`, `legend`) in R is an expression, the argument is interpreted as a mathematical expression and the output will be formatted according to TeX-like rules. Expressions can also be used for titles, subtitles and x- and y-axis labels (but not for axis labels on `persp` plots).

In most cases other language objects (names and calls, including formulas) are coerced to expressions and so can also be used.

## Details

A mathematical expression must obey the normal rules of syntax for any R expression, but it is interpreted according to very different rules than for normal R expressions.

It is possible to produce many different mathematical symbols, generate sub- or superscripts, produce fractions, etc.

The output from `demo(plotmath)` includes several tables which show the available features. In these tables, the columns of grey text show sample R expressions, and the columns of black text show the resulting output.

The available features are also described in the tables below:

Syntax	Meaning
<code>x + y</code>	x plus y
<code>x - y</code>	x minus y
<code>x*y</code>	juxtapose x and y
<code>x/y</code>	x forwardslash y
<code>x %+-% y</code>	x plus or minus y
<code>x %/% y</code>	x divided by y
<code>x %*% y</code>	x times y
<code>x %.% y</code>	x cdot y
<code>x[i]</code>	x subscript i
<code>x^2</code>	x superscript 2
<code>paste(x, y, z)</code>	juxtapose x, y, and z
<code>sqrt(x)</code>	square root of x
<code>sqrt(x, y)</code>	yth root of x
<code>x == y</code>	x equals y
<code>x != y</code>	x is not equal to y
<code>x &lt; y</code>	x is less than y
<code>x &lt;= y</code>	x is less than or equal to y
<code>x &gt; y</code>	x is greater than y
<code>x &gt;= y</code>	x is greater than or equal to y
<code>x %~~% y</code>	x is approximately equal to y
<code>x %~% y</code>	x and y are congruent
<code>x %==% y</code>	x is defined as y
<code>x %prop% y</code>	x is proportional to y
<code>plain(x)</code>	draw x in normal font
<code>bold(x)</code>	draw x in bold font
<code>italic(x)</code>	draw x in italic font
<code>bolditalic(x)</code>	draw x in bolditalic font
<code>symbol(x)</code>	draw x in symbol font
<code>list(x, y, z)</code>	comma-separated list
<code>...</code>	ellipsis (height varies)
<code>cdots</code>	ellipsis (vertically centred)
<code>ldots</code>	ellipsis (at baseline)
<code>x %subset% y</code>	x is a proper subset of y
<code>x %subteq% y</code>	x is a subset of y
<code>x %notsubset% y</code>	x is not a subset of y
<code>x %supset% y</code>	x is a proper superset of y
<code>x %supseteq% y</code>	x is a superset of y



<code>x %in% y</code>	$x$ is an element of $y$
<code>x %notin% y</code>	$x$ is not an element of $y$
<code>hat(x)</code>	$x$ with a circumflex
<code>tilde(x)</code>	$x$ with a tilde
<code>dot(x)</code>	$x$ with a dot
<code>ring(x)</code>	$x$ with a ring
<code>bar(xy)</code>	$xy$ with bar
<code>widehat(xy)</code>	$xy$ with a wide circumflex
<code>widetilde(xy)</code>	$xy$ with a wide tilde
<code>x %&lt;-&gt;% y</code>	$x$ double-arrow $y$
<code>x %-&gt;% y</code>	$x$ right-arrow $y$
<code>x %&lt;-% y</code>	$x$ left-arrow $y$
<code>x %up% y</code>	$x$ up-arrow $y$
<code>x %down% y</code>	$x$ down-arrow $y$
<code>x %&lt;=&gt;% y</code>	$x$ is equivalent to $y$
<code>x %=&gt;% y</code>	$x$ implies $y$
<code>x %&lt;=% y</code>	$y$ implies $x$
<code>x %dblup% y</code>	$x$ double-up-arrow $y$
<code>x %dbldown% y</code>	$x$ double-down-arrow $y$
<code>alpha - omega</code>	Greek symbols
<code>Alpha - Omega</code>	uppercase Greek symbols
<code>theta1, phi1, sigma1, omega1</code>	cursive Greek symbols
<code>Upsilon1</code>	capital upsilon with hook
<code>aleph</code>	first letter of Hebrew alphabet
<code>infinity</code>	infinity symbol
<code>partialdiff</code>	partial differential symbol
<code>nabla</code>	nabla, gradient symbol
<code>32*degree</code>	32 degrees
<code>60*minute</code>	60 minutes of angle
<code>30*second</code>	30 seconds of angle
<code>displaystyle(x)</code>	draw $x$ in normal size (extra spacing)
<code>textstyle(x)</code>	draw $x$ in normal size
<code>scriptstyle(x)</code>	draw $x$ in small size
<code>scriptscriptstyle(x)</code>	draw $x$ in very small size
<code>underline(x)</code>	draw $x$ underlined
<code>x ~~ y</code>	put extra space between $x$ and $y$
<code>x + phantom(0) + y</code>	leave gap for "0", but don't draw it
<code>x + over(1, phantom(0))</code>	leave vertical gap for "0" (don't draw)
<code>frac(x, y)</code>	$x$ over $y$
<code>over(x, y)</code>	$x$ over $y$
<code>atop(x, y)</code>	$x$ over $y$ (no horizontal bar)
<code>sum(x[i], i==1, n)</code>	sum $x[i]$ for $i$ equals 1 to $n$
<code>prod(plain(P) (X==x), x)</code>	product of $P(X=x)$ for all values of $x$
<code>integral(f(x)*dx, a, b)</code>	definite integral of $f(x)$ wrt $x$
<code>union(A[i], i==1, n)</code>	union of $A[i]$ for $i$ equals 1 to $n$
<code>intersect(A[i], i==1, n)</code>	intersection of $A[i]$
<code>lim(f(x), x %-&gt;% 0)</code>	limit of $f(x)$ as $x$ tends to 0
<code>min(g(x), x &gt; 0)</code>	minimum of $g(x)$ for $x$ greater than 0
<code>inf(S)</code>	infimum of $S$
<code>sup(S)</code>	supremum of $S$
<code>x^y + z</code>	normal operator precedence
<code>x^(y + z)</code>	visible grouping of operands

<code>x^{y + z}</code>	invisible grouping of operands
<code>group("(", list(a, b), ")")</code>	specify left and right delimiters
<code>bgroup("(", atop(x, y), ")")</code>	use scalable delimiters
<code>group(lceil, x, rceil)</code>	special delimiters

The symbol font uses Adobe Symbol encoding so, for example, a lower case mu can be obtained either by the special symbol `mu` or by `symbol("m")`. This provides access to symbols that have no special symbol name, for example, the universal, or forall, symbol is `symbol("\042")`. To see what symbols are available in this way use `TestChars(font=5)` as given in the examples for [points](#): some are only available on some devices.

Note to TeX users: TeX's `\Upsilon` is `Upsilon1`, TeX's `\varepsilon` is close to `epsilon`, and there is no equivalent of TeX's `\epsilon`. TeX's `\varpi` is close to `omega1`. `vartheta`, `varphi` and `varsigma` are allowed as synonyms for `thetal`, `phil` and `sigma1`. `sigma1` is also known as `sigma`, its Unicode name.

Control characters (e.g. `\n`) are not interpreted in character strings in plotmath, unlike normal plotting.

The fonts used are taken from the current font family, and so can be set by `par(family=)` in base graphics, and `gpar(fontfamily=)` in package **grid**.

Note that `bold`, `italic` and `bolditalic` do not apply to symbols, and hence not to the Greek *symbols* such as `mu` which are displayed in the symbol font.

## Other symbols

On many OSes and some graphics devices many other symbols are available as part of the standard text font, and all of the symbols in the Adobe Symbol encoding are in principle available *via* changing the font face or (see ‘Details’) plotmath: see the examples section of [points](#) for a function to display them. (‘In principle’ because some of the glyphs are missing from some implementations of the symbol font.) Unfortunately, [postscript](#) and [pdf](#) have support for little more than European (not Greek) and CJK characters and the Adobe Symbol encoding (and in a few fonts, also Cyrillic characters).

In a UTF-8 locale any Unicode character can be entered, perhaps as a `\uxxxx` or `\Uxxxxxxxx` escape sequence, but the issue is whether the graphics device is able to display the character. The widest range of characters is likely to be available in the [X11](#) device using `cairo`: see its help page for how installing additional fonts can help. This can often be used to display Greek *letters* in bold or italic.

In non-UTF-8 locales there is normally no support for symbols not in the languages for which the current encoding was intended.

## References

Murrell, P. and Ihaka, R. (2000) An approach to providing mathematical annotation in plots. *Journal of Computational and Graphical Statistics*, **9**, 582–599.

The symbol codes can be found in octal in the Adobe reference manuals, e.g. for Postscript <http://www.adobe.com/products/postscript/pdfs/PLRM.pdf> or PDF [http://www.adobe.com/devnet/acrobat/pdfs/pdf\\_reference\\_1-7.pdf](http://www.adobe.com/devnet/acrobat/pdfs/pdf_reference_1-7.pdf) and in decimal, octal and hex at <http://www.stat.auckland.ac.nz/~paul/R/CM/AdobeSym.html>.

## See Also

`demo(plotmath)`, [axis](#), [mtext](#), [text](#), [title](#), [substitute quote](#), [bquote](#)

**Examples**

```

require(graphics)

x <- seq(-4, 4, len = 101)
y <- cbind(sin(x), cos(x))
matplot(x, y, type = "l", xaxt = "n",
        main = expression(paste(plain(sin) * phi, " and ",
                                plain(cos) * phi)),
        ylab = expression("sin" * phi, "cos" * phi), # only 1st is taken
        xlab = expression(paste("Phase Angle ", phi)),
        col.main = "blue")
axis(1, at = c(-pi, -pi/2, 0, pi/2, pi),
     labels = expression(-pi, -pi/2, 0, pi/2, pi))

## How to combine "math" and numeric variables :
plot(1:10, type="n", xlab="", ylab="", main = "plot math & numbers")
theta <- 1.23 ; mtext(bquote(hat(theta) == .(theta)), line= .25)
for(i in 2:9)
  text(i,i+1, substitute(list(xi,eta) == group("(",list(x,y),")"),
                        list(x=i, y=i+1)))
## note that both of these use calls rather than expressions.
##
text(1,10, "Derivatives:", adj=0)
text(1,9.6, expression(
  "      first: {f * minute}(x) " == {f * minute}(x)), adj=0)
text(1,9.0, expression(
  "      second: {f * second}(x) " == {f * second}(x)), adj=0)

plot(1:10, 1:10)
text(4, 9, expression(hat(beta) == (X^t * X)^{-1} * X^t * y))
text(4, 8.4, "expression(hat(beta) == (X^t * X)^{-1} * X^t * y)",
     cex = .8)
text(4, 7, expression(bar(x) == sum(frac(x[i], n), i==1, n)))
text(4, 6.4, "expression(bar(x) == sum(frac(x[i], n), i==1, n))",
     cex = .8)
text(8, 5, expression(paste(frac(1, sigma*sqrt(2*pi)), " ",
                            plain(e)^{frac(-(x-mu)^2, 2*sigma^2)})),
     cex = 1.2)

## some other useful symbols
plot.new(); plot.window(c(0,4), c(15,1))
text(1, 1, "universal", adj=0); text(2.5, 1, "\\042")
text(3, 1, expression(symbol("\\042")))
text(1, 2, "existential", adj=0); text(2.5, 2, "\\044")
text(3, 2, expression(symbol("\\044")))
text(1, 3, "suchthat", adj=0); text(2.5, 3, "\\047")
text(3, 3, expression(symbol("\\047")))
text(1, 4, "therefore", adj=0); text(2.5, 4, "\\134")
text(3, 4, expression(symbol("\\134")))
text(1, 5, "perpendicular", adj=0); text(2.5, 5, "\\136")
text(3, 5, expression(symbol("\\136")))
text(1, 6, "circlemultiply", adj=0); text(2.5, 6, "\\304")
text(3, 6, expression(symbol("\\304")))
text(1, 7, "circleplus", adj=0); text(2.5, 7, "\\305")

```

```

text(3, 7, expression(symbol("\305")))
text(1, 8, "emptyset", adj=0); text(2.5, 8, "\306")
text(3, 8, expression(symbol("\306")))
text(1, 9, "angle", adj=0); text(2.5, 9, "\320")
text(3, 9, expression(symbol("\320")))
text(1, 10, "leftangle", adj=0); text(2.5, 10, "\341")
text(3, 10, expression(symbol("\341")))
text(1, 11, "rightangle", adj=0); text(2.5, 11, "\361")
text(3, 11, expression(symbol("\361")))

```

---

png

*BMP, JPEG, PNG and TIFF graphics devices*

---

## Description

Graphics devices for JPEG, PNG or TIFF format bitmap files.

## Usage

```

bmp(filename = "Rplot%03d.bmp",
     width = 480, height = 480, units = "px",
     pointsize = 12, bg = "white", res = NA, ...,
     type = c("cairo", "Xlib", "quartz"), antialias)

jpeg(filename = "Rplot%03d.jpeg",
     width = 480, height = 480, units = "px",
     pointsize = 12, quality = 75, bg = "white", res = NA, ...,
     type = c("cairo", "Xlib", "quartz"), antialias)

png(filename = "Rplot%03d.png",
     width = 480, height = 480, units = "px",
     pointsize = 12, bg = "white", res = NA, ...,
     type = c("cairo", "Xlib", "quartz"), antialias)

tiff(filename = "Rplot%03d.tiff",
     width = 480, height = 480, units = "px", pointsize = 12,
     compression = c("none", "rle", "lzw", "jpeg", "zip"),
     bg = "white", res = NA, ...,
     type = c("cairo", "Xlib", "quartz"), antialias)

```

## Arguments

filename	the name of the output file. The page number is substituted if a C integer format is included in the character string, as in the default. (The result must be less than <code>PATH_MAX</code> characters long, and may be truncated if not. See <a href="#">postscript</a> for further details.) Tilde expansion is performed where supported by the platform.
width	the width of the device.
height	the height of the device.
units	The units in which height and width are given. Can be <code>px</code> (pixels, the default), <code>in</code> (inches), <code>cm</code> or <code>mm</code> .

<code>pointsize</code>	the default pointsize of plotted text, interpreted as big points (1/72 inch) at <code>res</code> dpi.
<code>bg</code>	the initial background colour: can be overridden by setting <code>par("bg")</code> .
<code>quality</code>	the ‘quality’ of the JPEG image, as a percentage. Smaller values will give more compression but also more degradation of the image.
<code>compression</code>	the type of compression to be used.
<code>res</code>	The nominal resolution in dpi which will be recorded in the bitmap file, if a positive integer. Also used for <code>units</code> other than the default, and to convert points to pixels.
<code>...</code>	for <code>type = "Xlib"</code> only, additional arguments to the underlying <code>X11</code> device, such as <code>gamma</code> and <code>fonts</code> .
<code>type</code>	character string, one of <code>"Xlib"</code> or <code>"quartz"</code> (some Mac OS X builds) or <code>"cairo"</code> . The latter will only be available if the system was compiled with support for <code>cairo</code> – otherwise <code>"Xlib"</code> will be used. The default is set by <code>getOption("bitmapType")</code> – the ‘out of the box’ default is <code>"quartz"</code> or <code>"cairo"</code> where available, otherwise <code>"Xlib"</code> .
<code>antialias</code>	for <code>type = "cairo"</code> , giving the type of anti-aliasing (if any) to be used. See <code>X11</code> . The default is set by <code>X11.options</code> .

## Details

Plots in PNG and JPEG format can easily be converted to many other bitmap formats, and both can be displayed in modern web browsers. The PNG format is lossless and is best for line diagrams and blocks of colour. The JPEG format is lossy, but may be useful for image plots, for example. BMP is a standard format on Windows. TIFF is a meta-format: the default format written by `tiff` is lossless and stores RGB (and alpha where appropriate) values uncompressed—such files are widely accepted, which is their main virtue over PNG.

`png` supports transparent backgrounds: use `bg = "transparent"`. Not all PNG viewers render files with transparency correctly. When transparency is in use in the `type = "Xlib"` variant a very light grey is used as the background and so appear as transparent if used in the plot. This allows opaque white to be used, as in the example. The `type = "cairo"` and `type = "cairo1"` variants allows semi-transparent colours, including on a transparent or semi-transparent background.

`tiff(type = "cairo")` supports semi-transparent colours, including on a transparent or semi-transparent background.

R can be compiled without support for each of these devices: this will be reported if you attempt to use them on a system where they are not supported. For `type = "Xlib"` they may not be usable unless the X11 display is available to the owner of the R process. `type = "cairo"` requires `cairo 1.2` or later. `type = "quartz"` uses the `quartz` device and so is only available where that is (on some Mac OS X builds: see `capabilities("aqua")`).

By default no resolution is recorded in the file. Viewers will often assume a nominal resolution of 72dpi when none is recorded. As resolutions in PNG files are recorded in pixels/metre, the reported dpi value will be changed slightly.

For graphics parameters that make use of dimensions in inches (including font sizes in points) the resolution used is `res` (or 72dpi if unset).

`png` will use a palette if there are less than 256 colours on the page, and record a 24-bit RGB file otherwise (or a 32-bit RGBA file if `type = "cairo"` and non-opaque colours are used).

**Value**

A plot device is opened: nothing is returned to the R interpreter.

**Warnings**

Note that by default the `width` and `height` are in pixels not inches. A warning will be issued if both are less than 20.

If you plot more than one page on one of these devices and do not include something like `%d` for the sequence number in `file`, the file will contain the last page plotted.

**Conventions**

This section describes the implementation of the conventions for graphics devices set out in the “R Internals Manual”.

- The default device size is in pixels.
- Font sizes are in big points interpreted at `res` dpi.
- The default font family is Helvetica.
- Line widths in 1/96 inch, minimum one pixel for `type = "Xlib"`, 0.01 for `type = "cairo"`.
- For `type = "Xlib"` circle radii are in pixels with minimum one.
- Colours are interpreted by the viewing application.

For `type = "quartz"` see the help for [quartz](#).

**Note**

For `type = "Xlib"` these devices are based on the [X11](#) device. The colour model used will be that set up by `X11.options` at the time the first Xlib-based devices was opened (or the first after all such devices have been closed).

**Author(s)**

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**See Also**

[Devices](#), [dev.print](#)

[capabilities](#) to see if these devices are supported by this build of R, and if `type = "cairo"` is supported.

[bitmap](#) provides an alternative way to generate PNG and JPEG plots that does not depend on accessing the X11 display but does depend on having GhostScript installed. (Devices `GDD` in CRAN package **GDD** and `CairoJPEG / CairoPNG` in CRAN package **Cairo** are further alternatives using several other additional pieces of software.)

**Examples**

```
## these examples will work only if the devices are available
## and cairo or an X11 display or a Mac OS X display is available.

## copy current plot to a (large) PNG file
## Not run: dev.print(png, file="myplot.png", width=1024, height=768)

png(file="myplot.png", bg="transparent")
plot(1:10)
rect(1, 5, 3, 7, col="white")
dev.off()

## will make myplot1.jpeg and myplot2.jpeg
jpeg(file="myplot%d.jpeg")
example(rect)
dev.off()
```

---

postscript

*PostScript Graphics*


---

**Description**

postscript starts the graphics device driver for producing PostScript graphics.

**Usage**

```
postscript(file = ifelse(onefile, "Rplots.ps", "Rplot%03d.ps"),
           onefile, family, title, fonts, encoding, bg, fg,
           width, height, horizontal, pointsize,
           paper, pagecentre, print.it, command,
           colormodel, useKerning, fillOddEven)
```

**Arguments**

file	a character string giving the name of the file. If it is "", the output is piped to the command given by the argument <code>command</code> . If it is of the form " <code> cmd</code> ", the output is piped to the command given by ' <code>cmd</code> '. For use with <code>onefile = FALSE</code> give a printf format such as " <code>Rplot%03d.ps</code> " (the default in that case). The string should not otherwise contain a %: if it is really necessary, use %% in the string for % in the file name. A single integer format matching the <a href="#">regular expression</a> " <code>%[#0 +=-]*[0-9.]*[diouxX]</code> " is allowed.
onefile	logical: if true (the default) allow multiple figures in one file. If false, generate a file name containing the page number for each page and use an EPSF header and no DocumentMedia comment. Defaults to the TRUE.
family	the initial font family to be used, normally as a character string. See the section 'Families'. Defaults to "Helvetica".
title	title string to embed as the Title comment in the file. Defaults to "R Graphics Output".

fonts	a character vector specifying additional R graphics font family names for font families whose declarations will be included in the PostScript file and are available for use with the device. See ‘Families’ below. Defaults to NULL.
encoding	the name of an encoding file. Defaults to "default". The latter is interpreted as "ISOLatin1.enc" unless the locale is recognized as corresponding to a language using ISO 8859- $\{5,7,13,15\}$ or KOI8- $\{R,U\}$ . The file is looked for in the ‘enc’ directory of package <b>grDevices</b> if the path does not contain a path separator. An extension ".enc" can be omitted.
bg	the initial background color to be used. If "transparent" (or any other non-opaque colour), no background is painted. Defaults to "transparent".
fg	the initial foreground color to be used. Defaults to "black".
width, height	the width and height of the graphics region in inches. Default to t0. If <code>paper != "special"</code> and <code>width</code> or <code>height</code> is less than 0.1 or too large to give a total margin of 0.5 inch, it is reset to the corresponding paper dimension minus 0.5.
horizontal	the orientation of the printed image, a logical. Defaults to true, that is landscape orientation on paper sizes with width less than height.
pointsize	the default point size to be used. Strictly speaking, in bp, that is 1/72 of an inch, but approximately in points. Defaults to 12.
paper	the size of paper in the printer. The choices are "a4", "letter" (or "us"), "legal" and "executive" (and these can be capitalized). Also, "special" can be used, when arguments <code>width</code> and <code>height</code> specify the paper size. A further choice is "default" (the default): If this is selected, the <code>papersize</code> is taken from the option "papersize" if that is set and to "a4" if it is unset or empty.
pagecentre	logical: should the device region be centred on the page? Defaults to true.
print.it	logical: should the file be printed when the device is closed? (This only applies if <code>file</code> is a real file name.) Defaults to false.
command	the command to be used for ‘printing’. Defaults to "default", the value of option "printcmd". The length limit is $2 * \text{PATH\_MAX}$ , typically 8096 bytes.
colormodel	a character string describing the color model: currently allowed values are "rgb", "rgb-nogray", "gray" and "cmyk". Defaults to "rgb".
useKerning	logical. Should kerning corrections be included in setting text and calculating string widths? Defaults to TRUE.
fillOddEven	logical controlling the polygon fill mode: see <a href="#">polygon</a> for details. Default FALSE.

## Details

All arguments except `file` default to values given by `ps.options()`. The ultimate defaults are quoted in the arguments section.

`postscript` opens the file `file` and the PostScript commands needed to plot any graphics requested are written to that file. This file can then be printed on a suitable device to obtain hard copy.

The `file` argument is interpreted as a C integer format as used by `sprintf`, with integer argument the page number. The default gives files ‘Rplot001.ps’, ..., ‘Rplot999.ps’, ‘Rplot1000.ps’, ...



The postscript produced for a single R plot is EPS (*Encapsulated PostScript*) compatible, and can be included into other documents, e.g., into LaTeX, using `\includegraphics{<filename>}`. For use in this way you will probably want to use `setEPS()` to set the defaults as `horizontal = FALSE`, `onefile = FALSE`, `paper = "special"`. Note that the bounding box is for the *device* region: if you find the white space around the plot region excessive, reduce the margins of the figure region via `par(mar=)`.

Most of the PostScript prologue used is taken from the R character vector `.ps.prolog`. This is marked in the output, and can be changed by changing that vector. (This is only advisable for PostScript experts: the standard version is in `namespace:grDevices`.)

A PostScript device has a default family, which can be set by the user via `family`. If other font families are to be used when drawing to the PostScript device, these must be declared when the device is created via `fonts`; the font family names for this argument are R graphics font family names (see the documentation for `postscriptFonts`).

Line widths as controlled by `par(lwd=)` are in multiples of 1/96 inch: multiples less than 1 are allowed. `pch="."` with `cex = 1` corresponds to a square of side 1/72 inch, which is also the 'pixel' size assumed for graphics parameters such as `"cra"`.

When the background colour is fully transparent (as is the initial default value), the PostScript produced does not paint the background. Almost all PostScript viewers will use a white canvas so the visual effect is if the background were white. This will not be the case when printing onto coloured paper, though.

## Families

Font families are collections of fonts covering the five font faces, (conventionally plain, bold, italic, bold-italic and symbol) selected by the graphics parameter `par(font=)` or the grid parameter `gpar(fontface=)`. Font families can be specified either as an initial/default font family for the device via the `family` argument or after the device is opened by the graphics parameter `par(family=)` or the grid parameter `gpar(fontfamily=)`. Families which will be used in addition to the initial family must be specified in the `fonts` argument when the device is opened.

Font families are declared via a call to `postscriptFonts`.

The argument `family` specifies the initial/default font family to be used. In normal use it is one of "AvantGarde", "Bookman", "Courier", "Helvetica", "Helvetica-Narrow", "NewCenturySchoolbook", "Palatino" or "Times", and refers to the standard Adobe PostScript fonts families of those names which are included (or cloned) in all common PostScript devices.

Many PostScript emulators (including those based on `ghostscript`) use the URW equivalents of these fonts, which are "URWGothic", "URWBookman", "NimbusMon", "NimbusSan", "NimbusSanCond", "CenturySch", "URWPalladio" and "NimbusRom" respectively. If your PostScript device is using URW fonts, you will obtain access to more characters and more appropriate metrics by using these names. To make these easier to remember, "URWHelvetica" == "NimbusSan" and "URWTimes" == "NimbusRom" are also supported.

Another type of family makes use of CID-keyed fonts for East Asian languages – see `postscriptFonts`.

The `family` argument is normally a character string naming a font family, but family objects generated by `Type1Font` and `CIDFont` are also accepted. For compatibility with earlier versions of R, the initial family can also be specified as a vector of four or five afm files.

Note that R does not embed the font(s) used in the PostScript output: see `embedFonts` for a utility to help do so.

Viewers and embedding applications frequently substitute fonts for those specified in the family, and the substitute will often have slightly different font metrics. `useKerning=TRUE` spaces the

letters in the string using kerning corrections for the intended family: this may look uglier than `useKerning=FALSE`.

## Encodings

Encodings describe which glyphs are used to display the character codes (in the range 0–255). Most commonly `R` uses `ISOLatin1` encoding, and the examples for `text` are in that encoding. However, the encoding used on machines running `R` may well be different, and by using the `encoding` argument the glyphs can be matched to encoding in use. This suffices for European and Cyrillic languages, but not for CJK languages. For the latter, composite CID fonts are used. These fonts are useful for other languages: for example they may contain Greek glyphs. (The rest of this section applies only when CID fonts are not used.)

None of this will matter if only ASCII characters (codes 32–126) are used as all the encodings (except `"TeXtext"`) agree over that range. Some encodings are supersets of `ISOLatin1`, too. However, if accented and special characters do not come out as you expect, you may need to change the encoding. Some other encodings are supplied with `R`: `"WinAnsi.enc"` and `"MacRoman.enc"` correspond to the encodings normally used on Windows and Classic Mac OS (at least by Adobe), and `"PDFDoc.enc"` is the first 256 characters of the Unicode encoding, the standard for PDF. There are also encodings `"ISOLatin2.enc"`, `"CP1250.enc"`, `"ISOLatin7.enc"` (ISO 8859-13), `"CP1257.enc"`, and `"ISOLatin9.enc"` (ISO 8859-15), `"Cyrillic.enc"` (ISO 8859-5), `"KOI8-R.enc"`, `"KOI8-U.enc"`, `"CP1251.enc"`, `"Greek.enc"` (ISO 8859-7) and `"CP1253.enc"`. Note that many glyphs in these encodings are not in the fonts corresponding to the standard families. (The Adobe ones for all but Courier, Helvetica and Times cover little more than Latin-1, whereas the URW ones also cover Latin-2, Latin-7, Latin-9 and Cyrillic but no Greek. The Adobe exceptions cover the Latin character sets, but not the Euro.)

If you specify the encoding, it is your responsibility to ensure that the PostScript font contains the glyphs used. One issue here is the Euro symbol which is in the `WinAnsi` and `MacRoman` encodings but may well not be in the PostScript fonts. (It is in the URW variants; it is not in the supplied Adobe Font Metric files.)

There is an exception. Character 45 ("–") is always set as minus (its value in Adobe `ISOLatin1`) even though it is hyphen in the other encodings. Hyphen is available as character 173 (octal 0255) in all the Latin encodings, Cyrillic and Greek. (This can be entered as `"\uad"` in a UTF-8 locale.) There are some discrepancies in accounts of glyphs 39 and 96: the supplied encodings (except `CP1250` and `CP1251`) treat these as ‘quoteright’ and ‘quoteleft’ (rather than ‘quotesingle’/‘acute’ and ‘grave’ respectively), as they are in the Adobe documentation.

## TeX fonts

TeX has traditionally made use of fonts such as Computer Modern which are encoded rather differently, in a 7-bit encoding. This encoding can be specified by `encoding = "TeXtext.enc"`, taking care that the ASCII characters `<` `>` `\` `_` `{` `}` are not available in those fonts.

There are supplied families `"ComputerModern"` and `"ComputerModernItalic"` which use this encoding, and which are only supported for `postscript` (and not `pdf`). They are intended to use with the Type 1 versions of the TeX CM fonts. It will normally be possible to include such output in TeX or LaTeX provided it is processed with `dvips -Ppfb -j0` or the equivalent on your system. (`-j0` turns off font subsetting.) When `family = "ComputerModern"` is used, the italic/bold-italic fonts used are slanted fonts (`cmsl10` and `cmbxsl10`). To use text italic fonts instead, set `family = "ComputerModernItalic"`.

These families use the TeX math italic and symbol fonts for a comprehensive but incomplete coverage of the glyphs covered by the Adobe symbol font in other families. This is achieved by special-casing the postscript code generated from the supplied `'CM_symbol_10.afm'`.

## Color models

The default color model is RGB, with pure gray colors expressed as greyscales. Color model "rgb-nogray" uses only RGB, model "cmyk" only CMYK, and model "gray" only greyscales (and selecting any other colour is an error). Nothing in R specifies the interpretation of the RGB or CMYK color spaces, and the simplest possible conversion to CMYK is used ([http://en.wikipedia.org/wiki/CMYK\\_color\\_model#Mapping\\_RGB\\_to\\_CMYK](http://en.wikipedia.org/wiki/CMYK_color_model#Mapping_RGB_to_CMYK)).

## Printing

A postscript plot can be printed via `postscript` in two ways.

1. Setting `print.it = TRUE` causes the command given in argument `command` to be called with argument "file" when the device is closed. Note that the plot file is not deleted unless `command` arranges to delete it.
2. `file=""` or `file="|cmd"` can be used to print using a pipe on systems that support 'popen'. Failure to open the command will probably be reported to the terminal but not to 'popen', in which case close the device by `dev.off` immediately.

## Conventions

This section describes the implementation of the conventions for graphics devices set out in the "R Internals Manual".

- The default device size is 7 inches square.
- Font sizes are in big points.
- The default font family is Helvetica.
- Line widths are as a multiple of 1/96 inch, with no minimum.
- Circle of any radius are allowed.
- Colours are interpreted by the viewing/printing application.

## Note

If you see problems with postscript output, do remember that the problem is much more likely to be in your viewer than in R. Try another viewer if possible. Symptoms for which the viewer has been at fault are apparent grids on image plots (turn off graphics anti-aliasing in your viewer if you can) and missing or incorrect glyphs in text (viewers silently doing font substitution).

Unfortunately the default viewers on most Linux and Mac OS X systems have these problems, and no obvious way to turn off graphics anti-aliasing.

## Author(s)

Support for Computer Modern fonts is based on a contribution by Brian D'Urso <durso@hussle.harvard.edu>.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`postscriptFonts`, `Devices`, and `check.options` which is called from both `ps.options` and `postscript.cairo_ps` for another device that can produce PostScript.

More details of font families and encodings and especially handling text in a non-Latin-1 encoding and embedding fonts can be found in

Paul Murrell and Brian Ripley (2006) Non-standard fonts in PostScript and PDF graphics. *R News*, 6(2):41–47. [http://cran.r-project.org/doc/Rnews/Rnews\\_2006-2.pdf](http://cran.r-project.org/doc/Rnews/Rnews_2006-2.pdf).

**Examples**

```
require(graphics)
## Not run:
# open the file "foo.ps" for graphics output
postscript("foo.ps")
# produce the desired graph(s)
dev.off()          # turn off the postscript device
postscript("|lp -dlw")
# produce the desired graph(s)
dev.off()          # plot will appear on printer

# for URW PostScript devices
postscript("foo.ps", family = "NimbusSan")

## for inclusion in Computer Modern TeX documents, perhaps
postscript("cm_test.eps", width = 4.0, height = 3.0,
          horizontal = FALSE, onefile = FALSE, paper = "special",
          family = "ComputerModern", encoding = "TeXtext.enc")
## The resultant postscript file can be used by dvips -Ppfb -j0.

## To test out encodings, you can use
TestChars <- function(encoding="ISOLatin1", family="URWHelvetica")
{
  postscript(encoding=encoding, family=family)
  par(pty="s")
  plot(c(-1,16), c(-1,16), type="n", xlab="", ylab="",
        xaxs="i", yaxs="i")
  title(paste("Centred chars in encoding", encoding))
  grid(17, 17, lty=1)
  for(i in c(32:255)) {
    x <- i %% 16
    y <- i %/% 16
    points(x, y, pch=i)
  }
  dev.off()
}
## there will be many warnings. We use URW to get a complete enough
## set of font metrics.
TestChars()
TestChars("ISOLatin2")
TestChars("WinAnsi")

## End(Not run)
```

---

postscriptFonts      *PostScript and PDF Font Families*

---

## Description

These functions handle the translation of a R graphics font family name to a PostScript or PDF font description, used by the `postscript` or `pdf` graphics devices.

## Usage

```
postscriptFonts(...)
pdfFonts(...)
```

## Arguments

...                    either character strings naming mappings to display, or named arguments specifying mappings to add or change.

## Details

If these functions are called with no argument they list all the existing mappings, whereas if they are called with named arguments they add (or change) mappings.

A PostScript or PDF device is created with a default font family (see the documentation for `postscript`), but it is also possible to specify a font family when drawing to the device (for example, see the documentation for "family" in `par` and for "fontfamily" in `gpar` in the **grid** package).

The font family sent to the device is a simple string name, which must be mapped to a set of PostScript fonts. Separate lists of mappings for `postscript` and `pdf` devices are maintained for the current R session and can be added to by the user.

The `postscriptFonts` and `pdfFonts` functions can be used to list existing mappings and to define new mappings. The `Type1Font` and `CIDFont` functions can be used to create new mappings, when the `xxxFonts` function is used to add them to the database. See the examples.

Default mappings are provided for three device-independent family names: "sans" for a sans-serif font (to "Helvetica"), "serif" for a serif font (to "Times") and "mono" for a monospaced font (to "Courier").

Mappings for a number of standard Adobe fonts (and URW equivalents) are also provided: "AvantGarde", "Bookman", "Courier", "Helvetica", "Helvetica-Narrow", "NewCenturySchoolbook", "Palatino" and "Times"; "URWGothic", "URWBookman", "NimbusMon", "NimbusSan" (synonym "URWHelvetica"), "NimbusSanCond", "CenturySch", "URWPalladio" and "NimbusRom" (synonym "URWTimes").

There are also mappings for "ComputerModern" and "ComputerModernItalic".

Finally, there are some default mappings for East Asian locales described in a separate section.

The specification of font metrics and encodings is described in the help for the `postscript` function.

The fonts are not embedded in the resulting PostScript or PDF file, so software including the PostScript or PDF plot file should either embed the font outlines (usually from '.pfb' or '.pfa')

files) or use DSC comments to instruct the print spooler or including application to do so (see also [embedFonts](#)).

A font family has both an R-level name, the argument name used when `postscriptFonts` was called, and an internal name, the `family` component. These two names are the same for all the pre-defined font families.

Once a font family is in use it cannot be changed. 'In use' means that it has been specified *via* a `family` or `fonts` argument to an invocation of the same graphics device already in the R session. (For these purposes `xfig` counts the same as `postscript` but only uses some of the predefined mappings.)

**Value**

A list of one or more font mappings.

**East Asian fonts**

There are some default mappings for East Asian locales:

"Japan1", "Japan1HeiMin", "Japan1GothicBBB", and "Japan1Ryumin" for Japanese; "Korea1" and "Korea1deb" for Korean; "GB1" (Simplified Chinese) for mainland China and Singapore; "CNS1" (Traditional Chinese) for Hong Kong and Taiwan.

These refer to the following fonts

Japan1 (PS)	HeiseiKakuGo-W5 Linotype Japanese printer font
Japan1 (PDF)	KozMinPro-Regular-Acro from Adobe Reader 7.0 Japanese Font Pack
Japan1HeiMin (PS)	HeiseiMin-W3 Linotype Japanese printer font
Japan1HeiMin (PDF)	HeiseiMin-W3-Acro from Adobe Reader 7.0 Japanese Font Pack
Japan1GothicBBB	GothicBBB-Medium Japanese-market PostScript printer font
Japan1Ryumin	Ryumin-Light Japanese-market PostScript printer font
Korea1 (PS)	Baekmuk-Batang TrueType font found on some Linux systems
Korea1 (PDF)	HYSMyeongJoStd-Medium-Acro from Adobe Reader 7.0 Korean Font Pack
Korea1deb (PS)	Batang-Regular another name for Baekmuk-Batang
Korea1deb (PDF)	HYGothic-Medium-Acro from Adobe Reader 4.0 Korean Font Pack
GB1 (PS)	BousungEG-Light-GB TrueType font found on some Linux systems
GB1 (PDF)	STSong-Light-Acro from Adobe Reader 7.0 Simplified Chinese Font Pack
CNS1 (PS)	MOESung-Regular Ken Lunde's CJKV resources
CNS1 (PDF)	MSungStd-Light-Acro from Adobe Reader 7.0 Traditional Chinese Font Pack

Baekmuk-Batang can be found at <ftp://ftp.mizi.com/pub/baekmuk/>. BousungEG-Light-GB can be found at <ftp://ftp.gnu.org/pub/non-gnu/chinese-fonts-truetype/>. Ken Lunde's CJKV resources are at <ftp://ftp.oreilly.com/pub/examples/nutshell/cjkv/adobe/samples/>. These will need to be installed or otherwise made available to the postscript/PDF interpreter such as ghostscript (and not all interpreters can handle TrueType fonts).

You may well find that your postscript/PDF interpreters has been set up to provide aliases for many of these fonts. For example, ghostscript on Windows can optionally be installed to map common CJK fonts names to Windows TrueType fonts. (You may want to add the `-Acro` versions as well.)

Adding a mapping for a CID-keyed font is for gurus only.

### Author(s)

Support for Computer Modern fonts is based on a contribution by Brian D'Urso <durso@hussle.harvard.edu>.

### See Also

[postscript](#) and [pdf](#); [Type1Font](#) and [CIDFont](#) for specifying new font mappings.

### Examples

```
postscriptFonts()
## This duplicates "ComputerModernItalic".
CMitalic <- Type1Font("ComputerModern2",
                    c("CM_regular_10.afm", "CM_boldx_10.afm",
                      "cmti10.afm", "cmbxti10.afm",
                      "CM_symbol_10.afm"),
                    encoding = "TeXtext.enc")
postscriptFonts(CMitalic = CMitalic)

## A CID font for Japanese using a different CMap and
## corresponding cmapEncoding.
`Jp_UCS-2` <- CIDFont("TestUCS2",
                    c("Adobe-Japan1-UniJIS-UCS2-H.afm",
                      "Adobe-Japan1-UniJIS-UCS2-H.afm",
                      "Adobe-Japan1-UniJIS-UCS2-H.afm",
                      "Adobe-Japan1-UniJIS-UCS2-H.afm"),
                    "UniJIS-UCS2-H", "UCS-2")
pdfFonts(`Jp_UCS-2` = `Jp_UCS-2`)
names(pdfFonts())
```

---

ps.options

*Auxiliary Function to Set/View Defaults for Arguments of postscript*

---

### Description

The auxiliary function `ps.options` can be used to set or view (if called without arguments) the default values for some of the arguments to `postscript`.

`ps.options` needs to be called before calling `postscript`, and the default values it sets can be overridden by supplying arguments to `postscript`.

**Usage**

```
ps.options(..., reset = FALSE, override.check = FALSE)

setEPS(...)
setPS(...)
```

**Arguments**

`...` **arguments** onefile, family, title, fonts, encoding, bg, fg, width, height, horizontal, pointsize, paper, pagecentre, print.it, command, colormodel and fillOddEven can be supplied. onefile, horizontal and paper are *ignored* for setEPS and setPS.

`reset` **logical**: should the defaults be reset to their ‘factory-fresh’ values?

`override.check` **logical** argument passed to `check.options`. See the Examples.

**Details**

If both `reset = TRUE` and `...` are supplied the defaults are first reset to the ‘factory-fresh’ values and then the new values are applied.

For backwards compatibility argument `append` is accepted but ignored with a warning.

`setEPS` and `setPS` are wrappers to set defaults appropriate for figures for inclusion in documents (the default size is 7 inches square unless `width` or `height` is supplied) and for spooling to a PostScript printer respectively. For historical reasons the latter is the ultimate default.

**Value**

A named list of all the previous defaults. If `...` or `reset = TRUE` is supplied the result has the visibility flag turned off.

**See Also**

[postscript](#), [pdf.options](#)

**Examples**

```
ps.options(bg = "pink")
utils::str(ps.options())

### ---- error checking of arguments: ----
ps.options(width=0:12, onefile=0, bg=pi)
# override the check for 'width', but not 'bg':
ps.options(width=0:12, bg=pi, override.check = c(TRUE,FALSE))
utils::str(ps.options())
ps.options(reset = TRUE) # back to factory-fresh
```



---

quartz

*MacOS X Quartz Device*


---

## Description

quartz starts a graphics device driver for the Mac OS X System. It supports plotting both to the screen (the default) and to various graphics file formats.

## Usage

```
quartz(title, width, height, pointsize, family, fontsmooth, antialias,
        type, file = NULL, bg, canvas, dpi)
```

```
quartz.options(..., reset = FALSE)
```

## Arguments

title	title for the Quartz window (applies to on-screen output only), default "Quartz %d". A C-style format for an integer will be substituted by the device number (see the <code>file</code> argument to <code>postscript</code> for further details).
width	the width of the plotting area in inches. Default 7.
height	the height of the plotting area in inches. Default 7.
pointsize	the default pointsize to be used. Default 12.
family	this is the family name of the font that will be used by the device. Default "Helvetica".
fontsmooth	logical specifying if fonts should be smoothed. Default TRUE. Currently unused.
antialias	whether to use antialiasing. Default TRUE.
type	the type of output to use. See 'Details' for more information. Default "native".
file	an optional target for the graphics device. The default, NULL, selects a default name where one is needed. See 'Details' for more information.
bg	the initial background colour to use for the device. Default "transparent". An opaque colour such as "white" will normally be required on off-screen types that support transparency such as "png" and "tiff".
canvas	canvas colour to use for an on-screen device. Default "white", and will be forced to be an opaque colour.
dpi	resolution of the output. The default ( <code>NA_real_</code> ) for an on-screen display defaults to the resolution of the main screen, and to 72 dpi otherwise. See 'Details'.
...	Any of the arguments to quartz except file.
reset	logical: should the defaults be reset to their defaults?

## Details

The defaults for all but one of the arguments of `quartz` are set by `quartz.options`: the ‘Arguments’ section gives the ‘factory-fresh’ defaults.

The Quartz graphics device supports a variety of output types. On-screen output types are "" or "native" (picks the best possible on-screen output), "Cocoa" (Mac OS X 10.4 and later) and "Carbon" (not currently implemented – potentially Mac OS X 10.3 and earlier). Off-screen output types produce output files and utilize the `file` argument. `type = "pdf"` gives PDF output. The following bitmap formats may be supported (on OS X 10.4 and later): "png", "jpeg", "jpg", "jpeg2000", "tif", "tiff", "gif", "psd" (Adobe Photoshop), "bmp" (Windows bitmap), "sgi" and "pict". (The availability of some formats is OS-version-dependent.)

To reproduce the default of older Quartz devices on-screen, set `dpi = 72` (for a permanent solution set `quartz.options(dpi = 72)`).

The `file` argument is used for off-screen drawing. The actual file is only created when the device is closed (e.g. using `dev.off()`). For the bitmap devices, the page number is substituted if a C integer format is included in the character string, e.g. `Rplot%03d.png`. (The result must be less than `PATH_MAX` characters long, and may be truncated if not. See [postscript](#) for further details.) If a `file` argument is not supplied, the default is `Rplots.pdf` or `Rplot%03d.type`.

If a device-independent R graphics font family is specified (e.g., via `par(family=)` in the graphics package), the Quartz device makes use of the Quartz font database (see `quartzFonts`) to convert the R graphics font family to a Quartz-specific font family description.

On-screen devices are launched with a semi-transparent canvas. Once a new plot is created, the canvas is first painted with the `canvas` colour and then the current background colour (which can be transparent or semi-transparent). Off-screen devices have no canvas colour, and so start with a transparent background where possible (e.g. `type="png"` and `type="tiff"`) – otherwise it appears that a solid white canvas is assumed in the Quartz code.

`title` can be used for on-screen output. It must be a single character string with an optional integer printf-style format that will be substituted by the device number. It is also optionally used (without a format) to give a title to a PDF file.

Calling `quartz()` sets `.Device` to "quartz" for on-screen devices and to "quartz\_off\_screen" otherwise.

## Conventions

This section describes the implementation of the conventions for graphics devices set out in the “R Internals Manual”.

- The default device size is 7 inches square.
- Font sizes are in big points.
- The default font family is Arial.
- Line widths are a multiple of 1/96 inch with no minimum set by R.
- Circle radii are real-valued with no minimum set by R.
- Colour interpretation is by the viewer, including the screen display.

## See Also

[quartzFonts](#), [Devices](#).

[png](#) for way to access the bitmap types of this device via R’s standard bitmap devices.

**Examples**

```
## Not run:
## put something this is your .Rprofile to customize the defaults
setHook(packageEvent("grDevices", "onLoad"),
        function(...) grDevices::quartz.options(width=8, height=6,
                                                pointsize=10))

## End(Not run)
```

---

quartzFonts

*quartz Fonts*


---

**Description**

These functions handle the translation of a device-independent R graphics font family name to a quartz font description.

**Usage**

```
quartzFont (family)
```

```
quartzFonts (...)
```

**Arguments**

family	a character vector containing the four PostScript font names for plain, bold, italic, and bolditalic versions of a font family.
...	either character strings naming mappings to display, or new (named) mappings to define.

**Details**

A quartz device is created with a default font (see the documentation for `quartz`), but it is also possible to specify a font family when drawing to the device (for example, see the documentation for `gpar` in the `grid` package).

The font family sent to the device is a simple string name, which must be mapped to something more specific to quartz fonts. A list of mappings is maintained and can be modified by the user.

The `quartzFonts` function can be used to list existing mappings and to define new mappings. The `quartzFont` function can be used to create a new mapping.

Default mappings are provided for three device-independent font family names: "sans" for a sans-serif font, "serif" for a serif font and "mono" for a monospaced font.

**See Also**

[quartz](#)

**Examples**

```
quartzFonts()
quartzFonts("mono")
## Not run:
## for CJK locales you can use something like
quartzFonts(sans = quartzFont(rep("AppleGothic", 4)),
             serif = quartzFont(rep("AppleMyungjp", 4)))
## since the default fonts may well not have the glyphs needed

## End(Not run)
```

---

recordGraphics	<i>Record Graphics Operations</i>
----------------	-----------------------------------

---

**Description**

Records arbitrary code on the graphics engine display list. Useful for encapsulating calculations with graphical output that depends on the calculations. Intended *only* for expert use.

**Usage**

```
recordGraphics(expr, list, env)
```

**Arguments**

<code>expr</code>	object of mode <code>expression</code> or <code>call</code> or an unevaluated expression.
<code>list</code>	a list defining the environment in which <code>expr</code> is to be evaluated.
<code>env</code>	An <code>environment</code> specifying where R looks for objects not found in <code>envir</code> .

**Details**

The code in `expr` is evaluated in an environment constructed from `list`, with `env` as the parent of that environment.

All three arguments are saved on the graphics engine display list so that on a device resize or copying between devices, the original evaluation environment can be recreated and the code can be re-evaluated to reproduce the graphical output.

**Value**

The value from evaluating `expr`.

**Warning**

This function is not intended for general use. Incorrect or improper use of this function could lead to unintended and/or undesirable results.

An example of acceptable use is querying the current state of a graphics device or graphics system setting and then calling a graphics function.

An example of improper use would be calling the `assign` function to performing assignments in the global environment.

**See Also**[eval](#)**Examples**

```
require(graphics)

plot(1:10)
# This rectangle remains 1inch wide when the device is resized
recordGraphics(
  {
    rect(4, 2,
        4 + diff(par("usr")[1:2])/par("pin")[1], 3)
  },
  list(),
  getNamespace("graphics"))
```

---

`recordPlot`*Record and Replay Plots*

---

**Description**

Functions to save the current plot in an R variable, and to replay it.

**Usage**

```
recordPlot()
replayPlot(x)
```

**Arguments**

`x`                    A saved plot.

**Details**

These functions record and replay the displaylist of the current graphics device. The returned object is of class "recordedplot", and `replayPlot` acts as a `print` method for that class.

**Value**

`recordPlot` returns an object of class "recordedplot".  
`replayPlot` has no return value.

**Warning**

The format of recorded plots may change between R versions. Recorded plots should **not** be used as a permanent storage format for R plots.

R will always attempt to replay a recorded plot, but if the plot was recorded with a different R version then bad things may happen.

---

`rgb`*RGB Color Specification*

---

**Description**

This function creates colors corresponding to the given intensities (between 0 and `max`) of the red, green and blue primaries.

An alpha transparency value can also be specified (0 means fully transparent and `max` means opaque). If `alpha` is not specified, an opaque colour is generated.

The `names` argument may be used to provide names for the colors.

The values returned by these functions can be used with a `col=` specification in graphics functions or in `par`.

**Usage**

```
rgb(red, green, blue, alpha, names = NULL, maxColorValue = 1)
```

**Arguments**

`red`, `blue`, `green`, `alpha`

numeric vectors with values in  $[0, M]$  where  $M$  is `maxColorValue`. When this is 255, the `red`, `blue`, `green`, and `alpha` values are coerced to integers in  $0:255$  and the result is computed most efficiently.

`names`

character. The names for the resulting vector.

`maxColorValue`

number giving the maximum of the color values range, see above.

**Details**

The colors may be specified by passing a matrix or dataframe as argument `red`, and leaving `blue` and `green` missing. In this case the first three columns of `red` are taken to be the red, green and blue values.

Semi-transparent colors ( $0 < \text{alpha} < 1$ ) are supported only on some devices: at the time of writing on the `pdf`, `windows`, `quartz` and `X11 (type="cairo")` devices and associated bitmap devices (`jpeg`, `png`, `bmp`, `tiff` and `bitmap`). They are supported by several third-party devices such as those in packages **Cairo**, **cairoDevice** and **JavaGD**. Only some of these devices support semi-transparent backgrounds.

Most other graphics devices plot semi-transparent colors as fully transparent, usually with a warning when first encountered.

**Value**

A character vector with elements of 7 or 9 characters, "#" followed by the red, blue, green and optionally alpha values in hexadecimal (after rescaling to  $0 \dots 255$ ).

**See Also**

`col2rgb` for translating R colors to RGB vectors; `rainbow`, `hsv`, `hcl`, `gray`.

**Examples**

```

rgb(0,1,0)

rgb((0:15)/15, green=0, blue=0, names=paste("red",0:15,sep="."))

rgb(0, 0:12, 0, max = 255)# integer input

ramp <- colorRamp(c("red", "white"))
rgb( ramp(seq(0, 1, length = 5)), max = 255)

```

---

rgb2hsv

*RGB to HSV Conversion*


---

**Description**

rgb2hsv transforms colors from RGB space (red/green/blue) into HSV space (hue/saturation/value).

**Usage**

```
rgb2hsv(r, g = NULL, b = NULL, gamma = 1, maxColorValue = 255)
```

**Arguments**

**r** vector of 'red' values in  $[0, M]$ , ( $M = \text{maxColorValue}$ ) or 3-row rgb matrix.  
**g** vector of 'green' values, or `NULL` when **r** is a matrix.  
**b** vector of 'blue' values, or `NULL` when **r** is a matrix.  
**gamma** a gamma-correction (supposedly applied to the r,g,b values previously), see `hsv(..., gamma)`.  
**maxColorValue** number giving the maximum of the RGB color values range. The default 255 corresponds to the typical 0:255 RGB coding as in `col2rgb()`.

**Details**

Value (brightness) gives the amount of light in the color.  
Hue describes the dominant wavelength.  
Saturation is the amount of Hue mixed into the color.

**Value**

A matrix with a column for each color. The three rows of the matrix indicate hue, saturation and value and are named "h", "s", and "v" accordingly.

**Author(s)**

R interface by Wolfram Fischer <wolfram@fischer-zim.ch>;  
C code mainly by Nicholas Lewin-Koh <nikko@hailmail.net>.

**See Also**

[hsv](#), [col2rgb](#), [rgb](#).

**Examples**

```

## These (saturated, bright ones) only differ by hue
(rc <- col2rgb(c("red", "yellow","green","cyan", "blue", "magenta")))
(hc <- rgb2hsv(rc))
6 * hc["h",] # the hues are equispaced

(rgb3 <- floor(256 * matrix(stats::runif(3*12), 3,12)))
(hsv3 <- rgb2hsv(rgb3))
## Consistency :
stopifnot(rgb3 == col2rgb(hsv(h=hsv3[1,], s=hsv3[2,], v=hsv3[3,])),
          all.equal(hsv3, rgb2hsv(rgb3/255, maxColorValue = 1)))

## A (simplified) pure R version -- originally by Wolfram Fischer --
## showing the exact algorithm:
rgb2hsvR <- function(rgb, gamma = 1, maxColorValue = 255)
{
  if(!is.numeric(rgb)) stop("rgb matrix must be numeric")
  d <- dim(rgb)
  if(d[1] != 3) stop("rgb matrix must have 3 rows")
  n <- d[2]
  if(n == 0) return(cbind(c(h=1,s=1,v=1))[,0])
  rgb <- rgb/maxColorValue
  if(gamma != 1) rgb <- rgb ^ (1/gamma)

  ## get the max and min
  v <- apply( rgb, 2, max)
  s <- apply( rgb, 2, min)
  D <- v - s # range

  ## set hue to zero for undefined values (gray has no hue)
  h <- numeric(n)
  notgray <- ( s != v )

  ## blue hue
  idx <- (v == rgb[3,] & notgray )
  if (any (idx))
    h[idx] <- 2/3 + 1/6 * (rgb[1,idx] - rgb[2,idx]) / D[idx]
  ## green hue
  idx <- (v == rgb[2,] & notgray )
  if (any (idx))
    h[idx] <- 1/3 + 1/6 * (rgb[3,idx] - rgb[1,idx]) / D[idx]
  ## red hue
  idx <- (v == rgb[1,] & notgray )
  if (any (idx))
    h[idx] <- 1/6 * (rgb[2,idx] - rgb[3,idx]) / D[idx]

  ## correct for negative red
  idx <- (h < 0)
  h[idx] <- 1+h[idx]

  ## set the saturation
  s[! notgray] <- 0;
  s[notgray] <- 1 - s[notgray] / v[notgray]

  rbind( h=h, s=s, v=v )
}

```



```

}

## confirm the equivalence:
all.equal(rgb2hsv (rgb3),
          rgb2hsvR(rgb3), tol=1e-14) # TRUE

```

---

savePlot

*Save Cairo X11 Plot to File*


---

## Description

Save the current page of a cairo [X11](#) () device to a file.

## Usage

```

savePlot(filename = paste("Rplot", type, sep="."),
         type = c("png", "jpeg", "tiff", "bmp"),
         device = dev.cur())

```

## Arguments

filename	filename to save to.
type	file type: only "png" will be accepted for cairo version 1.0.
device	the device to save from.

## Details

Only X11 devices of types "cairo" and "nbcairo" are supported.

This works by copying the image surface to a file. For PNG will always be a 24-bit per pixel PNG 'DirectClass' file, for JPEG the quality is 75% and for TIFF there is no compression.

At present the plot is saved after rendering onto the canvas (default opaque white), so for the default `bg = "transparent"` the effective background colour is the canvas colour.

## Value

Invisible `NULL`.

## Note

There is a similar function of the same name but more types for windows devices on Windows.

## See Also

[X11](#), [dev.copy](#), [dev.print](#)

---

trans3d

*3D to 2D Transformation for Perspective Plots*


---

**Description**

Projection of 3-dimensional to 2-dimensional points using a 4x4 viewing transformation matrix. Mainly for adding to perspective plots such as [persp](#).

**Usage**

```
trans3d(x, y, z, pmat)
```

**Arguments**

*x*, *y*, *z*        numeric vectors of equal length, specifying points in 3D space.

*pmat*            a  $4 \times 4$  viewing transformation matrix, suitable for projecting the 3D coordinates  $(x, y, z)$  into the 2D plane using homogeneous 4D coordinates  $(x, y, z, t)$ ; such matrices are returned by [persp\(\)](#).

**Value**

a list with two components

*x*, *y*            the projected 2d coordinates of the 3d input  $(x, y, z)$ .

**See Also**

[persp](#)

**Examples**

```
## See help(persp) {after attaching the 'graphics' package}
## -----
```

---

Type1Font

*Type 1 and CID Fonts*


---

**Description**

These functions are used to define the translation of a R graphics font family name to a Type 1 or CID font descriptions, used by both the [postscript](#) and [pdf](#) graphics devices.

**Usage**

```
Type1Font(family, metrics, encoding = "default")
```

```
CIDFont(family, cmap, cmapEncoding, pdfresource = "")
```

**Arguments**

<code>family</code>	a character string giving the name to be used internally for a Type 1 or CID-keyed font family. This needs to uniquely identify each family, so if you modify a family which is in use (see <a href="#">postscriptFonts</a> ) you need to change the family name.
<code>metrics</code>	a character vector of four or five strings giving paths to the afm (Adobe Font Metric) files for the font.
<code>cmap</code>	the name of a CMap file for a CID-keyed font.
<code>encoding</code>	for <code>Type1Font</code> , the name of an encoding file. Defaults to "default", which maps on Unix-alikes to "ISOLatin1.enc" and on Windows to "WinAnsi.enc". Otherwise, a file name in the 'enc' directory of the <b>grDevices</b> package, which is used if the path does not contain a path separator. An extension ".enc" can be omitted.
<code>cmapEncoding</code>	The name of a character encoding to be used with the named CMap file: strings will be translated to this encoding when written to the file.
<code>pdfresource</code>	A chunk of PDF code; only required for using a CID-keyed font on pdf; users should not be expected to provide this.

**Details**

For `Type1Fonts`, if four '.afm' files are supplied the fifth is taken to be "Symbol.afm". Relative paths are taken relative to the directory '[R\\_HOME](#)/library/grDevices/afm'. The fifth (symbol) font must be in `AdobeSym` encoding. However, the glyphs in the first four fonts are referenced by name and any encoding given within the '.afm' files is not used.

Glyphs in CID-keyed fonts are accessed by ID (number) and not by name. The CMap file maps encoded strings (usually in a MBCS) to IDs, so `cmap` and `cmapEncoding` specifications must match. There are no real bold or italic versions of CID fonts (bold/italic were very rarely used in traditional CJK typography), and for the `pdf` device all four font faces will be identical. However, for the `postscript` device, bold and italic (and bold italic) are emulated.

CID-keyed fonts are intended only for use for the glyphs of CJK languages, which are all monospaced and are all treated as filling the same bounding box. (Thus `plotmath` will work with such characters, but the spacing will be less carefully controlled than with Western glyphs.) The CID-keyed fonts do contain other characters, including a Latin alphabet: non-CJK glyphs are regarded as monospaced with half the width of CJK glyphs. This is often the case, but sometimes Latin glyphs designed for proportional spacing are used (and may look odd). We strongly recommend that CID-keyed fonts are **only** used for CJK glyphs.

**Value**

A list of class "Type1Font" or "CIDFont".

**See Also**

[postscript](#), [pdf](#), [postscriptFonts](#), and [pdfFonts](#).

**Examples**

```
## This duplicates "ComputerModernItalic".
CMitalic <- Type1Font("ComputerModern2",
                    c("CM_regular_10.afm", "CM_boldx_10.afm",
                      "cmti10.afm", "cmbxti10.afm",
```

```

        "CM_symbol_10.afm"),
        encoding = "TeXtext.enc")

## Not run:
## This could be used by
postscript(family = CMitalic)
## or
postscriptFonts(CMitalic = CMitalic) # once in a session
postscript(family = "CMitalic", encoding = "TeXtext.enc")

## End(Not run)

```

---

x11

*X Window System Graphics*


---

## Description

X11 starts a graphics device driver for the X Window System (version 11). This can only be done on machines/accounts that have access to an X server.

x11 is recognized as a synonym for X11.

## Usage

```

X11(display = "", width, height, pointsize, gamma, bg, canvas,
     fonts, xpos, ypos, title, type, antialias)

```

```

X11.options(..., reset = FALSE)

```

## Arguments

display	the display on which the graphics window will appear. The default is to use the value in the user's environment variable <code>DISPLAY</code> . This is ignored (with a warning) if an X11 device is already open on another display.
width, height	the width and height of the plotting window, in inches. If NA, taken from the resources and if not specified there defaults to 7 inches. See also 'Resources'.
pointsize	the default pointsize to be used. Defaults to 12.
gamma	the gamma correction factor. This value is used to help ensure that the colours perceived are linearly related to RGB values (see <a href="#">hsv</a> ). By default 1 (default correction).
bg	colour, the initial background colour. Default "transparent".
canvas	colour. The colour of the canvas, which is visible only when the background colour is transparent. Should be a solid colour (and any alpha value will be ignored). Default "white".
fonts	X11 font description strings into which weight, slant and size will be substituted. There are two, the first for fonts 1 to 4 and the second for font 5, the symbol font. See section 'Fonts'.

<code>xpos, ypos</code>	integer: initial position of the top left corner of the window, in pixels. Negative values are from the opposite corner, e.g. <code>xpos=-100</code> says the top right corner should be 100 pixels from the right edge of the screen. If NA (the default), successive devices are cascaded in 20 pixel steps from the top left. See also ‘Resources’.
<code>title</code>	character string, up to 100 bytes. With the default, "", a suitable title is created internally. A C-style format for an integer will be substituted by the device number (see the <code>file</code> argument to <code>postscript</code> for further details). How non-ASCII titles are handled is implementation-dependent.
<code>type</code>	character string, one of "Xlib" (the only type prior to R 2.7.0) or "cairo" or "nbcairo". The latter two will only be available if the system was compiled with support for cairo. Default "cairo" where available, otherwise "Xlib".
<code>antialias</code>	for cairo types, the type of anti-aliasing (if any) to be used. One of <code>c("default", "none", "gray", "subpixel")</code> .
<code>reset</code>	logical: should the defaults be reset to their defaults?
<code>...</code>	Any of the arguments to X11, plus <code>colortype</code> and <code>maxcubsize</code> (see section ‘Colour Rendering’).

### Details

The defaults for all of the arguments of `X11` are set by `X11.options`: the ‘Arguments’ section gives the ‘factory-fresh’ defaults.

The initial size and position are only hints, and may not be acted on by the window manager. Also, some systems (especially laptops) are set up to appear to have a screen of a different size to the physical screen.

Option `type` selects between two separate devices: R can be built with support for neither, `type = "Xlib"` or both. Where both are available, types "cairo" and "nbcairo" offer

- anti-aliasing of text and lines.
- translucent colours.
- scalable text, including to sizes like 4.5 pt.
- full support for UTF-8, so on systems with suitable fonts you can plot in many languages on a single figure (and this will work even in non-UTF-8 locales). The output should be locale-independent.

`type = "nbcairo"` is the same device as `type="cairo"` without buffering: which is faster will depend on the X11 connection. Both will be slower than `type = "Xlib"`, especially on a slow X11 connection as all the rendering is done on the machine running R rather than in the X server.

All devices which use an X11 server (including the `type = "Xlib"` versions of bitmap devices such as `png`) share internal structures, which means that they must use the same `display` and `visual`. If you want to change `display`, first close all such devices.

### X11 Fonts

This section applies only to `type = "Xlib"`.

An initial/default font family for the device can be specified via the `fonts` argument, but if a device-independent R graphics font family is specified (e.g., via `par(family=)` in the graphics package), the X11 device makes use of the X11 font database (see `X11Fonts`) to convert the R graphics font family to an X11-specific font family description.

X11 chooses fonts by matching to a pattern, and it is quite possible that it will choose a font in the wrong encoding or which does not contain glyphs for your language (particularly common in iso10646-1 fonts).

The `fonts` argument is a two-element character vector, and the first element will be crucial in successfully using non-Western-European fonts. Settings that have proved useful include

```
"*-mincho-%s-%s-***%d-***-***-***-***" for CJK languages and "-cronyx-helvetica-%s-%s-***%d-***-***-***-***" for Russian.
```

For UTF-8 locales, the `XLC_LOCALE` databases provide mappings between character encodings, and you may need to add an entry for your locale (e.g. Fedora Core 3 lacked one for `ru_RU.utf8`).

## Cairo Fonts

The cairo-based device works directly with font family names such as "Helvetica" which should be selected by `par` or `gpar`. There are mappings for the three device-independent font families, "sans" for a sans-serif font (to "Helvetica"), "serif" for a serif font (to "Times") and "mono" for a monospaced font (to "Courier").

The font selection is handled by `Pango` (usually) or `cairo` (on Mac OS X and perhaps elsewhere). Both make use of `fontconfig` (<http://www.fontconfig.org>) to select fonts and so the results depend on the fonts installed on the system running R – setting the environment variable `FC_DEBUG` to 1 allows some tracing of the selection process.

This works best when high-quality scalable fonts are installed, usually in Type 1 or TrueType formats: see the “R Installation and Administration Manual” for advice on how to obtain and install such fonts.

Because of known problems with font selection on Mac OS X without `Pango`, `type="cairo"` is not the default (as from R 2.11.0) unless `Pango` is available. These problems include mixing up bold and italic and selecting incorrect glyphs.

## Resources

The standard X11 resource `geometry` can be used to specify the window position and/or size, but will be overridden by values specified as arguments or non-NA defaults set in `X11.options`. The class looked for is `R_x11`. Note that the resource specifies the width and height in pixels and not in inches. See for example [http://web.mit.edu/answers/xwindows/xwindows\\_resources.html](http://web.mit.edu/answers/xwindows/xwindows_resources.html) and perhaps ‘`man X`’ (or <http://www.xfree86.org/current/X.7.html>). An example line in ‘`~/Xresources`’ might be

```
R_x11*geometry: 900x900-0+0
```

which specifies a 900 x 900 pixel window at the top right of the screen.

## Colour Rendering

X11 supports several ‘visual’ types, and nowadays almost all systems support ‘truecolor’ which X11 will use by default. This uses a direct specification of any RGB colour up to the depth supported (usually 8 bits per colour). Other visuals make use of a palette to support fewer colours, only grays or even only black/white. The palette is shared between all X11 clients, so it can be necessary to limit the number of colours used by R.

Cairo-based devices currently support only ‘truecolor’ visuals. (Cairo 1.6 will support other visuals.)

The default for `type="Xlib"` is to use the best possible colour model for the visual of the X11 server. This can be overridden by the `colortype` argument of `X11.options`. **Note:** All X11



---

X11Fonts

*X11 Fonts*


---

## Description

These functions handle the translation of a device-independent R graphics font family name to an X11 font description.

## Usage

```
X11Font(font)
```

```
X11Fonts(...)
```

## Arguments

<code>font</code>	a character string containing an X11 font description.
<code>...</code>	either character strings naming mappings to display, or new (named) mappings to define.

## Details

These functions apply only to an [X11](#) device with `type = "Xlib"` - X11 (`type = "Cairo"` uses a different mechanism to select fonts).

Such a device is created with a default font (see the documentation for [X11](#)), but it is also possible to specify a font family when drawing to the device (for example, see the documentation for `"family"` in [par](#) and for `"fontfamily"` in [gpar](#) in the [grid](#) package).

The font family sent to the device is a simple string name, which must be mapped to something more specific to X11 fonts. A list of mappings is maintained and can be modified by the user.

The `X11Fonts` function can be used to list existing mappings and to define new mappings. The `X11Font` function can be used to create a new mapping.

Default mappings are provided for three device-independent font family names: `"sans"` for a sans-serif font, `"serif"` for a serif font and `"mono"` for a monospaced font.

## See Also

[X11](#)

## Examples

```
X11Fonts()
X11Fonts("mono")
utopia <- X11Font("--utopia-*****-*****-*****")
X11Fonts(utopia=utopia)
```



xfig

*XFig Graphics Device***Description**

xfig starts the graphics device driver for producing XFig (version 3.2) graphics.

The auxiliary function `ps.options` can be used to set and view (if called without arguments) default values for the arguments to `xfig` and `postscript`.

**Usage**

```
xfig(file = ifelse(onefile, "Rplots.fig", "Rplot%03d.fig"),
     onefile = FALSE, encoding = "none",
     paper = "default", horizontal = TRUE,
     width = 0, height = 0, family = "Helvetica",
     pointsize = 12, bg = "transparent", fg = "black",
     pagecentre = TRUE, defaultfont = FALSE, textspecial = FALSE)
```

**Arguments**

file	a character string giving the name of the file. For use with <code>onefile = FALSE</code> give a C integer format such as "Rplot%03d.fig" (the default in that case). (See <a href="#">postscript</a> for further details.)
onefile	logical: if true allow multiple figures in one file. If false, assume only one page per file and generate a file number containing the page number.
encoding	The encoding in which to write text strings. The default is not to re-encode. This can be any encoding recognized by <code>iconv</code> : in a Western UTF-8 locale you probably want to select an 8-bit encoding such as <code>latin1</code> , and in an East Asian locale an EUC encoding. If re-encoding fails, the text strings will be written in the current encoding with a warning.
paper	the size of paper region. The choices are "A4", "Letter" and "Legal" (and these can be lowercase). A further choice is "default", which is the default. If this is selected, the <code>papersize</code> is taken from the option "papersize" if that is set to a non-empty value, otherwise "A4".
horizontal	the orientation of the printed image, a logical. Defaults to true, that is landscape orientation.
width, height	the width and height of the graphics region in inches. The default is to use the entire page less a 0.5 inch overall margin in each direction. (See <a href="#">postscript</a> for further details.)
family	the font family to be used. This must be one of "AvantGarde", "Bookman", "Courier", "Helvetica" (the default), "Helvetica-Narrow", "NewCenturySchoolbook", "Palatino" or "Times". Any other value is replaced by "Helvetica", with a warning.
pointsize	the default point size to be used.
bg	the initial background color to be used.
fg	the initial foreground color to be used.
pagecentre	logical: should the device region be centred on the page?

`defaultfont` logical: should the device use xfig's default font?  
`textspecial` logical: should the device set the `textspecial` flag for all text elements. This is useful when generating `ps` from xfig figures.

### Details

Although `xfig` can produce multiple plots in one file, the XFig format does not say how to separate or view them. So `onefile = FALSE` is the default.

The `file` argument is interpreted as a C integer format as used by `sprintf`, with integer argument the page number. The default gives files 'Rplot001.fig', ..., 'Rplot999.fig', 'Rplot1000.fig', ....

Line widths as controlled by `par(lwd=)` are in multiples of  $5/6 * 1/72$  inch. Multiples less than 1 are allowed. `pch="."` with `cex = 1` corresponds to a square of side  $1/72$  inch.

Windows users can make use of WinFIG (<http://www.schmidt-web-berlin.de/WinFIG.htm>, shareware), or XFig under Cygwin.

### Conventions

This section describes the implementation of the conventions for graphics devices set out in the "R Internals Manual".

- The default device size is the paper size with a 0.25 inch border on all sides.
- Font sizes are in big points.
- The default font family is Helvetica.
- Line widths are integers, multiples of  $5/432$  inch.
- Circle radii are multiples of  $1/1200$  inch.
- Colours are interpreted by the viewing/printing application.

### Note

Only some line textures ( $0 \leq lty < 4$ ) are used. Eventually this may be partially remedied, but the XFig file format does not allow as general line textures as the R model. Unimplemented line textures are displayed as *dash-double-dotted*.

There is a limit of 512 colours (plus white and black) per file.

### Author(s)

Brian Ripley. Support for `defaultFont` and `textSpecial` contributed by Sebastian Fischmeister.

### See Also

[Devices](#), [postscript](#), [ps.options](#).

xy.coords

*Extracting Plotting Structures***Description**

xy.coords is used by many functions to obtain x and y coordinates for plotting. The use of this common mechanism across all relevant R functions produces a measure of consistency.

**Usage**

```
xy.coords(x, y = NULL, xlab = NULL, ylab = NULL, log = NULL,
          recycle = FALSE)
```

**Arguments**

x, y	the x and y coordinates of a set of points. Alternatively, a single argument x can be provided.
xlab, ylab	names for the x and y variables to be extracted.
log	character, "x", "y" or both, as for plot. Sets negative values to NA and gives a warning.
recycle	logical; if TRUE, recycle (rep) the shorter of x or y if their lengths differ.

**Details**

An attempt is made to interpret the arguments x and y in a way suitable for bivariate plotting (or other bivariate procedures).

If y is NULL and x is a

**formula:** of the form `yvar ~ xvar`. `xvar` and `yvar` are used as x and y variables.

**list:** containing components x and y, these are used to define plotting coordinates.

**time series:** the x values are taken to be `time(x)` and the y values to be the time series.

**matrix or data.frame with two or more columns:** the first is assumed to contain the x values and the second the y values. *Note* that is also true if x has columns named "x" and "y"; these names will be irrelevant here.

In any other case, the x argument is coerced to a vector and returned as y component where the resulting x is just the index vector 1:n. In this case, the resulting xlab component is set to "Index".

If x (after transformation as above) inherits from class "POSIXt" it is coerced to class "POSIXct".

**Value**

A list with the components

x	numeric (i.e., "double") vector of abscissa values.
y	numeric vector of the same length as x.
xlab	character(1) or NULL, the 'label' of x.
ylab	character(1) or NULL, the 'label' of y.

**See Also**

`plot.default`, `lines`, `points` and `lowess` are examples of functions which use this mechanism.

**Examples**

```
xy.coords(stats::fft(c(1:10)), NULL)

with(cars, xy.coords(dist ~ speed, NULL)$xlab ) # = "speed"

xy.coords(1:3, 1:2, recycle=TRUE)
xy.coords(-2:10, NULL, log="y")
##> warning: 3 y values <=0 omitted ..
```

xyTable

*Multiplicities of (x,y) Points, e.g., for a Sunflower Plot***Description**

Given (x,y) points, determine their multiplicity – checking for equality only up to some (crude kind of) noise. Note that this is special kind of 2D binning.

**Usage**

```
xyTable(x, y = NULL, digits)
```

**Arguments**

<code>x, y</code>	numeric vectors of the same length; alternatively other (x,y) argument combinations as allowed by <code>xy.coords(x, y)</code> .
<code>digits</code>	integer specifying the significant digits to be used for determining equality of coordinates. These are compared after rounding them via <code>signif(*, digits)</code> .

**Value**

A list with three components of same length,

<code>x</code>	x coordinates, rounded and sorted.
<code>y</code>	y coordinates, rounded (and sorted within x).
<code>number</code>	multiplicities (positive integers); i.e., <code>number[i]</code> is the multiplicity of <code>(x[i], y[i])</code> .

**See Also**

`sunflowerplot` which typically uses `xyTable()`; `signif`.

**Examples**

```

xyTable(iris[,3:4], digits = 6)

## Discretized uncorrelated Gaussian:

require(stats)
xy <- data.frame(x = round(sort(rnorm(100))), y = rnorm(100))
xyTable(xy, digits = 1)

```

xyz.coords

*Extracting Plotting Structures***Description**

Utility for obtaining consistent x, y and z coordinates and labels for three dimensional (3D) plots.

**Usage**

```

xyz.coords(x, y = NULL, z = NULL,
           xlab = NULL, ylab = NULL, zlab = NULL,
           log = NULL, recycle = FALSE)

```

**Arguments**

<code>x, y, z</code>	the x, y and z coordinates of a set of points. Both y and z can be left at NULL. In this case, an attempt is made to interpret x in a way suitable for plotting. If the argument is a formula <code>zvar ~ xvar + yvar</code> , <code>xvar</code> , <code>yvar</code> and <code>zvar</code> are used as x, y and z variables; if the argument is a list containing components x, y and z, these are assumed to define plotting coordinates; if the argument is a matrix or <code>data.frame</code> with three or more columns, the first is assumed to contain the x values, the 2nd the y ones, and the 3rd the z ones – independently of any column names that x may have. Alternatively two arguments x and y can be provided (leaving <code>z = NULL</code> ). One may be real, the other complex; in any other case, the arguments are coerced to vectors and the values plotted against their indices.
<code>xlab, ylab, zlab</code>	names for the x, y and z variables to be extracted.
<code>log</code>	character, "x", "y", "z" or combinations. Sets negative values to NA and gives a warning.
<code>recycle</code>	logical; if TRUE, recycle ( <a href="#">rep</a> ) the shorter ones of x, y or z if their lengths differ.

**Value**

A list with the components

<code>x</code>	numeric (i.e., <a href="#">double</a> ) vector of abscissa values.
<code>y</code>	numeric vector of the same length as x.
<code>z</code>	numeric vector of the same length as x.
<code>xlab</code>	character (1) or NULL, the axis label of x.
<code>ylab</code>	character (1) or NULL, the axis label of y.
<code>zlab</code>	character (1) or NULL, the axis label of z.

**Author(s)**

Uwe Ligges and Martin Maechler

**See Also**

[xy.coords](#) for 2D.

**Examples**

```
xyz.coords(data.frame(10*1:9, -4), y = NULL, z = NULL)

xyz.coords(1:6, stats::fft(1:6), z = NULL, xlab = "X", ylab = "Y")

y <- 2 * (x2 <- 10 + (x1 <- 1:10))
xyz.coords(y ~ x1 + x2, y = NULL, z = NULL)

xyz.coords(data.frame(x = -1:9, y = 2:12, z = 3:13), y = NULL, z = NULL,
              log = "xy")
##> Warning message: 2 x values <= 0 omitted ...
```



## Chapter 4

# The graphics package

---

graphics-package    *The R Graphics Package*

---

### Description

R functions for base graphics

### Details

This package contains functions for ‘base’ graphics. Base graphics are traditional S-like graphics, as opposed to the more recent [grid](#) graphics.

For a complete list of functions with individual help pages, use `library(help="graphics")`.

### Author(s)

R Development Core Team and contributors worldwide

Maintainer: R Core Team <R-core@r-project.org>

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

---

abline                      *Add Straight Lines to a Plot*

---

### Description

This function adds one or more straight lines through the current plot.

### Usage

```
abline(a = NULL, b = NULL, h = NULL, v = NULL, reg = NULL,  
       coef = NULL, untf = FALSE, ...)
```



**Arguments**

<code>a, b</code>	the intercept and slope, single values.
<code>untf</code>	logical asking whether to <i>untransform</i> . See ‘Details’.
<code>h</code>	the y-value(s) for horizontal line(s).
<code>v</code>	the x-value(s) for vertical line(s).
<code>coef</code>	a vector of length two giving the intercept and slope.
<code>reg</code>	an object with a <code>coef</code> method. See ‘Details’.
<code>...</code>	graphical parameters such as <code>col</code> , <code>lty</code> and <code>lwd</code> (possibly as vectors: see ‘Details’) and the line characteristics <code>lend</code> , <code>ljoin</code> and <code>lmitre</code> .

**Details**

Typical usages are

```
abline(a, b, untf = FALSE, ...)
abline(h=, untf = FALSE, ...)
abline(v=, untf = FALSE, ...)
abline(coef=, untf = FALSE, ...)
abline(reg=, untf = FALSE, ...)
```

The first form specifies the line in intercept/slope form (alternatively `a` can be specified on its own and is taken to contain the slope and intercept in vector form).

The `h=` and `v=` forms draw horizontal and vertical lines at the specified coordinates.

The `coef` form specifies the line by a vector containing the slope and intercept.

`reg` is a regression object with a `coef` method. If this returns a vector of length 1 then the value is taken to be the slope of a line through the origin, otherwise, the first 2 values are taken to be the intercept and slope.

If `untf` is true, and one or both axes are log-transformed, then a curve is drawn corresponding to a line in original coordinates, otherwise a line is drawn in the transformed coordinate system. The `h` and `v` parameters always refer to original coordinates.

The graphical parameters `col`, `lty` and `lwd` can be specified; see [par](#) for details. For the `h=` and `v=` usages they can be vectors of length greater than one, recycled as necessary.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

**See Also**

[lines](#) and [segments](#) for connected and arbitrary lines given by their *endpoints*. [par](#).

**Examples**

```
## Setup up coordinate system (with x==y aspect ratio):
plot(c(-2,3), c(-1,5), type = "n", xlab="x", ylab="y", asp = 1)
## the x- and y-axis, and an integer grid
abline(h=0, v=0, col = "gray60")
text(1,0, "abline( h = 0 )", col = "gray60", adj = c(0, -.1))
```

```

abline(h = -1:5, v = -2:3, col = "lightgray", lty=3)
abline(a=1, b=2, col = 2)
text(1,3, "abline( 1, 2 )", col=2, adj=c(-.1,-.1))

## Simple Regression Lines:
require(stats)
sale5 <- c(6, 4, 9, 7, 6, 12, 8, 10, 9, 13)
plot(sale5)
abline(lsfit(1:10,sale5))
abline(lsfit(1:10,sale5, intercept = FALSE), col= 4) # less fitting

z <- lm(dist ~ speed, data = cars)
plot(cars)
abline(z) # equivalent to abline(reg = z) or
abline(coef = coef(z))

## trivial intercept model
abline(mC <- lm(dist ~ 1, data = cars)) ## the same as
abline(a = coef(mC), b = 0, col = "blue")

```

---

arrows

*Add Arrows to a Plot*


---

## Description

Draw arrows between pairs of points.

## Usage

```

arrows(x0, y0, x1 = x0, y1 = y0, length = 0.25, angle = 30, code = 2,
       col = par("fg"), lty = par("lty"), lwd = par("lwd"),
       ...)

```

## Arguments

<code>x0, y0</code>	coordinates of points <b>from</b> which to draw.
<code>x1, y1</code>	coordinates of points <b>to</b> which to draw. At least one must be supplied.
<code>length</code>	length of the edges of the arrow head (in inches).
<code>angle</code>	angle from the shaft of the arrow to the edge of the arrow head.
<code>code</code>	integer code, determining <i>kind</i> of arrows to be drawn.
<code>col, lty, lwd</code>	graphical parameters, possible vectors. NA values in <code>col</code> cause the arrow to be omitted.
<code>...</code>	graphical parameters such as <code>xpd</code> and the line characteristics <code>lend</code> , <code>ljoin</code> and <code>lmitre</code> : see <a href="#">par</a> .

**Details**

For each  $i$ , an arrow is drawn between the point  $(x0[i], y0[i])$  and the point  $(x1[i], y1[i])$ . The coordinate vectors will be recycled to the length of the longest.

If `code=1` an arrowhead is drawn at  $(x0[i], y0[i])$  and if `code=2` an arrowhead is drawn at  $(x1[i], y1[i])$ . If `code=3` a head is drawn at both ends of the arrow. Unless `length = 0`, when no head is drawn.

The graphical parameters `col`, `lty` and `lwd` can be vectors of length greater than one and will be recycled if necessary.

The direction of a zero-length arrow is indeterminate, and hence so is the direction of the arrowheads. To allow for rounding error, arrowheads are omitted (with a warning) on any arrow of length less than 1/1000 inch.

**Note**

The first four arguments in the comparable S function are named `x1`, `y1`, `x2`, `y2`.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[segments](#) to draw segments.

**Examples**

```
x <- stats::runif(12); y <- stats::rnorm(12)
i <- order(x,y); x <- x[i]; y <- y[i]
plot(x,y, main="arrows(.) and segments(.)")
## draw arrows from point to point :
s <- seq(length(x)-1)# one shorter than data
arrows(x[s], y[s], x[s+1], y[s+1], col= 1:3)
s <- s[-length(s)]
segments(x[s], y[s], x[s+2], y[s+2], col= 'pink')
```

---

 assocplot

*Association Plots*


---

**Description**

Produce a Cohen-Friendly association plot indicating deviations from independence of rows and columns in a 2-dimensional contingency table.

**Usage**

```
assocplot(x, col = c("black", "red"), space = 0.3,
          main = NULL, xlab = NULL, ylab = NULL)
```

**Arguments**

<code>x</code>	a two-dimensional contingency table in matrix form.
<code>col</code>	a character vector of length two giving the colors used for drawing positive and negative Pearson residuals, respectively.
<code>space</code>	the amount of space (as a fraction of the average rectangle width and height) left between each rectangle.
<code>main</code>	overall title for the plot.
<code>xlab</code>	a label for the x axis. Defaults to the name (if any) of the row dimension in <code>x</code> .
<code>ylab</code>	a label for the y axis. Defaults to the name (if any) of the column dimension in <code>x</code> .

**Details**

For a two-way contingency table, the signed contribution to Pearson's  $\chi^2$  for cell  $i, j$  is  $d_{ij} = (f_{ij} - e_{ij})/\sqrt{e_{ij}}$ , where  $f_{ij}$  and  $e_{ij}$  are the observed and expected counts corresponding to the cell. In the Cohen-Friendly association plot, each cell is represented by a rectangle that has (signed) height proportional to  $d_{ij}$  and width proportional to  $\sqrt{e_{ij}}$ , so that the area of the box is proportional to the difference in observed and expected frequencies. The rectangles in each row are positioned relative to a baseline indicating independence ( $d_{ij} = 0$ ). If the observed frequency of a cell is greater than the expected one, the box rises above the baseline and is shaded in the color specified by the first element of `col`, which defaults to black; otherwise, the box falls below the baseline and is shaded in the color specified by the second element of `col`, which defaults to red.

A more flexible and extensible implementation of association plots written in the grid graphics system is provided in the function `assoc` in the contributed package `vcd` (Meyer, Zeileis and Hornik, 2005).

**References**

Cohen, A. (1980), On the graphical display of the significant components in a two-way contingency table. *Communications in Statistics—Theory and Methods*, **A9**, 1025–1041.

Friendly, M. (1992), Graphical methods for categorical data. *SAS User Group International Conference Proceedings*, **17**, 190–200. <http://www.math.yorku.ca/SCS/sugi/sugi17-paper.html>

Meyer, D., Zeileis, A., and Hornik, K. (2005) The struplot framework: Visualizing multi-way contingency tables with `vcd`. *Report 22*, Department of Statistics and Mathematics, Wirtschaftsuniversität Wien, Research Report Series. [http://epub.wu-wien.ac.at/dyn/openURL?id=oai:epub.wu-wien.ac.at:pub-wu-01\\_8a1](http://epub.wu-wien.ac.at/dyn/openURL?id=oai:epub.wu-wien.ac.at:pub-wu-01_8a1)

**See Also**

`mosaicplot`, `chisq.test`.

**Examples**

```
## Aggregate over sex:
x <- margin.table(HairEyeColor, c(1, 2))
x
assocplot(x, main = "Relation between hair and eye color")
```

---

Axis

*Generic Function to Add an Axis to a Plot*


---

**Description**

Generic function to add a suitable axis to the current plot.

**Usage**

```
Axis(x = NULL, at = NULL, ..., side, labels = NULL)
```

**Arguments**

<code>x</code>	an object which indicates the range over which an axis should be drawn
<code>at</code>	the points at which tick-marks are to be drawn.
<code>side</code>	an integer specifying which side of the plot the axis is to be drawn on. The axis is placed as follows: 1=below, 2=left, 3=above and 4=right.
<code>labels</code>	this can either be a logical value specifying whether (numerical) annotations are to be made at the tickmarks, or a character or expression vector of labels to be placed at the tickpoints. If this is specified as a character or expression vector, <code>at</code> should be supplied and they should be the same length.
<code>...</code>	Arguments to be passed to methods and perhaps then to <a href="#">axis</a> .

**Details**

This is a generic function. It works in a slightly non-standard way: if `x` is supplied and non-NULL it dispatches on `x`, otherwise if `at` is supplied and non-NULL it dispatches on `at`, and the default action is to call [axis](#), omitting argument `x`.

The idea is that for plots for which either or both of the axes are numerical but with a special interpretation, the standard plotting functions (including [boxplot](#), [contour](#), [coplot](#), [filled.contour](#), [pairs](#), [plot.default](#), [rug](#) and [stripchart](#)) will set up user coordinates and `Axis` will be called to label them appropriately.

There are "Date", "POSIXct" and "POSIXlt" methods which can pass an argument `format` onto the appropriate `axis` method (see [axis.POSIXct](#)).

**Value**

The numeric locations on the axis scale at which tick marks were drawn when the plot was first drawn (see 'Details').

This function is usually invoked for its side effect, which is to add an axis to an already existing plot.

**See Also**

[axis](#).

axis

*Add an Axis to a Plot***Description**

Adds an axis to the current plot, allowing the specification of the side, position, labels, and other options.

**Usage**

```
axis(side, at = NULL, labels = TRUE, tick = TRUE, line = NA,
      pos = NA, outer = FALSE, font = NA, lty = "solid",
      lwd = 1, lwd.ticks = lwd, col = NULL, col.ticks = NULL,
      hadj = NA, padj = NA, ...)
```

**Arguments**

side	an integer specifying which side of the plot the axis is to be drawn on. The axis is placed as follows: 1=below, 2=left, 3=above and 4=right.
at	the points at which tick-marks are to be drawn. Non-finite (infinite, NaN or NA) values are omitted. By default (when NULL) tickmark locations are computed, see ‘Details’ below.
labels	this can either be a logical value specifying whether (numerical) annotations are to be made at the tickmarks, or a character or expression vector of labels to be placed at the tickpoints. (Other objects are coerced by <code>as.graphicsAnnot()</code> .) If this is not logical, <code>at</code> should also be supplied and of the same length. If <code>labels</code> is of length zero after coercion, it has the same effect as supplying TRUE.
tick	a logical value specifying whether tickmarks and an axis line should be drawn.
line	the number of lines into the margin at which the axis line will be drawn, if not NA.
pos	the coordinate at which the axis line is to be drawn: if not NA this overrides the value of <code>line</code> .
outer	a logical value indicating whether the axis should be drawn in the outer plot margin, rather than the standard plot margin.
font	font for text. Defaults to <code>par("font")</code> .
lty	line type for both the axis line and the tick marks.
lwd, lwd.ticks	line widths for the axis line and the tick marks. Zero or negative values will suppress the line or ticks.
col, col.ticks	colors for the axis line and the tick marks respectively. <code>col = NULL</code> means to use <code>par("fg")</code> , possibly specified inline, and <code>col=NULL</code> means to use whatever color <code>col</code> resolved to.
hadj	adjustment (see <code>par("adj")</code> ) for all labels <i>parallel</i> (‘horizontal’) to the reading direction. If this is not a finite value, the default is used (centring for strings parallel to the axis, justification of the end nearest the axis otherwise).

`padj` adjustment for each tick label *perpendicular* to the reading direction. For labels parallel to the axes, `padj=0` means right or top alignment, and `padj=1` means left or bottom alignment. This can be a vector given a value for each string, and will be recycled as necessary.

If `padj` is not a finite value (the default), the value of `par("las")` determines the adjustment. For strings plotted perpendicular to the axis the default is to centre the string.

... other graphical parameters may also be passed as arguments to this function, particularly, `cex.axis`, `col.axis` and `font.axis` for axis annotation, `mgp` and `xaxp` or `yaxp` for positioning, `tck` or `tcl` for tick mark length and direction, `las` for vertical/horizontal label orientation, or `fg` instead of `col`, and `xpd` for clipping. See [par](#) on these.

Parameters `xaxt` (sides 1 and 3) and `yaxt` (sides 2 and 4) control if the axis is plotted at all.

Note that `lab` will partial match to argument `labels` unless the latter is also supplied. (Since the default axes have already been set up by `plot.window`, `lab` will not be acted on by `axis`.)

## Details

The axis line is drawn from the lowest to the highest value of `at`, but will be clipped at the plot region. By default, only ticks which are drawn from points within the plot region (up to a tolerance for rounding error) are plotted, but the ticks and their labels may well extend outside the plot region. Use `xpd=TRUE` or `xpd=NA` to allow axes to extend further.

When `at = NULL`, pretty tick mark locations are computed internally (the same way `axTicks(side)` would) from `par("xaxp")` or `"yaxp"` and `par("xlog")` (or `"ylog"`). Note that these locations may change if an on-screen plot is resized (for example, if the `plot` argument `asp` (see `plot.window`) is set.)

If `labels` is not specified, the numeric values supplied or calculated for `at` are converted to character strings as if they were a numeric vector printed by `print.default(digits=7)`.

The code tries hard not to draw overlapping tick labels, and so will omit labels where they would abut or overlap previously drawn labels. This can result in, for example, every other tick being labelled. (The ticks are drawn left to right or bottom to top, and space at least the size of an 'm' is left between labels.)

If either `line` or `pos` is set, they (rather than `par("mgp")[3]`) determine the position of the axis line and tick marks, and the tick labels are placed `par("mgp")[2]` further lines into (or towards for `pos`) the margin.

Several of the graphics parameters affect the way axes are drawn. The vertical (for sides 1 and 3) positions of the axis and the tick labels are controlled by `mgp[2:3]` and `mex`, the size and direction of the ticks is controlled by `tck` and `tcl` and the appearance of the tick labels by `cex.axis`, `col.axis` and `font.axis` with orientation controlled by `las` (but not `srt`, unlike S which uses `srt` if `at` is supplied and `las` if it is not). Note that `adj` is not supported and labels are always centered. See [par](#) for details.

## Value

The numeric locations on the axis scale at which tick marks were drawn when the plot was first drawn (see 'Details').

This function is usually invoked for its side effect, which is to add an axis to an already existing plot.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[Axis](#) for a generic interface.

[axTicks](#) returns the axis tick locations corresponding to `at=NULL`; [pretty](#) is more flexible for computing pretty tick coordinates and does *not* depend on (nor adapt to) the coordinate system in use.

Several graphics parameters affecting the appearance are documented in [par](#).

## Examples

```
require(stats) # for rnorm
plot(1:4, rnorm(4), axes = FALSE)
axis(1, 1:4, LETTERS[1:4])
axis(2)
box() #- to make it look "as usual"

plot(1:7, rnorm(7), main = "axis() examples",
     type = "s", xaxt = "n", frame = FALSE, col = "red")
axis(1, 1:7, LETTERS[1:7], col.axis = "blue")
# unusual options:
axis(4, col = "violet", col.axis="dark violet", lwd = 2)
axis(3, col = "gold", lty = 2, lwd = 0.5)

# one way to have a custom x axis
plot(1:10, xaxt = "n")
axis(1, xaxp=c(2, 9, 7))
```

---

axis.POSIXct

*Date and Date-time Plotting Functions*


---

## Description

Functions to plot objects of classes "POSIXlt", "POSIXct" and "Date" representing calendar dates and times.

## Usage

```
axis.POSIXct(side, x, at, format, labels = TRUE, ...)
axis.Date(side, x, at, format, labels = TRUE, ...)

## S3 method for class 'POSIXct':
plot(x, y, xlab = "", ...)
## S3 method for class 'POSIXlt':
plot(x, y, xlab = "", ...)
## S3 method for class 'Date':
plot(x, y, xlab = "", ...)
```



**Arguments**

<code>x</code> , <code>at</code>	A date-time or date object.
<code>y</code>	numeric values to be plotted against <code>x</code> .
<code>xlab</code>	a character string giving the label for the x axis.
<code>side</code>	See <a href="#">axis</a> .
<code>format</code>	See <a href="#">strptime</a> .
<code>labels</code>	Either a logical value specifying whether annotations are to be made at the tick-marks, or a vector of character strings to be placed at the tickpoints.
<code>...</code>	Further arguments to be passed from or to other methods, typically graphical parameters or arguments of <a href="#">plot.default</a> . For the plot methods, also <code>format</code> .

**Details**

The functions plot against an x-axis of date-times. `axis.POSIXct` and `axis.Date` work quite hard to choose suitable time units (years, months, days, hours, minutes or seconds) and a sensible output format, but this can be overridden by supplying a `format` specification.

If `at` is supplied it specifies the locations of the ticks and labels whereas if `x` is specified a suitable grid of labels is chosen. Printing of tick labels can be suppressed by using `labels = FALSE`.

As from R 2.9.0 the date-times for a "POSIXct" input are interpreted in the timezone give by the "tzzone" attribute if there is one, otherwise the current timezone. (Earlier versions always used the current timezone.)

**Value**

The locations on the axis scale at which tick marks were drawn.

**See Also**

[DateTimeClasses](#), [Dates](#) for details of the classes.

**Examples**

```
with(beaver1, {
  time <- strptime(paste(1990, day, time %/% 100, time %% 100),
                  "%Y %j %H %M")
  plot(time, temp, type="l") # axis at 4-hour intervals.
  # now label every hour on the time axis
  plot(time, temp, type="l", xaxt="n")
  r <- as.POSIXct(round(range(time), "hours"))
  axis.POSIXct(1, at=seq(r[1], r[2], by="hour"), format="%H")
})

plot(.leap.seconds, seq_along(.leap.seconds), type="n", yaxt="n",
     xlab="leap seconds", ylab="", bty="n")
rug(.leap.seconds)
## or as dates
lps <- as.Date(.leap.seconds)
plot(lps, seq_along(.leap.seconds),
     type = "n", yaxt = "n", xlab = "leap seconds",
     ylab = "", bty = "n")
rug(lps)
```

```
## 100 random dates in a 10-week period
random.dates <- as.Date("2001/1/1") + 70*sort(stats::runif(100))
plot(random.dates, 1:100)
# or for a better axis labelling
plot(random.dates, 1:100, xaxt="n")
axis.Date(1, at=seq(as.Date("2001/1/1"), max(random.dates)+6, "weeks"))
axis.Date(1, at=seq(as.Date("2001/1/1"), max(random.dates)+6, "days"),
         labels = FALSE, tcl = -0.2)
```

---

axTicks

*Compute Axis Tickmark Locations*


---

### Description

Compute pretty tickmark locations, the same way as R does internally. This is only non-trivial when `log` coordinates are active. By default, gives the `at` values which `axis(side)` would use.

### Usage

```
axTicks(side, axp = NULL, usr = NULL, log = NULL)
```

### Arguments

<code>side</code>	integer in 1:4, as for <code>axis</code> .
<code>axp</code>	numeric vector of length three, defaulting to <code>par("xaxp")</code> or <code>par("yaxp")</code> depending on the <code>side</code> argument.
<code>usr</code>	numeric vector of length four, defaulting to <code>par("usr")</code> giving horizontal ('x') and vertical ('y') user coordinate limits.
<code>log</code>	logical indicating if log coordinates are active; defaults to <code>par("xlog")</code> or <code>par("ylog")</code> .

### Details

The `axp`, `usr`, and `log` arguments must be consistent as their default values (the `par(...)` results) are. If you specify all three (as non-NULL), the graphics environment is not used at all. Note that the meaning of `axp` alters very much when `log` is TRUE, see the documentation on `par(xaxp=.)`.

`axTicks()` can be regarded as an R implementation of the C function `CreateAtVector()` in `'.../src/main/plot.c'` which is called by `axis(side,*)` when no argument `at` is specified.

### Value

numeric vector of coordinate values at which axis tickmarks can be drawn. By default, when only the first argument is specified, these values should be identical to those that `axis(side)` would use or has used.

### See Also

`axis`, `par`. `pretty` uses the same algorithm (but independently of the graphics environment) and has more options. However it is not available for `log = TRUE`.

**Examples**

```

plot(1:7, 10*21:27)
axTicks(1)
axTicks(2)
stopifnot(identical(axTicks(1), axTicks(3)),
           identical(axTicks(2), axTicks(4)))

## Show how axTicks() and axis() correspond :
op <- par(mfrow = c(3,1))
for(x in 9999*c(1,2,8)) {
  plot(x, 9, log = "x")
  cat(formatC(par("xaxp"), width=5), ";", T <- axTicks(1), "\n")
  rug(T, col="red")
}
par(op)

```

barplot

*Bar Plots***Description**

Creates a bar plot with vertical or horizontal bars.

**Usage**

```

barplot(height, ...)

## Default S3 method:
barplot(height, width = 1, space = NULL,
        names.arg = NULL, legend.text = NULL, beside = FALSE,
        horiz = FALSE, density = NULL, angle = 45,
        col = NULL, border = par("fg"),
        main = NULL, sub = NULL, xlab = NULL, ylab = NULL,
        xlim = NULL, ylim = NULL, xpd = TRUE, log = "",
        axes = TRUE, axisnames = TRUE,
        cex.axis = par("cex.axis"), cex.names = par("cex.axis"),
        inside = TRUE, plot = TRUE, axis.lty = 0, offset = 0,
        add = FALSE, args.legend = NULL, ...)

```

**Arguments**

height	either a vector or matrix of values describing the bars which make up the plot. If <code>height</code> is a vector, the plot consists of a sequence of rectangular bars with heights given by the values in the vector. If <code>height</code> is a matrix and <code>beside</code> is <code>FALSE</code> then each bar of the plot corresponds to a column of <code>height</code> , with the values in the column giving the heights of stacked sub-bars making up the bar. If <code>height</code> is a matrix and <code>beside</code> is <code>TRUE</code> , then the values in each column are juxtaposed rather than stacked.
width	optional vector of bar widths. Re-cycled to length the number of bars drawn. Specifying a single value will have no visible effect unless <code>xlim</code> is specified.

space	the amount of space (as a fraction of the average bar width) left before each bar. May be given as a single number or one number per bar. If <code>height</code> is a matrix and <code>beside</code> is <code>TRUE</code> , <code>space</code> may be specified by two numbers, where the first is the space between bars in the same group, and the second the space between the groups. If not given explicitly, it defaults to <code>c(0, 1)</code> if <code>height</code> is a matrix and <code>beside</code> is <code>TRUE</code> , and to <code>0.2</code> otherwise.
<code>names.arg</code>	a vector of names to be plotted below each bar or group of bars. If this argument is omitted, then the names are taken from the <code>names</code> attribute of <code>height</code> if this is a vector, or the column names if it is a matrix.
<code>legend.text</code>	a vector of text used to construct a legend for the plot, or a logical indicating whether a legend should be included. This is only useful when <code>height</code> is a matrix. In that case given legend labels should correspond to the rows of <code>height</code> ; if <code>legend.text</code> is true, the row names of <code>height</code> will be used as labels if they are non-null.
<code>beside</code>	a logical value. If <code>FALSE</code> , the columns of <code>height</code> are portrayed as stacked bars, and if <code>TRUE</code> the columns are portrayed as juxtaposed bars.
<code>horiz</code>	a logical value. If <code>FALSE</code> , the bars are drawn vertically with the first bar to the left. If <code>TRUE</code> , the bars are drawn horizontally with the first at the bottom.
<code>density</code>	a vector giving the density of shading lines, in lines per inch, for the bars or bar components. The default value of <code>NULL</code> means that no shading lines are drawn. Non-positive values of <code>density</code> also inhibit the drawing of shading lines.
<code>angle</code>	the slope of shading lines, given as an angle in degrees (counter-clockwise), for the bars or bar components.
<code>col</code>	a vector of colors for the bars or bar components. By default, grey is used if <code>height</code> is a vector, and a gamma-corrected grey palette if <code>height</code> is a matrix.
<code>border</code>	the color to be used for the border of the bars. Use <code>border = NA</code> to omit borders. If there are shading lines, <code>border = TRUE</code> means use the same colour for the border as for the shading lines.
<code>main, sub</code>	overall and sub title for the plot.
<code>xlab</code>	a label for the x axis.
<code>ylab</code>	a label for the y axis.
<code>xlim</code>	limits for the x axis.
<code>ylim</code>	limits for the y axis.
<code>xpd</code>	logical. Should bars be allowed to go outside region?
<code>log</code>	string specifying if axis scales should be logarithmic; see <code>plot.default</code> .
<code>axes</code>	logical. If <code>TRUE</code> , a vertical (or horizontal, if <code>horiz</code> is true) axis is drawn.
<code>axisnames</code>	logical. If <code>TRUE</code> , and if there are <code>names.arg</code> (see above), the other axis is drawn (with <code>lty=0</code> ) and labeled.
<code>cex.axis</code>	expansion factor for numeric axis labels.
<code>cex.names</code>	expansion factor for axis names (bar labels).
<code>inside</code>	logical. If <code>TRUE</code> , the lines which divide adjacent (non-stacked!) bars will be drawn. Only applies when <code>space = 0</code> (which it partly is when <code>beside = TRUE</code> ).
<code>plot</code>	logical. If <code>FALSE</code> , nothing is plotted.
<code>axis.lty</code>	the graphics parameter <code>lty</code> applied to the axis and tick marks of the categorical (default horizontal) axis. Note that by default the axis is suppressed.

<code>offset</code>	a vector indicating how much the bars should be shifted relative to the x axis.
<code>add</code>	logical specifying if bars should be added to an already existing plot; defaults to FALSE.
<code>args.legend</code>	list of additional arguments to pass to <code>legend()</code> ; names of the list are used as argument names. Only used if <code>legend.text</code> is supplied.
<code>...</code>	arguments to be passed to/from other methods. For the default method these can include further arguments (such as <code>axes</code> , <code>asp</code> and <code>main</code> ) and graphical parameters (see <code>par</code> ) which are passed to <code>plot.window()</code> , <code>title()</code> and <code>axis</code> .

### Details

This is a generic function, it currently only has a default method. A formula interface may be added eventually.

### Value

A numeric vector (or matrix, when `beside = TRUE`), say `mp`, giving the coordinates of *all* the bar midpoints drawn, useful for adding to the graph.

If `beside` is true, use `colMeans(mp)` for the midpoints of each *group* of bars, see example.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

### See Also

`plot(..., type="h")`, `dotchart`, `hist`.

### Examples

```
require(grDevices) # for colours
tN <- table(Ni <- stats::rpois(100, lambda=5))
r <- barplot(tN, col=rainbow(20))
#- type = "h" plotting *is* 'bar'plot
lines(r, tN, type='h', col='red', lwd=2)

barplot(tN, space = 1.5, axisnames=FALSE,
        sub = "barplot(..., space= 1.5, axisnames = FALSE)")

barplot(VADeaths, plot = FALSE)
barplot(VADeaths, plot = FALSE, beside = TRUE)

mp <- barplot(VADeaths) # default
tot <- colMeans(VADeaths)
text(mp, tot + 3, format(tot), xpd = TRUE, col = "blue")
barplot(VADeaths, beside = TRUE,
        col = c("lightblue", "mistyrose", "lightcyan",
               "lavender", "cornsilk"),
        legend = rownames(VADeaths), ylim = c(0, 100))
title(main = "Death Rates in Virginia", font.main = 4)
```

```

hh <- t(VADeaths)[, 5:1]
mybarcol <- "gray20"
mp <- barplot(hh, beside = TRUE,
             col = c("lightblue", "mistyrose",
                    "lightcyan", "lavender"),
             legend = colnames(VADeaths), ylim= c(0,100),
             main = "Death Rates in Virginia", font.main = 4,
             sub = "Faked upper 2*sigma error bars", col.sub = mybarcol,
             cex.names = 1.5)
segments(mp, hh, mp, hh + 2*sqrt(1000*hh/100), col = mybarcol, lwd = 1.5)
stopifnot(dim(mp) == dim(hh))# corresponding matrices
mtext(side = 1, at = colMeans(mp), line = -2,
      text = paste("Mean", formatC(colMeans(hh))), col = "red")

# Bar shading example
barplot(VADeaths, angle = 15+10*1:5, density = 20, col = "black",
      legend = rownames(VADeaths))
title(main = list("Death Rates in Virginia", font = 4))

# border :
barplot(VADeaths, border = "dark blue")

# log scales (not much sense here):
barplot(tN, col=heat.colors(12), log = "y")
barplot(tN, col=gray.colors(20), log = "xy")

# args.legend
barplot(height = cbind(x = c(465, 91) / 465 * 100,
                      y = c(840, 200) / 840 * 100,
                      z = c(37, 17) / 37 * 100),
      beside = FALSE,
      width = c(465, 840, 37),
      col = c(1, 2),
      legend.text = c("A", "B"),
      args.legend = list(x = "topleft"))

```

---

box

*Draw a Box around a Plot*


---

## Description

This function draws a box around the current plot in the given color and linetype. The `bty` parameter determines the type of box drawn. See [par](#) for details.

## Usage

```
box(which = "plot", lty = "solid", ...)
```

## Arguments

<code>which</code>	character, one of "plot", "figure", "inner" and "outer".
<code>lty</code>	line type of the box.
<code>...</code>	further graphical parameters, such as <code>bty</code> , <code>col</code> , or <code>lwd</code> , see <a href="#">par</a> . Note that <code>xpd</code> is not accepted as clipping is always to the device region.

**Details**

The choice of colour is complicated. If `col` was supplied and is not `NA`, it is used. Otherwise, if `fg` was supplied and is not `NA`, it is used. The final default is `par("col")`.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`rect` for drawing of arbitrary rectangles.

**Examples**

```
plot(1:7, abs(stats::rnorm(7)), type = 'h', axes = FALSE)
axis(1, at = 1:7, labels = letters[1:7])
box(lty = '1373', col = 'red')
```

---

 boxplot

*Box Plots*


---

**Description**

Produce box-and-whisker plot(s) of the given (grouped) values.

**Usage**

```
boxplot(x, ...)

## S3 method for class 'formula':
boxplot(formula, data = NULL, ..., subset, na.action = NULL)

## Default S3 method:
boxplot(x, ..., range = 1.5, width = NULL, varwidth = FALSE,
        notch = FALSE, outline = TRUE, names, plot = TRUE,
        border = par("fg"), col = NULL, log = "",
        pars = list(boxwex = 0.8, staplewex = 0.5, outwex = 0.5),
        horizontal = FALSE, add = FALSE, at = NULL)
```

**Arguments**

<code>formula</code>	a formula, such as <code>y ~ grp</code> , where <code>y</code> is a numeric vector of data values to be split into groups according to the grouping variable <code>grp</code> (usually a factor).
<code>data</code>	a <code>data.frame</code> (or list) from which the variables in <code>formula</code> should be taken.
<code>subset</code>	an optional vector specifying a subset of observations to be used for plotting.
<code>na.action</code>	a function which indicates what should happen when the data contain <code>NA</code> s. The default is to ignore missing values in either the response or the group.

<code>x</code>	for specifying data from which the boxplots are to be produced. Either a numeric vector, or a single list containing such vectors. Additional unnamed arguments specify further data as separate vectors (each corresponding to a component boxplot). <code>NA</code> s are allowed in the data.
<code>...</code>	For the <code>formula</code> method, named arguments to be passed to the default method. For the default method, unnamed arguments are additional data vectors (unless <code>x</code> is a list when they are ignored), and named arguments are arguments and graphical parameters to be passed to <code>bxp</code> in addition to the ones given by argument <code>pars</code> (and override those in <code>pars</code> ).
<code>range</code>	this determines how far the plot whiskers extend out from the box. If <code>range</code> is positive, the whiskers extend to the most extreme data point which is no more than <code>range</code> times the interquartile range from the box. A value of zero causes the whiskers to extend to the data extremes.
<code>width</code>	a vector giving the relative widths of the boxes making up the plot.
<code>varwidth</code>	if <code>varwidth</code> is <code>TRUE</code> , the boxes are drawn with widths proportional to the square-roots of the number of observations in the groups.
<code>notch</code>	if <code>notch</code> is <code>TRUE</code> , a notch is drawn in each side of the boxes. If the notches of two plots do not overlap this is ‘strong evidence’ that the two medians differ (Chambers <i>et al.</i> , 1983, p. 62). See <code>boxplot.stats</code> for the calculations used.
<code>outline</code>	if <code>outline</code> is not true, the outliers are not drawn (as points whereas S+ uses lines).
<code>names</code>	group labels which will be printed under each boxplot. Can be a character vector or an <a href="#">expression</a> (see <code>plotmath</code> ).
<code>boxwex</code>	a scale factor to be applied to all boxes. When there are only a few groups, the appearance of the plot can be improved by making the boxes narrower.
<code>staplewex</code>	staple line width expansion, proportional to box width.
<code>outwex</code>	outlier line width expansion, proportional to box width.
<code>plot</code>	if <code>TRUE</code> (the default) then a boxplot is produced. If not, the summaries which the boxplots are based on are returned.
<code>border</code>	an optional vector of colors for the outlines of the boxplots. The values in <code>border</code> are recycled if the length of <code>border</code> is less than the number of plots.
<code>col</code>	if <code>col</code> is non-null it is assumed to contain colors to be used to colour the bodies of the box plots. By default they are in the background colour.
<code>log</code>	character indicating if <code>x</code> or <code>y</code> or both coordinates should be plotted in log scale.
<code>pars</code>	a list of (potentially many) more graphical parameters, e.g., <code>boxwex</code> or <code>outpch</code> ; these are passed to <code>bxp</code> (if <code>plot</code> is true); for details, see there.
<code>horizontal</code>	logical indicating if the boxplots should be horizontal; default <code>FALSE</code> means vertical boxes.
<code>add</code>	logical, if true <code>add</code> boxplot to current plot.
<code>at</code>	numeric vector giving the locations where the boxplots should be drawn, particularly when <code>add = TRUE</code> ; defaults to <code>1:n</code> where <code>n</code> is the number of boxes.

## Details

The generic function `boxplot` currently has a default method (`boxplot.default`) and a formula interface (`boxplot.formula`).



If multiple groups are supplied either as multiple arguments or via a formula, parallel boxplots will be plotted, in the order of the arguments or the order of the levels of the factor (see [factor](#)).

Missing values are ignored when forming boxplots.

### Value

List with the following components:

<code>stats</code>	a matrix, each column contains the extreme of the lower whisker, the lower hinge, the median, the upper hinge and the extreme of the upper whisker for one group/plot. If all the inputs have the same class attribute, so will this component.
<code>n</code>	a vector with the number of observations in each group.
<code>conf</code>	a matrix where each column contains the lower and upper extremes of the notch.
<code>out</code>	the values of any data points which lie beyond the extremes of the whiskers.
<code>group</code>	a vector of the same length as <code>out</code> whose elements indicate to which group the outlier belongs.
<code>names</code>	a vector of names for the groups.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Chambers, J. M., Cleveland, W. S., Kleiner, B. and Tukey, P. A. (1983) *Graphical Methods for Data Analysis*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

See also [boxplot.stats](#).

### See Also

[boxplot.stats](#) which does the computation, [bxp](#) for the plotting and more examples; and [stripchart](#) for an alternative (with small data sets).

### Examples

```
## boxplot on a formula:
boxplot(count ~ spray, data = InsectSprays, col = "lightgray")
# *add* notches (somewhat funny here):
boxplot(count ~ spray, data = InsectSprays,
        notch = TRUE, add = TRUE, col = "blue")

boxplot(decrease ~ treatment, data = OrchardSprays,
        log = "y", col = "bisque")

rb <- boxplot(decrease ~ treatment, data = OrchardSprays, col="bisque")
title("Comparing boxplot()s and non-robust mean +/- SD")

mn.t <- tapply(OrchardSprays$decrease, OrchardSprays$treatment, mean)
sd.t <- tapply(OrchardSprays$decrease, OrchardSprays$treatment, sd)
xi <- 0.3 + seq(rb$n)
points(xi, mn.t, col = "orange", pch = 18)
arrows(xi, mn.t - sd.t, xi, mn.t + sd.t,
       code = 3, col = "pink", angle = 75, length = .1)
```

```
## boxplot on a matrix:
mat <- cbind(Uni05 = (1:100)/21, Norm = rnorm(100),
             `5T` = rt(100, df = 5), Gam2 = rgamma(100, shape = 2))
boxplot(as.data.frame(mat),
        main = "boxplot(as.data.frame(mat), main = ...)")
par(las=1)# all axis labels horizontal
boxplot(as.data.frame(mat), main = "boxplot(*, horizontal = TRUE)",
        horizontal = TRUE)

## Using 'at = ' and adding boxplots -- example idea by Roger Bivand :

boxplot(len ~ dose, data = ToothGrowth,
        boxwex = 0.25, at = 1:3 - 0.2,
        subset = supp == "VC", col = "yellow",
        main = "Guinea Pigs' Tooth Growth",
        xlab = "Vitamin C dose mg",
        ylab = "tooth length",
        xlim = c(0.5, 3.5), ylim = c(0, 35), yaxs = "i")
boxplot(len ~ dose, data = ToothGrowth, add = TRUE,
        boxwex = 0.25, at = 1:3 + 0.2,
        subset = supp == "OJ", col = "orange")
legend(2, 9, c("Ascorbic acid", "Orange juice"),
      fill = c("yellow", "orange"))

## more examples in help(bxp)
```

---

boxplot.matrix

*Draw a Boxplot for each Column (Row) of a Matrix*


---

## Description

Interpreting the columns (or rows) of a matrix as different groups, draw a boxplot for each.

## Usage

```
## S3 method for class 'matrix':
boxplot(x, use.cols = TRUE, ...)
```

## Arguments

<code>x</code>	a numeric matrix.
<code>use.cols</code>	logical indicating if columns (by default) or rows ( <code>use.cols=FALSE</code> ) should be plotted.
<code>...</code>	Further arguments to <code>boxplot</code> .

## Value

A list as for `boxplot`.

## Author(s)

Martin Maechler, 1995, for S+, then R package `sfsmisc`.

**See Also**

`boxplot.default` which already works nowadays with `data.frames`; `boxplot.formula`, `plot.factor` which work with (the more general concept) of a grouping factor.

**Examples**

```
## Very similar to the example in ?boxplot
mat <- cbind(Uni05 = (1:100)/21, Norm = rnorm(100),
            T5 = rt(100, df = 5), Gam2 = rgamma(100, shape = 2))
boxplot(mat, main = "boxplot.matrix(..., main = ...)",
        notch = TRUE, col = 1:4)
```

bxp

*Draw Box Plots from Summaries***Description**

`bxp` draws box plots based on the given summaries in `z`. It is usually called from within `boxplot`, but can be invoked directly.

**Usage**

```
bxp(z, notch = FALSE, width = NULL, varwidth = FALSE,
    outline = TRUE, notch.frac = 0.5, log = "",
    border = par("fg"), pars = NULL, frame.plot = axes,
    horizontal = FALSE, add = FALSE, at = NULL, show.names = NULL,
    ...)
```

**Arguments**

<code>z</code>	a list containing data summaries to be used in constructing the plots. These are usually the result of a call to <code>boxplot</code> , but can be generated in any fashion.
<code>notch</code>	if <code>notch</code> is <code>TRUE</code> , a notch is drawn in each side of the boxes. If the notches of two plots do not overlap then the medians are significantly different at the 5 percent level.
<code>width</code>	a vector giving the relative widths of the boxes making up the plot.
<code>varwidth</code>	if <code>varwidth</code> is <code>TRUE</code> , the boxes are drawn with widths proportional to the square-roots of the number of observations in the groups.
<code>outline</code>	if <code>outline</code> is not true, the outliers are not drawn.
<code>notch.frac</code>	numeric in (0,1). When <code>notch=TRUE</code> , the fraction of the box width that the notches should use.
<code>border</code>	character or numeric (vector), the color of the box borders. Is recycled for multiple boxes. Is used as default for the <code>boxcol</code> , <code>medcol</code> , <code>whiskcol</code> , <code>staplecol</code> , and <code>outcol</code> options (see below).
<code>log</code>	character, indicating if any axis should be drawn in logarithmic scale, as in <code>plot.default</code> .
<code>frame.plot</code>	logical, indicating if a 'frame' (box) should be drawn; defaults to <code>TRUE</code> , unless <code>axes = FALSE</code> is specified.

<code>horizontal</code>	logical indicating if the boxplots should be horizontal; default <code>FALSE</code> means vertical boxes.
<code>add</code>	logical, if true <i>add</i> boxplot to current plot.
<code>at</code>	numeric vector giving the locations where the boxplots should be drawn, particularly when <code>add = TRUE</code> ; defaults to <code>1:n</code> where <code>n</code> is the number of boxes.
<code>show.names</code>	Set to <code>TRUE</code> or <code>FALSE</code> to override the defaults on whether an x-axis label is printed for each group.
<code>pars, ...</code>	graphical parameters (etc) can be passed as arguments to this function, either as a list ( <code>pars</code> ) or normally( <code>...</code> ), see the following. (Those in <code>...</code> take precedence over those in <code>pars</code> .)

Currently, `yaxs` and `ylim` are used 'along the boxplot', i.e., vertically, when `horizontal` is false, and `xlim` horizontally. `xaxt`, `yaxt`, `las`, `cex.axis`, and `col.axis` are passed to `axis`, and `main`, `cex.main`, `col.main`, `sub`, `cex.sub`, `col.sub`, `xlab`, `ylab`, `cex.lab`, and `col.lab` are passed to `title`.

In addition, `axes` is accepted (see `plot.window`), with default `TRUE`.

The following arguments (or `pars` components) allow further customization of the boxplot graphics. Their defaults are typically determined from the non-prefixed version (e.g., `boxlty` from `lty`), either from the specified argument or `pars` component or the corresponding `par` one.

**boxwex:** a scale factor to be applied to all boxes. When there are only a few groups, the appearance of the plot can be improved by making the boxes narrower. The default depends on `at` and typically is 0.8.

**staplewex, outwex:** staple and outlier line width expansion, proportional to box width; both default to 0.5.

**boxlty, boxlwd, boxcol, boxfill:** box outline type, width, color, and fill color (which currently defaults to `col` and will in future default to `par("bg")`).

**medlty, medlwd, medpch, medcex, medcol, medbg:** median line type, line width, point character, point size expansion, color, and background color. The default `medpch = NA` suppresses the point, and `medlty = "blank"` does so for the line. Note that `medlwd` defaults to  $3 \times$  the default `lwd`.

**whisklty, whisklwd, whiskcol:** whisker line type (default: `"dashed"`), width, and color.

**staplelty, staplelwd, staplecol:** staple (= end of whisker) line type, width, and color.

**outlty, outlwd, outpch, outcex, outcol, outbg:** outlier line type, line width, point character, point size expansion, color, and background color. The default `outlty = "blank"` suppresses the lines and `outpch = NA` suppresses points.

### Value

An invisible vector, actually identical to the `at` argument, with the coordinates ("x" if horizontal is false, "y" otherwise) of box centers, useful for adding to the plot.

### Note

if `add = FALSE`, the default is `xlim = c(0.5, n + 0.5)`. It will usually be a good idea to specify the latter if the "x" axis has a log scale or `at` is specified or `width` is far from uniform.

**Author(s)**

The R Core development team and Arni Magnusson (then at U Washington) who has provided most changes for the `box*`, `med*`, `whisk*`, `staple*`, and `out*` arguments.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**Examples**

```
require(stats)
set.seed(753)
(bx.p <- boxplot(split(rt(100, 4), gl(5,20))))
op <- par(mfrow= c(2,2))
bxp(bx.p, xaxt = "n")
bxp(bx.p, notch = TRUE, axes = FALSE, pch = 4, boxfill=1:5)
bxp(bx.p, notch = TRUE, boxfill= "lightblue", frame= FALSE,
    outl= FALSE, main = "bxp(*, frame= FALSE, outl= FALSE)")
bxp(bx.p, notch = TRUE, boxfill= "lightblue", border= 2:6,
    ylim = c(-4,4), pch = 22, bg = "green", log = "x",
    main = "... log='x', ylim=*")
par(op)
op <- par(mfrow= c(1,2))

## single group -- no label
boxplot(weight ~ group, data = PlantGrowth, subset = group=="ctrl")
## with label
bx <- boxplot(weight ~ group, data = PlantGrowth,
    subset = group=="ctrl", plot = FALSE)
bxp(bx, show.names=TRUE)
par(op)

z <- split(rnorm(1000), rpois(1000,2.2))
boxplot(z, whisklty=3, main="boxplot(z, whisklty = 3)")

## Colour support similar to plot.default:
op <- par(mfrow=1:2, bg="light gray", fg="midnight blue")
boxplot(z, col.axis="skyblue3", main="boxplot(*, col.axis=..,main=..)")
plot(z[[1]], col.axis="skyblue3", main="plot(*, col.axis=..,main=..)")
mtext("par(bg=\"light gray\", fg=\"midnight blue\")",
    outer = TRUE, line = -1.2)
par(op)

## Mimic S-Plus:
splus <- list(boxwex=0.4, staplewex=1, outwex=1, boxfill="grey40",
    medlwd=3, medcol="white", whisklty=3, outlty=1, outpch=NA)
boxplot(z, pars=splus)
## Recycled and "sweeping" parameters
op <- par(mfrow=c(1,2))
boxplot(z, border=1:5, lty = 3, medlty = 1, medlwd = 2.5)
boxplot(z, boxfill=1:3, pch=1:5, lwd = 1.5, medcol="white")
par(op)
## too many possibilities
boxplot(z, boxfill= "light gray", outpch = 21:25, outlty = 2,
```

```
bg = "pink", lwd = 2,
medcol = "dark blue", medcex = 2, medpch = 20)
```

cdplot

*Conditional Density Plots***Description**

Computes and plots conditional densities describing how the conditional distribution of a categorical variable  $y$  changes over a numerical variable  $x$ .

**Usage**

```
cdplot(x, ...)
```

```
## Default S3 method:
cdplot(x, y,
  plot = TRUE, tol.ylab = 0.05, ylevels = NULL,
  bw = "nrd0", n = 512, from = NULL, to = NULL,
  col = NULL, border = 1, main = "", xlab = NULL, ylab = NULL,
  yaxlabels = NULL, xlim = NULL, ylim = c(0, 1), ...)
```

```
## S3 method for class 'formula':
cdplot(formula, data = list(),
  plot = TRUE, tol.ylab = 0.05, ylevels = NULL,
  bw = "nrd0", n = 512, from = NULL, to = NULL,
  col = NULL, border = 1, main = "", xlab = NULL, ylab = NULL,
  yaxlabels = NULL, xlim = NULL, ylim = c(0, 1), ...,
  subset = NULL)
```

**Arguments**

<code>x</code>	an object, the default method expects either a single numerical variable.
<code>y</code>	a "factor" interpreted to be the dependent variable
<code>formula</code>	a "formula" of type $y \sim x$ with a single dependent "factor" and a single numerical explanatory variable.
<code>data</code>	an optional data frame.
<code>plot</code>	logical. Should the computed conditional densities be plotted?
<code>tol.ylab</code>	convenience tolerance parameter for y-axis annotation. If the distance between two labels drops under this threshold, they are plotted equidistantly.
<code>ylevels</code>	a character or numeric vector specifying in which order the levels of the dependent variable should be plotted.
<code>bw, n, from, to, ...</code>	arguments passed to <code>density</code>
<code>col</code>	a vector of fill colors of the same length as <code>levels(y)</code> . The default is to call <code>gray.colors</code> .
<code>border</code>	border color of shaded polygons.
<code>main, xlab, ylab</code>	character strings for annotation

`yaxlabels` character vector for annotation of y axis, defaults to `levels(y)`.  
`xlim, ylim` the range of x and y values with sensible defaults.  
`subset` an optional vector specifying a subset of observations to be used for plotting.

### Details

`cdplot` computes the conditional densities of  $x$  given the levels of  $y$  weighted by the marginal distribution of  $y$ . The densities are derived cumulatively over the levels of  $y$ .

This visualization technique is similar to spinograms (see `spineplot`) and plots  $P(y|x)$  against  $x$ . The conditional probabilities are not derived by discretization (as in the spinogram), but using a smoothing approach via `density`.

Note, that the estimates of the conditional densities are more reliable for high-density regions of  $x$ . Conversely, they are less reliable in regions with only few  $x$  observations.

### Value

The conditional density functions (cumulative over the levels of  $y$ ) are returned invisibly.

### Author(s)

Achim Zeileis <Achim.Zeileis@R-project.org>

### References

Hofmann, H., Theus, M. (2005), *Interactive graphics for visualizing conditional distributions*, Unpublished Manuscript.

### See Also

`spineplot`, `density`

### Examples

```
## NASA space shuttle o-ring failures
fail <- factor(c(2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 2, 1, 2, 1, 1, 1,
               1, 2, 1, 1, 1, 1, 1),
              levels = 1:2, labels = c("no", "yes"))
temperature <- c(53, 57, 58, 63, 66, 67, 67, 67, 68, 69, 70, 70,
                70, 70, 72, 73, 75, 75, 76, 76, 78, 79, 81)

## CD plot
cdplot(fail ~ temperature)
cdplot(fail ~ temperature, bw = 2)
cdplot(fail ~ temperature, bw = "SJ")

## compare with spinogram
(spineplot(fail ~ temperature, breaks = 3))

## highlighting for failures
cdplot(fail ~ temperature, ylevels = 2:1)

## scatter plot with conditional density
cdens <- cdplot(fail ~ temperature, plot = FALSE)
plot(I(as.numeric(fail) - 1) ~ jitter(temperature, factor = 2),
```

```
      xlab = "Temperature", ylab = "Conditional failure probability")
lines(53:81, 1 - cdens[[1]](53:81), col = 2)
```

---

clip

*Set Clipping Region*

---

## Description

Set clipping region in user coordinates

## Usage

```
clip(x1, x2, y1, y2)
```

## Arguments

```
x1, x2, y1, y2
      user coordinates of clipping rectangle
```

## Details

How the clipping rectangle is set depends on the setting of `par("xpd")`: this function changes the current setting until the next high-level plotting command resets it.

Exactly when the clipping region will be reset can be hard to predict. `plot.new` always resets it. Functions such as `lines` and `text` only reset it if `par("xpd")` has been changed. However, functions such as `box`, `mtext`, `title` and `plot.dendrogram` can manipulate the `xpd` setting.

## See Also

[par](#)

## Examples

```
x <- rnorm(1000)
hist(x, xlim=c(-4,4))
usr <- par("usr")
clip(usr[1], -2, usr[3], usr[4])
hist(x, col = 'red', add = TRUE)
clip(2, usr[2], usr[3], usr[4])
hist(x, col = 'blue', add = TRUE)
do.call("clip", as.list(usr)) # reset to plot region
```



contour

*Display Contours***Description**

Create a contour plot, or add contour lines to an existing plot.

**Usage**

```
contour(x, ...)

## Default S3 method:
contour(x = seq(0, 1, length.out = nrow(z)),
        y = seq(0, 1, length.out = ncol(z)),
        z,
        nlevels = 10, levels = pretty(zlim, nlevels),
        labels = NULL,
        xlim = range(x, finite = TRUE),
        ylim = range(y, finite = TRUE),
        zlim = range(z, finite = TRUE),
        labcex = 0.6, drawlabels = TRUE, method = "flattest",
        vfont, axes = TRUE, frame.plot = axes,
        col = par("fg"), lty = par("lty"), lwd = par("lwd"),
        add = FALSE, ...)
```

**Arguments**

<code>x, y</code>	locations of grid lines at which the values in <code>z</code> are measured. These must be in ascending order. By default, equally spaced values from 0 to 1 are used. If <code>x</code> is a list, its components <code>x\$x</code> and <code>x\$y</code> are used for <code>x</code> and <code>y</code> , respectively. If the list has component <code>z</code> this is used for <code>z</code> .
<code>z</code>	a matrix containing the values to be plotted (NAs are allowed). Note that <code>x</code> can be used instead of <code>z</code> for convenience.
<code>nlevels</code>	number of contour levels desired <b>iff</b> <code>levels</code> is not supplied.
<code>levels</code>	numeric vector of levels at which to draw contour lines.
<code>labels</code>	a vector giving the labels for the contour lines. If <code>NULL</code> then the levels are used as labels, otherwise this is coerced by <code>as.character</code> .
<code>labcex</code>	<code>cex</code> for contour labelling. This is an absolute size, not a multiple of <code>par("cex")</code> .
<code>drawlabels</code>	logical. Contours are labelled if <code>TRUE</code> .
<code>method</code>	character string specifying where the labels will be located. Possible values are "simple", "edge" and "flattest" (the default). See the 'Details' section.
<code>vfont</code>	if <code>NULL</code> , the current font family and face are used for the contour labels. If a character vector of length 2 then Hershey vector fonts are used for the contour labels. The first element of the vector selects a typeface and the second element selects a fontindex (see <code>text</code> for more information). The default is <code>NULL</code> on graphics devices with high-quality rotation of text and <code>c("sans serif", "plain")</code> otherwise.

<code>xlim, ylim, zlim</code>	x-, y- and z-limits for the plot.
<code>axes, frame.plot</code>	logical indicating whether axes or a box should be drawn, see <code>plot.default</code> .
<code>col</code>	color for the lines drawn.
<code>lty</code>	line type for the lines drawn.
<code>lwd</code>	line width for the lines drawn.
<code>add</code>	logical. If TRUE, add to a current plot.
<code>...</code>	additional arguments to <code>plot.window</code> , <code>title</code> , <code>Axis</code> and <code>box</code> , typically graphical parameters such as <code>cex.axis</code> .

### Details

`contour` is a generic function with only a default method in base R.

The methods for positioning the labels on contours are "simple" (draw at the edge of the plot, overlaying the contour line), "edge" (draw at the edge of the plot, embedded in the contour line, with no labels overlapping) and "flattest" (draw on the flattest section of the contour, embedded in the contour line, with no labels overlapping). The second and third may not draw a label on every contour line.

For information about vector fonts, see the help for `text` and `Hershey`.

Notice that `contour` interprets the `z` matrix as a table of  $f(x[i], y[j])$  values, so that the `x` axis corresponds to row number and the `y` axis to column number, with column 1 at the bottom, i.e. a 90 degree clockwise rotation of the conventional textual layout.

Alternatively, use `contourplot` from the `lattice` package where the `formula` notation allows to use vectors `x`, `y`, `z` of the same length.

There is limited control over the axes and frame as arguments `col`, `lwd` and `lty` refer to the contour lines (rather than being general graphical parameters). For more control, add contours to a plot, or add axes and frame to a contour plot.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

`options("max.contour.segments")` for the maximal complexity of a single contour line. `contourLines`, `filled.contour` for color-filled contours, `contourplot` (and `levelplot`) from package `lattice`. Further, `image` and the graphics demo which can be invoked as `demo(graphics)`.

### Examples

```
require(grDevices) # for colours
x <- -6:16
op <- par(mfrow = c(2, 2))
contour(outer(x, x), method = "edge", vfont = c("sans serif", "plain"))
z <- outer(x, sqrt(abs(x)), FUN = "/")
image(x, x, z)
contour(x, x, z, col = "pink", add = TRUE, method = "edge",
        vfont = c("sans serif", "plain"))
```

```

contour(x, x, z, ylim = c(1, 6), method = "simple", labcex = 1)
contour(x, x, z, ylim = c(-6, 6), nlev = 20, lty = 2, method = "simple")
par(op)

## Persian Rug Art:
x <- y <- seq(-4*pi, 4*pi, len = 27)
r <- sqrt(outer(x^2, y^2, "+"))
opar <- par(mfrow = c(2, 2), mar = rep(0, 4))
for(f in pi^(0:3))
  contour(cos(r^2)*exp(-r/f),
          drawlabels = FALSE, axes = FALSE, frame = TRUE)

rx <- range(x <- 10*1:nrow(volcano))
ry <- range(y <- 10*1:ncol(volcano))
ry <- ry + c(-1,1) * (diff(rx) - diff(ry))/2
tcol <- terrain.colors(12)
par(opar); opar <- par(pty = "s", bg = "lightcyan")
plot(x = 0, y = 0, type = "n", xlim = rx, ylim = ry, xlab = "", ylab = "")
u <- par("usr")
rect(u[1], u[3], u[2], u[4], col = tcol[8], border = "red")
contour(x, y, volcano, col = tcol[2], lty = "solid", add = TRUE,
        vfont = c("sans serif", "plain"))
title("A Topographic Map of Maunga Whau", font = 4)
abline(h = 200*0:4, v = 200*0:4, col = "lightgray", lty = 2, lwd = 0.1)

## contourLines produces the same contour lines as contour
line.list <- contourLines(x, y, volcano)
plot(x = 0, y = 0, type = "n", xlim = rx, ylim = ry, xlab = "", ylab = "")
u <- par("usr")
rect(u[1], u[3], u[2], u[4], col = tcol[8], border = "red")
contour(x, y, volcano, col = tcol[2], lty = "solid", add = TRUE,
        vfont = c("sans serif", "plain"))
templines <- function(clines) {
  lines(clines[[2]], clines[[3]])
}
invisible(lapply(line.list, templines))
par(opar)

```

---

convertXY

---

*Convert between Graphics Coordinate Systems*


---

## Description

Convert between graphics coordinate systems.

## Usage

```

grconvertX(x, from = "user", to = "user")
grconvertY(y, from = "user", to = "user")

```

## Arguments

<code>x, y</code>	numeric vector of coordinates.
<code>from, to</code>	character strings giving the coordinate systems to convert between.

**Details**

The coordinate systems are

"user" user coordinates.

"inches" inches.

"device" the device coordinate system.

"ndc" normalized device coordinates.

"nfc" normalized figure coordinates.

"npc" normalized plot coordinates.

"nic" normalized inner region coordinates. (The 'inner region' is that inside the outer margins.)

(These names can be partially matched.) For the 'normalized' coordinate systems the lower left has value 0 and the top right value 1.

Device coordinates are those in which the device works: they are usually in pixels where that makes sense and in big points (1/72 inch) otherwise (e.g. [pdf](#) and [postscript](#)).

**Value**

A numeric vector of the same length as the input.

**Examples**

```
op <- par(omd=c(0.1, 0.9, 0.1, 0.9), mfrow = c(1, 2))
plot(1:4)
for(tp in c("in", "dev", "ndc", "nfc", "npc", "nic"))
  print(grconvertX(c(1.0, 4.0), "user", tp))
par(op)
```

---

 coplot

*Conditioning Plots*


---

**Description**

This function produces two variants of the **conditioning plots** discussed in the reference below.

**Usage**

```
coplot(formula, data, given.values, panel = points, rows, columns,
       show.given = TRUE, col = par("fg"), pch = par("pch"),
       bar.bg = c(num = gray(0.8), fac = gray(0.95)),
       xlab = c(x.name, paste("Given :", a.name)),
       ylab = c(y.name, paste("Given :", b.name)),
       subscripts = FALSE,
       axlabels = function(f) abbreviate(levels(f)),
       number = 6, overlap = 0.5, xlim, ylim, ...)
co.intervals(x, number = 6, overlap = 0.5)
```

**Arguments**

<code>formula</code>	<p>a formula describing the form of conditioning plot. A formula of the form <math>y \sim x \mid a</math> indicates that plots of <math>y</math> versus <math>x</math> should be produced conditional on the variable <math>a</math>. A formula of the form <math>y \sim x \mid a * b</math> indicates that plots of <math>y</math> versus <math>x</math> should be produced conditional on the two variables <math>a</math> and <math>b</math>.</p> <p>All three or four variables may be either numeric or factors. When <math>x</math> or <math>y</math> are factors, the result is almost as if <code>as.numeric()</code> was applied, whereas for factor <math>a</math> or <math>b</math>, the conditioning (and its graphics if <code>show.given</code> is true) are adapted.</p>
<code>data</code>	a data frame containing values for any variables in the formula. By default the environment where <code>coplot</code> was called from is used.
<code>given.values</code>	<p>a value or list of two values which determine how the conditioning on <math>a</math> and <math>b</math> is to take place.</p> <p>When there is no <math>b</math> (i.e., conditioning only on <math>a</math>), usually this is a matrix with two columns each row of which gives an interval, to be conditioned on, but it can also be a single vector of numbers or a set of factor levels (if the variable being conditioned on is a factor). In this case (no <math>b</math>), the result of <code>co.intervals</code> can be used directly as <code>given.values</code> argument.</p>
<code>panel</code>	a <code>function(x, y, col, pch, ...)</code> which gives the action to be carried out in each panel of the display. The default is <code>points</code> .
<code>rows</code>	the panels of the plot are laid out in a <code>rows</code> by <code>columns</code> array. <code>rows</code> gives the number of rows in the array.
<code>columns</code>	the number of columns in the panel layout array.
<code>show.given</code>	logical (possibly of length 2 for 2 conditioning variables): should conditioning plots be shown for the corresponding conditioning variables (default TRUE).
<code>col</code>	a vector of colors to be used to plot the points. If too short, the values are recycled.
<code>pch</code>	a vector of plotting symbols or characters. If too short, the values are recycled.
<code>bar.bg</code>	a named vector with components "num" and "fac" giving the background colors for the (shingle) bars, for <b>numeric</b> and <b>factor</b> conditioning variables respectively.
<code>xlab</code>	character; labels to use for the $x$ axis and the first conditioning variable. If only one label is given, it is used for the $x$ axis and the default label is used for the conditioning variable.
<code>ylab</code>	character; labels to use for the $y$ axis and any second conditioning variable.
<code>subscripts</code>	logical: if true the panel function is given an additional (third) argument <code>subscripts</code> giving the subscripts of the data passed to that panel.
<code>axlabels</code>	function for creating axis (tick) labels when $x$ or $y$ are factors.
<code>number</code>	integer; the number of conditioning intervals, for $a$ and $b$ , possibly of length 2. It is only used if the corresponding conditioning variable is not a <code>factor</code> .
<code>overlap</code>	numeric < 1; the fraction of overlap of the conditioning variables, possibly of length 2 for $x$ and $y$ direction. When <code>overlap</code> < 0, there will be <i>gaps</i> between the data slices.
<code>xlim</code>	the range for the $x$ axis.
<code>ylim</code>	the range for the $y$ axis.
<code>...</code>	additional arguments to the panel function.
<code>x</code>	a numeric vector.

## Details

In the case of a single conditioning variable `a`, when both `rows` and `columns` are unspecified, a ‘close to square’ layout is chosen with `columns >= rows`.

In the case of multiple `rows`, the *order* of the panel plots is from the bottom and from the left (corresponding to increasing `a`, typically).

A panel function should not attempt to start a new plot, but just plot within a given coordinate system: thus `plot` and `boxplot` are not panel functions.

The rendering of arguments `xlab` and `ylab` is not controlled by `par` arguments `cex.lab` and `font.lab` even though they are plotted by `mtext` rather than `title`.

## Value

`co.intervals(., number, .)` returns a  $(\text{number} \times 2)$  *matrix*, say `ci`, where `ci[k,]` is the *range* of `x` values for the `k`-th interval.

## References

Chambers, J. M. (1992) *Data for models*. Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

Cleveland, W. S. (1993) *Visualizing Data*. New Jersey: Summit Press.

## See Also

[pairs](#), [panel.smooth](#), [points](#).

## Examples

```
## Tonga Trench Earthquakes
coplot(lat ~ long | depth, data = quakes)
given.depth <- co.intervals(quakes$depth, number=4, overlap=.1)
coplot(lat ~ long | depth, data = quakes, given.v=given.depth, rows=1)

## Conditioning on 2 variables:
ll.dm <- lat ~ long | depth * mag
coplot(ll.dm, data = quakes)
coplot(ll.dm, data = quakes, number=c(4,7), show.given=c(TRUE,FALSE))
coplot(ll.dm, data = quakes, number=c(3,7),
       overlap=c(-.5,.1)) # negative overlap DROPS values

## given two factors
Index <- seq(length=nrow(warpbreaks)) # to get nicer default labels
coplot(breaks ~ Index | wool * tension, data = warpbreaks,
       show.given = 0:1)
coplot(breaks ~ Index | wool * tension, data = warpbreaks,
       col = "red", bg = "pink", pch = 21,
       bar.bg = c(fac = "light blue"))

## Example with empty panels:
with(data.frame(state.x77), {
  coplot(Life.Exp ~ Income | Illiteracy * state.region, number = 3,
        panel = function(x, y, ...) panel.smooth(x, y, span = .8, ...))
  ## y ~ factor -- not really sensible, but 'show off':
  coplot(Life.Exp ~ state.region | Income * state.division,
        panel = panel.smooth)
```

```
})
```

---

```
curve
```

### *Draw Function Plots*

---

## Description

Draws a curve corresponding to the given function or, for `curve()` also an expression (in `x`) over the interval `[from, to]`.

## Usage

```
curve(expr, from = NULL, to = NULL, n = 101, add = FALSE,
      type = "l", ylab = NULL, log = NULL, xlim = NULL, ...)

## S3 method for class 'function':
plot(x, y = 0, to = 1, from = y, xlim = NULL, ...)
```

## Arguments

<code>expr</code>	an expression written as a function of <code>x</code> , or alternatively the name of a function which will be plotted.
<code>x</code>	a ‘vectorizing’ numeric R function.
<code>from, to</code>	the range over which the function will be plotted.
<code>n</code>	integer; the number of <code>x</code> values at which to evaluate.
<code>add</code>	logical; if TRUE add to already existing plot.
<code>xlim</code>	numeric of length 2; if specified, it serves as default for <code>c(from, to)</code> .
<code>type</code>	plot type: see <code>plot.default</code> .
<code>y</code>	alias for <code>from</code> for compatibility with <code>plot()</code>
<code>ylab, log, ...</code>	labels and graphical parameters can also be specified as arguments. <code>plot.function</code> passes all these to <code>curve</code> .

## Details

The evaluation of `expr` is at `n` points equally spaced over the range `[from, to]`, possibly adapted to log scale. The points determined in this way are then joined with straight lines. `x(t)` or `expr` (with `x` inside) must return a numeric of the same length as the argument `t` or `x`.

For `curve()`, if either of `from` or `to` is `NULL`, it defaults to the corresponding element of `xlim`, and `xlim` defaults to the `x`-limits of the current plot. For `plot(<function>, ...)`, the defaults for `(from, to)` are `(0, 1)`.

`log` is taken from the current plot only when `add` is true, and otherwise defaults to "" indicating linear scales on both axes.

This used to be a quick hack which now seems to serve a useful purpose, but can give bad results for functions which are not smooth.

For expensive-to-compute expressions, you should use smarter tools.

**Value**

A list with components `x` and `y` of the points that were drawn is returned invisibly.

**See Also**

[splinefun](#) for spline interpolation, [lines](#).

**Examples**

```
plot(qnorm)
plot(qlogis, main = "The Inverse Logit : qlogis()")
abline(h=0, v=0:2/2, lty=3, col="gray")

curve(sin, -2*pi, 2*pi)
curve(tan, main = "curve(tan) --> same x-scale as previous plot")

op <- par(mfrow=c(2,2))
curve(x^3-3*x, -2, 2)
curve(x^2-2, add = TRUE, col = "violet")

## simple and sophisticated, quite similar:
plot(cos, -pi, 3*pi)
plot(cos, xlim = c(-pi,3*pi), n = 1001, col = "blue", add=TRUE)

chippy <- function(x) sin(cos(x)*exp(-x/2))
curve(chippy, -8, 7, n=2001)
plot(chippy, -8, -5)

for(ll in c("", "x", "y", "xy"))
  curve(log(1+x), 1,100, log=ll, sub=paste("log= ",ll,"",sep=""))
par(op)
```

---

dotchart

*Cleveland's Dot Plots*

---

**Description**

Draw a Cleveland dot plot.

**Usage**

```
dotchart(x, labels = NULL, groups = NULL, gdata = NULL,
         cex = par("cex"), pch = 21, gpch = 21, bg = par("bg"),
         color = par("fg"), gcolor = par("fg"), lcolor = "gray",
         xlim = range(x[is.finite(x)]),
         main = NULL, xlab = NULL, ylab = NULL, ...)
```

**Arguments**

`x` either a vector or matrix of numeric values (NAs are allowed). If `x` is a matrix the overall plot consists of juxtaposed dotplots for each row.

`labels` a vector of labels for each point. For vectors the default is to use names (`x`) and for matrices the row labels `dimnames(x)[[1]]`.



groups	an optional factor indicating how the elements of <code>x</code> are grouped. If <code>x</code> is a matrix, <code>groups</code> will default to the columns of <code>x</code> .
gdata	data values for the groups. This is typically a summary such as the median or mean of each group.
cex	the character size to be used. Setting <code>cex</code> to a value smaller than one can be a useful way of avoiding label overlap. Unlike many other graphics functions, this sets the actual size, not a multiple of <code>par("cex")</code> .
pch	the plotting character or symbol to be used.
gpch	the plotting character or symbol to be used for group values.
bg	the background color of plotting characters or symbols to be used; use <code>par(bg=*)</code> to set the background color of the whole plot.
color	the color(s) to be used for points and labels.
gcolor	the single color to be used for group labels and values.
lcolor	the color(s) to be used for the horizontal lines.
xlim	horizontal range for the plot, see <code>plot.window</code> , e.g.
main	overall title for the plot, see <code>title</code> .
xlab, ylab	axis annotations as in <code>title</code> .
...	graphical parameters can also be specified as arguments.

### Value

This function is invoked for its side effect, which is to produce two variants of dotplots as described in Cleveland (1985).

Dot plots are a reasonable substitute for bar plots.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Cleveland, W. S. (1985) *The Elements of Graphing Data*. Monterey, CA: Wadsworth.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

### Examples

```
dotchart(VADeaths, main = "Death Rates in Virginia - 1940")
op <- par(xaxs="i")# 0 -- 100%
dotchart(t(VADeaths), xlim = c(0,100),
         main = "Death Rates in Virginia - 1940")
par(op)
```

---

 filled.contour      *Level (Contour) Plots*


---

### Description

This function produces a contour plot with the areas between the contours filled in solid color (Cleveland calls this a level plot). A key showing how the colors map to  $z$  values is shown to the right of the plot.

### Usage

```
filled.contour(x = seq(0, 1, length.out = nrow(z)),
              y = seq(0, 1, length.out = ncol(z)),
              z,
              xlim = range(x, finite=TRUE),
              ylim = range(y, finite=TRUE),
              zlim = range(z, finite=TRUE),
              levels = pretty(zlim, nlevels), nlevels = 20,
              color.palette = cm.colors,
              col = color.palette(length(levels) - 1),
              plot.title, plot.axes, key.title, key.axes,
              asp = NA, xaxs = "i", yaxs = "i", las = 1,
              axes = TRUE, frame.plot = axes, ...)
```

### Arguments

<code>x, y</code>	locations of grid lines at which the values in $z$ are measured. These must be in ascending order. By default, equally spaced values from 0 to 1 are used. If $x$ is a list, its components $x\$x$ and $x\$y$ are used for $x$ and $y$ , respectively. If the list has component $z$ this is used for $z$ .
<code>z</code>	a matrix containing the values to be plotted (NAs are allowed). Note that $x$ can be used instead of $z$ for convenience.
<code>xlim</code>	$x$ limits for the plot.
<code>ylim</code>	$y$ limits for the plot.
<code>zlim</code>	$z$ limits for the plot.
<code>levels</code>	a set of levels which are used to partition the range of $z$ . Must be <b>strictly</b> increasing (and finite). Areas with $z$ values between consecutive levels are painted with the same color.
<code>nlevels</code>	if <code>levels</code> is not specified, the range of $z$ , values is divided into approximately this many levels.
<code>color.palette</code>	a color palette function to be used to assign colors in the plot.
<code>col</code>	an explicit set of colors to be used in the plot. This argument overrides any palette function specification.
<code>plot.title</code>	statements which add titles to the main plot.
<code>plot.axes</code>	statements which draw axes (and a <code>box</code> ) on the main plot. This overrides the default axes.
<code>key.title</code>	statements which add titles for the plot key.

<code>key.axes</code>	statements which draw axes on the plot key. This overrides the default axis.
<code>asp</code>	the $y/x$ aspect ratio, see <code>plot.window</code> .
<code>xaxs</code>	the x axis style. The default is to use internal labeling.
<code>yaxs</code>	the y axis style. The default is to use internal labeling.
<code>las</code>	the style of labeling to be used. The default is to use horizontal labeling.
<code>axes, frame.plot</code>	logicals indicating if axes and a box should be drawn, as in <code>plot.default</code> .
<code>...</code>	additional graphical parameters, currently only passed to <code>title()</code> .

**Note**

This function currently uses the `layout` function and so is restricted to a full page display. As an alternative consider the `levelplot` and `contourplot` functions from the **lattice** package which work in multipanel displays.

The output produced by `filled.contour` is actually a combination of two plots; one is the filled contour and one is the legend. Two separate coordinate systems are set up for these two plots, but they are only used internally - once the function has returned these coordinate systems are lost. If you want to annotate the main contour plot, for example to add points, you can specify graphics commands in the `plot.axes` argument. An example is given below.

**Author(s)**

Ross Ihaka.

**References**

Cleveland, W. S. (1993) *Visualizing Data*. Summit, New Jersey: Hobart.

**See Also**

`contour`, `image`, `palette`; `contourplot` from package **lattice**.

**Examples**

```
require(grDevices) # for colours
filled.contour(volcano, color = terrain.colors, asp = 1)# simple

x <- 10*1:nrow(volcano)
y <- 10*1:ncol(volcano)
filled.contour(x, y, volcano, color = terrain.colors,
  plot.title = title(main = "The Topography of Maunga Whau",
    xlab = "Meters North", ylab = "Meters West"),
  plot.axes = { axis(1, seq(100, 800, by = 100))
    axis(2, seq(100, 600, by = 100)) },
  key.title = title(main="Height\n(meters)"),
  key.axes = axis(4, seq(90, 190, by = 10)))# maybe also asp=1
mtext(paste("filled.contour(.) from", R.version.string),
  side = 1, line = 4, adj = 1, cex = .66)

# Annotating a filled contour plot
a <- expand.grid(1:20, 1:20)
b <- matrix(a[,1] + a[,2], 20)
filled.contour(x = 1:20, y = 1:20, z = b,
```

```

plot.axes={ axis(1); axis(2); points(10,10) }

## Persian Rug Art:
x <- y <- seq(-4*pi, 4*pi, len = 27)
r <- sqrt(outer(x^2, y^2, "+"))
filled.contour(cos(r^2)*exp(-r/(2*pi)), axes = FALSE)
## rather, the key *should* be labeled:
filled.contour(cos(r^2)*exp(-r/(2*pi)), frame.plot = FALSE,
               plot.axes = {})

```

fourfoldplot

*Fourfold Plots***Description**

Creates a fourfold display of a 2 by 2 by  $k$  contingency table on the current graphics device, allowing for the visual inspection of the association between two dichotomous variables in one or several populations (strata).

**Usage**

```

fourfoldplot(x, color = c("#99CCFF", "#6699CC"),
             conf.level = 0.95,
             std = c("margins", "ind.max", "all.max"),
             margin = c(1, 2), space = 0.2, main = NULL,
             mfrow = NULL, mfcoll = NULL)

```

**Arguments**

<code>x</code>	a 2 by 2 by $k$ contingency table in array form, or as a 2 by 2 matrix if $k$ is 1.
<code>color</code>	a vector of length 2 specifying the colors to use for the smaller and larger diagonals of each 2 by 2 table.
<code>conf.level</code>	confidence level used for the confidence rings on the odds ratios. Must be a single nonnegative number less than 1; if set to 0, confidence rings are suppressed.
<code>std</code>	a character string specifying how to standardize the table. Must be one of "margins", "ind.max", or "all.max", and can be abbreviated by the initial letter. If set to "margins", each 2 by 2 table is standardized to equate the margins specified by <code>margin</code> while preserving the odds ratio. If "ind.max" or "all.max", the tables are either individually or simultaneously standardized to a maximal cell frequency of 1.
<code>margin</code>	a numeric vector with the margins to equate. Must be one of 1, 2, or <code>c(1, 2)</code> (the default), which corresponds to standardizing the row, column, or both margins in each 2 by 2 table. Only used if <code>std</code> equals "margins".
<code>space</code>	the amount of space (as a fraction of the maximal radius of the quarter circles) used for the row and column labels.
<code>main</code>	character string for the fourfold title.
<code>mfrow</code>	a numeric vector of the form <code>c(nr, nc)</code> , indicating that the displays for the 2 by 2 tables should be arranged in an <code>nr</code> by <code>nc</code> layout, filled by rows.
<code>mfcoll</code>	a numeric vector of the form <code>c(nr, nc)</code> , indicating that the displays for the 2 by 2 tables should be arranged in an <code>nr</code> by <code>nc</code> layout, filled by columns.

## Details

The fourfold display is designed for the display of 2 by 2 by  $k$  tables.

Following suitable standardization, the cell frequencies  $f_{ij}$  of each 2 by 2 table are shown as a quarter circle whose radius is proportional to  $\sqrt{f_{ij}}$  so that its area is proportional to the cell frequency. An association (odds ratio different from 1) between the binary row and column variables is indicated by the tendency of diagonally opposite cells in one direction to differ in size from those in the other direction; color is used to show this direction. Confidence rings for the odds ratio allow a visual test of the null of no association; the rings for adjacent quadrants overlap if and only if the observed counts are consistent with the null hypothesis.

Typically, the number  $k$  corresponds to the number of levels of a stratifying variable, and it is of interest to see whether the association is homogeneous across strata. The fourfold display visualizes the pattern of association. Note that the confidence rings for the individual odds ratios are not adjusted for multiple testing.

## References

Friendly, M. (1994). A fourfold display for 2 by 2 by  $k$  tables. Technical Report 217, York University, Psychology Department. <http://www.math.yorku.ca/SCS/Papers/4fold/4fold.ps.gz>

## See Also

[mosaicplot](#)

## Examples

```
## Use the Berkeley admission data as in Friendly (1995).
x <- aperm(UCBAdmissions, c(2, 1, 3))
dimnames(x)[[2]] <- c("Yes", "No")
names(dimnames(x)) <- c("Sex", "Admit?", "Department")
stats::ftable(x)

## Fourfold display of data aggregated over departments, with
## frequencies standardized to equate the margins for admission
## and sex.
## Figure 1 in Friendly (1994).
fourfoldplot(margin.table(x, c(1, 2)))

## Fourfold display of x, with frequencies in each table
## standardized to equate the margins for admission and sex.
## Figure 2 in Friendly (1994).
fourfoldplot(x)

## Fourfold display of x, with frequencies in each table
## standardized to equate the margins for admission. but not
## for sex.
## Figure 3 in Friendly (1994).
fourfoldplot(x, margin = 2)
```

---

`frame`*Create / Start a New Plot Frame*

---

### Description

This function (`frame` is an alias for `plot.new`) causes the completion of plotting in the current plot (if there is one) and an advance to a new graphics frame. This is used in all high-level plotting functions and also useful for skipping plots when a multi-figure region is in use.

### Usage

```
plot.new()
frame()
```

### Details

The new page is painted with the background colour (`par("bg")`), which is often transparent. For devices with a *canvas* colour (the on-screen devices `X11`, `windows` and `quartz`), the window is first painted with the canvas colour and then the background colour.

There is a hook called `"plot.new"` (see `setHook`) called immediately after advancing the frame, which is used in the testing code to annotate the new page. The hook function(s) are called with no argument. (If the value is a character string, `get` is called on it from within the **graphics** name space.)

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (`frame`.)

### See Also

[plot.window](#), [plot.default](#).

---

`grid`*Add Grid to a Plot*

---

### Description

`grid` adds an `nx` by `ny` rectangular grid to an existing plot.

### Usage

```
grid(nx = NULL, ny = nx, col = "lightgray", lty = "dotted",
     lwd = par("lwd"), equilogs = TRUE)
```

**Arguments**

<code>nx, ny</code>	number of cells of the grid in x and y direction. When <code>NULL</code> , as per default, the grid aligns with the tick marks on the corresponding <i>default</i> axis (i.e., tick-marks as computed by <code>axTicks</code> ). When <code>NA</code> , no grid lines are drawn in the corresponding direction.
<code>col</code>	character or (integer) numeric; color of the grid lines.
<code>lty</code>	character or (integer) numeric; line type of the grid lines.
<code>lwd</code>	non-negative numeric giving line width of the grid lines.
<code>equilogs</code>	logical, only used when <i>log</i> coordinates and alignment with the axis tick marks are active. Setting <code>equilogs = FALSE</code> in that case gives <i>non equidistant</i> tick aligned grid lines.

**Note**

If more fine tuning is required, use `abline` (`h = .`, `v = .`) directly.

**References**

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

**See Also**

`plot`, `abline`, `lines`, `points`.

**Examples**

```
plot(1:3)
grid(NA, 5, lwd = 2) # grid only in y-direction

## maybe change the desired number of tick marks: par(lab=c(mx,my,7))
op <- par(mfcol = 1:2)
with(iris,
{
  plot(Sepal.Length, Sepal.Width, col = as.integer(Species),
       xlim = c(4, 8), ylim = c(2, 4.5), panel.first = grid(),
       main = "with(iris, plot(..., panel.first = grid(), ..) )")
  plot(Sepal.Length, Sepal.Width, col = as.integer(Species),
       panel.first = grid(3, lty=1,lwd=2),
       main = "... panel.first = grid(3, lty=1,lwd=2), ..")
}
)
par(op)
```

---

hist

*Histograms*


---

**Description**

The generic function `hist` computes a histogram of the given data values. If `plot=TRUE`, the resulting object of class "histogram" is plotted by `plot.histogram`, before it is returned.

**Usage**

```
hist(x, ...)

## Default S3 method:
hist(x, breaks = "Sturges",
     freq = NULL, probability = !freq,
     include.lowest = TRUE, right = TRUE,
     density = NULL, angle = 45, col = NULL, border = NULL,
     main = paste("Histogram of" , xname),
     xlim = range(breaks), ylim = NULL,
     xlab = xname, ylab,
     axes = TRUE, plot = TRUE, labels = FALSE,
     nclass = NULL, ...)
```

**Arguments**

<code>x</code>	a vector of values for which the histogram is desired.
<code>breaks</code>	one of: <ul style="list-style-type: none"> <li>• a vector giving the breakpoints between histogram cells,</li> <li>• a single number giving the number of cells for the histogram,</li> <li>• a character string naming an algorithm to compute the number of cells (see ‘Details’),</li> <li>• a function to compute the number of cells.</li> </ul> <p>In the last three cases the number is a suggestion only.</p>
<code>freq</code>	logical; if TRUE, the histogram graphic is a representation of frequencies, the counts component of the result; if FALSE, probability densities, component density, are plotted (so that the histogram has a total area of one). Defaults to TRUE <i>if and only if</i> breaks are equidistant (and probability is not specified).
<code>probability</code>	an <i>alias</i> for !freq, for S compatibility.
<code>include.lowest</code>	logical; if TRUE, an <code>x[i]</code> equal to the <code>breaks</code> value will be included in the first (or last, for <code>right = FALSE</code> ) bar. This will be ignored (with a warning) unless <code>breaks</code> is a vector.
<code>right</code>	logical; if TRUE, the histogram cells are right-closed (left open) intervals.
<code>density</code>	the density of shading lines, in lines per inch. The default value of NULL means that no shading lines are drawn. Non-positive values of <code>density</code> also inhibit the drawing of shading lines.
<code>angle</code>	the slope of shading lines, given as an angle in degrees (counter-clockwise).
<code>col</code>	a colour to be used to fill the bars. The default of NULL yields unfilled bars.
<code>border</code>	the color of the border around the bars. The default is to use the standard foreground color.
<code>main, xlab, ylab</code>	these arguments to <code>title</code> have useful defaults here.
<code>xlim, ylim</code>	the range of x and y values with sensible defaults. Note that <code>xlim</code> is <i>not</i> used to define the histogram (breaks), but only for plotting (when <code>plot = TRUE</code> ).
<code>axes</code>	logical. If TRUE (default), axes are draw if the plot is drawn.



plot	logical. If TRUE (default), a histogram is plotted, otherwise a list of breaks and counts is returned. In the latter case, a warning is used if (typically graphical) arguments are specified that only apply to the <code>plot = TRUE</code> case.
labels	logical or character. Additionally draw labels on top of bars, if not FALSE; see <a href="#">plot.histogram</a> .
nclass	numeric (integer). For S(-PLUS) compatibility only, <code>nclass</code> is equivalent to <code>breaks</code> for a scalar or character argument.
...	further arguments and graphical parameters passed to <a href="#">plot.histogram</a> and thence to <code>title</code> and <code>axis</code> (if <code>plot=TRUE</code> ).

## Details

The definition of *histogram* differs by source (with country-specific biases). R's default with equi-spaced breaks (also the default) is to plot the counts in the cells defined by `breaks`. Thus the height of a rectangle is proportional to the number of points falling into the cell, as is the area *provided* the breaks are equally-spaced.

The default with non-equi-spaced breaks is to give a plot of area one, in which the *area* of the rectangles is the fraction of the data points falling in the cells.

If `right = TRUE` (default), the histogram cells are intervals of the form  $(a, b]$ , i.e., they include their right-hand endpoint, but not their left one, with the exception of the first cell when `include.lowest` is TRUE.

For `right = FALSE`, the intervals are of the form  $[a, b)$ , and `include.lowest` means 'include highest'.

A numerical tolerance of  $10^{-7}$  times the median bin size is applied when counting entries on the edges of bins. This is not included in the reported `breaks` nor (as from R 2.11.0) in the calculation of `density`.

The default for `breaks` is "Sturges": see [nclass.Sturges](#). Other names for which algorithms are supplied are "Scott" and "FD" / "Freedman-Diaconis" (with corresponding functions [nclass.scott](#) and [nclass.FD](#)). Case is ignored and partial matching is used. Alternatively, a function can be supplied which will compute the intended number of breaks as a function of `x`.

## Value

an object of class "histogram" which is a list with components:

breaks	the $n+1$ cell boundaries (= <code>breaks</code> if that was a vector). These are the nominal breaks, not with the boundary fuzz.
counts	$n$ integers; for each cell, the number of <code>x[]</code> inside.
density	values $\hat{f}(x_i)$ , as estimated density values. If <code>all(diff(breaks) == 1)</code> , they are the relative frequencies <code>counts/n</code> and in general satisfy $\sum_i \hat{f}(x_i)(b_{i+1} - b_i) = 1$ , where $b_i = \text{breaks}[i]$ .
intensities	same as <code>density</code> . Deprecated, but retained for compatibility.
mids	the $n$ cell midpoints.
xname	a character string with the actual <code>x</code> argument name.
equidist	logical, indicating if the distances between <code>breaks</code> are all the same.

## References

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Springer.

## See Also

`nclass.Sturges`, `stem`, `density`, `truehist` in package **MASS**.

Typical plots with vertical bars are *not* histograms. Consider `barplot` or `plot(*, type = "h")` for such bar plots.

## Examples

```
op <- par(mfrow=c(2, 2))
hist(islands)
utils::str(hist(islands, col="gray", labels = TRUE))

hist(sqrt(islands), breaks = 12, col="lightblue", border="pink")
##-- For non-equidistant breaks, counts should NOT be graphed unscaled:
r <- hist(sqrt(islands), breaks = c(4*0:5, 10*3:5, 70, 100, 140),
          col='blue1')
text(r$midpoints, r$density, r$count, adj=c(.5, -.5), col='blue3')
sapply(r[2:3], sum)
sum(r$density * diff(r$breaks)) # == 1
lines(r, lty = 3, border = "purple") # -> lines.histogram(*)
par(op)

require(utils) # for str
str(hist(islands, breaks=12, plot= FALSE)) #-> 10 (~= 12) breaks
str(hist(islands, breaks=c(12,20,36,80,200,1000,17000), plot = FALSE))

hist(islands, breaks=c(12,20,36,80,200,1000,17000), freq = TRUE,
      main = "WRONG histogram") # and warning

require(stats)
set.seed(14)
x <- rchisq(100, df = 4)

## Comparing data with a model distribution should be done with qqplot()!
qqplot(x, qchisq(ppoints(x), df = 4)); abline(0,1, col = 2, lty = 2)

## if you really insist on using hist() ... :
hist(x, freq = FALSE, ylim = c(0, 0.2))
curve(dchisq(x, df = 4), col = 2, lty = 2, lwd = 2, add = TRUE)
```

---

hist.POSIXt

*Histogram of a Date or Date-Time Object*

---

## Description

Method for `hist` applied to date or date-time objects.

**Usage**

```
## S3 method for class 'POSIXt':
hist(x, breaks, ...,
      xlab = deparse(substitute(x)),
      plot = TRUE, freq = FALSE,
      start.on.monday = TRUE, format)

## S3 method for class 'Date':
hist(x, breaks, ...,
      xlab = deparse(substitute(x)),
      plot = TRUE, freq = FALSE,
      start.on.monday = TRUE, format)
```

**Arguments**

x	an object inheriting from class "POSIXt" or "Date".
breaks	a vector of cut points <i>or</i> number giving the number of intervals which x is to be cut into <i>or</i> an interval specification, one of "days", "weeks", "months", "quarters" or "years", plus "secs", "mins", "hours" for date-time objects.
...	graphical parameters, or arguments to <code>hist.default</code> such as <code>include.lowest</code> , <code>right</code> and <code>labels</code> .
xlab	a character string giving the label for the x axis, if plotted.
plot	logical. If TRUE (default), a histogram is plotted, otherwise a list of breaks and counts is returned.
freq	logical; if TRUE, the histogram graphic is a representation of frequencies, i.e, the counts component of the result; if FALSE, <i>relative</i> frequencies (probabilities) are plotted.
start.on.monday	logical. If <code>breaks = "weeks"</code> , should the week start on Mondays or Sundays?
format	for the x-axis labels. See <code>strptime</code> .

**Details**

Using `breaks = "quarters"` will create intervals of 3 calendar months, with the intervals beginning on January 1, April 1, July 1 or October 1, based upon `min(x)` as appropriate.

**Value**

An object of class "histogram": see `hist`.

**See Also**

`seq.POSIXt`, `axis.POSIXct`, `hist`

**Examples**

```
hist(.leap.seconds, "years", freq = TRUE)
hist(.leap.seconds,
      seq(ISoDate(1970, 1, 1), ISoDate(2010, 1, 1), "5 years"))
```

```
## 100 random dates in a 10-week period
random.dates <- as.Date("2001/1/1") + 70*stats::runif(100)
hist(random.dates, "weeks", format = "%d %b")
```

---

 identify

*Identify Points in a Scatter Plot*


---

### Description

`identify` reads the position of the graphics pointer when the (first) mouse button is pressed. It then searches the coordinates given in `x` and `y` for the point closest to the pointer. If this point is close enough to the pointer, its index will be returned as part of the value of the call.

### Usage

```
identify(x, ...)

## Default S3 method:
identify(x, y = NULL, labels = seq_along(x), pos = FALSE,
         n = length(x), plot = TRUE, atpen = FALSE, offset = 0.5,
         tolerance = 0.25, ...)
```

### Arguments

<code>x, y</code>	coordinates of points in a scatter plot. Alternatively, any object which defines coordinates (a plotting structure, time series etc: see <a href="#">xy.coords</a> ) can be given as <code>x</code> , and <code>y</code> left missing.
<code>labels</code>	an optional character vector giving labels for the points. Will be coerced using <a href="#">as.character</a> , and recycled if necessary to the length of <code>x</code> . Excess labels will be discarded, with a warning.
<code>pos</code>	if <code>pos</code> is <code>TRUE</code> , a component is added to the return value which indicates where text was plotted relative to each identified point: see <a href="#">Value</a> .
<code>n</code>	the maximum number of points to be identified.
<code>plot</code>	logical: if <code>plot</code> is <code>TRUE</code> , the labels are printed near the points and if <code>FALSE</code> they are omitted.
<code>atpen</code>	logical: if <code>TRUE</code> and <code>plot = TRUE</code> , the lower-left corners of the labels are plotted at the points clicked rather than relative to the points.
<code>offset</code>	the distance (in character widths) which separates the label from identified points. Negative values are allowed. Not used if <code>atpen = TRUE</code> .
<code>tolerance</code>	the maximal distance (in inches) for the pointer to be ‘close enough’ to a point.
<code>...</code>	further arguments passed to <a href="#">par</a> such as <code>cex</code> , <code>col</code> and <code>font</code> .

## Details

`identify` is a generic function, and only the default method is described here.

`identify` is only supported on screen devices such as `X11`, `windows` and `quartz`. On other devices the call will do nothing.

Clicking near (as defined by `tolerance`) a point adds it to the list of identified points. Points can be identified only once, and if the point has already been identified or the click is not near any of the points a message is printed immediately on the R console.

If `plot` is `TRUE`, the point is labelled with the corresponding element of `labels`. If `atpen` is `false` (the default) the labels are placed below, to the left, above or to the right of the identified point, depending on where the pointer was relative to the point. If `atpen` is `true`, the labels are placed with the bottom left of the string's box at the pointer.

For the usual `X11` device the identification process is terminated by pressing any mouse button other than the first. For the `quartz` device the process is terminated by pressing either the pop-up menu equivalent (usually second mouse button or `Ctrl`-click) or the `ESC` key.

On most devices which support `identify`, successful selection of a point is indicated by a bell sound unless `options(locatorBell = FALSE)` has been set.

If the window is resized or hidden and then exposed before the identification process has terminated, any labels drawn by `identify` will disappear. These will reappear once the identification process has terminated and the window is resized or hidden and exposed again. This is because the labels drawn by `identify` are not recorded in the device's display list until the identification process has terminated.

If you interrupt the `identify` call this leaves the graphics device in an undefined state, with points labelled but labels not recorded in the display list. Copying a device in that state will give unpredictable results.

## Value

If `pos` is `FALSE`, an integer vector containing the indices of the identified points, in the order they were identified.

If `pos` is `TRUE`, a list containing a component `ind`, indicating which points were identified and a component `pos`, indicating where the labels were placed relative to the identified points (1=below, 2=left, 3=above, 4=right and 0=no offset, used if `atpen = TRUE`).

## Technicalities

The algorithm used for placing labels is the same as used by `text` if `pos` is specified there, the difference being that the position of the pointer relative the identified point determines `pos` in `identify`.

For labels placed to the left of a point, the right-hand edge of the string's box is placed `offset` units to the left of the point, and analogously for points to the right. The baseline of the text is placed below the point so as to approximately centre string vertically. For labels placed above or below a point, the string is centered horizontally on the point. For labels placed above, the baseline of the text is placed `offset` units above the point, and for those placed below, the baseline is placed so that the top of the string's box is approximately `offset` units below the point. If you want more precise placement (e.g. centering) use `plot = FALSE` and plot via `text` or `points`: see the examples.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[locator](#), [text](#).

## Examples

```
## A function to use identify to select points, and overplot the
## points with another symbol as they are selected
identifyPch <- function(x, y=NULL, n=length(x), pch=19, ...)
{
  xy <- xy.coords(x, y); x <- xy$x; y <- xy$y
  sel <- rep(FALSE, length(x)); res <- integer(0)
  while(sum(sel) < n) {
    ans <- identify(x[!sel], y[!sel], n=1, plot=FALSE, ...)
    if(!length(ans)) break
    ans <- which(!sel)[ans]
    points(x[ans], y[ans], pch = pch)
    sel[ans] <- TRUE
    res <- c(res, ans)
  }
  res
}
```

---

image

*Display a Color Image*

---

## Description

Creates a grid of colored or gray-scale rectangles with colors corresponding to the values in *z*. This can be used to display three-dimensional or spatial data aka *images*. This is a generic function.

The functions [heat.colors](#), [terrain.colors](#) and [topo.colors](#) create heat-spectrum (red to white) and topographical color schemes suitable for displaying ordered data, with *n* giving the number of colors desired.

## Usage

```
image(x, ...)

## Default S3 method:
image(x, y, z, zlim, xlim, ylim, col = heat.colors(12),
      add = FALSE, xaxs = "i", yaxs = "i", xlab, ylab,
      breaks, oldstyle = FALSE, ...)
```

**Arguments**

<code>x, y</code>	locations of grid lines at which the values in <code>z</code> are measured. These must be finite, non-missing and in (strictly) ascending order. By default, equally spaced values from 0 to 1 are used. If <code>x</code> is a <code>list</code> , its components <code>x\$x</code> and <code>x\$y</code> are used for <code>x</code> and <code>y</code> , respectively. If the list has component <code>z</code> this is used for <code>z</code> .
<code>z</code>	a matrix containing the values to be plotted (NAs are allowed). Note that <code>x</code> can be used instead of <code>z</code> for convenience.
<code>zlim</code>	the minimum and maximum <code>z</code> values for which colors should be plotted, defaulting to the range of the finite values of <code>z</code> . Each of the given colors will be used to color an equispaced interval of this range. The <i>midpoints</i> of the intervals cover the range, so that values just outside the range will be plotted.
<code>xlim, ylim</code>	ranges for the plotted <code>x</code> and <code>y</code> values, defaulting to the ranges of <code>x</code> and <code>y</code> .
<code>col</code>	a list of colors such as that generated by <code>rainbow</code> , <code>heat.colors</code> , <code>topo.colors</code> , <code>terrain.colors</code> or similar functions.
<code>add</code>	logical; if <code>TRUE</code> , add to current plot (and disregard the following arguments). This is rarely useful because <code>image</code> ‘paints’ over existing graphics.
<code>xaxs, yaxs</code>	style of <code>x</code> and <code>y</code> axis. The default <code>"i"</code> is appropriate for images. See <code>par</code> .
<code>xlab, ylab</code>	each a character string giving the labels for the <code>x</code> and <code>y</code> axis. Default to the ‘call names’ of <code>x</code> or <code>y</code> , or to <code>" "</code> if these were unspecified.
<code>breaks</code>	a set of breakpoints for the colours: must give one more breakpoint than colour.
<code>oldstyle</code>	logical. If true the midpoints of the colour intervals are equally spaced, and <code>zlim[1]</code> and <code>zlim[2]</code> were taken to be midpoints. The default is to have colour intervals of equal lengths between the limits.
<code>...</code>	graphical parameters for <code>plot</code> may also be passed as arguments to this function, as can the plot aspect ratio <code>asp</code> and <code>axes</code> (see <code>plot.window</code> ).

**Details**

The length of `x` should be equal to the `nrow(z)+1` or `nrow(z)`. In the first case `x` specifies the boundaries between the cells: in the second case `x` specifies the midpoints of the cells. Similar reasoning applies to `y`. It probably only makes sense to specify the midpoints of an equally-spaced grid. If you specify just one row or column and a length-one `x` or `y`, the whole user area in the corresponding direction is filled.

Rectangles corresponding to missing values are not plotted (and so are transparent and (unless `add=TRUE`) the default background painted in `par("bg")` will show though and if that is transparent, the canvas colour will be seen).

If `breaks` is specified then `zlim` is unused and the algorithm used follows `cut`, so intervals are closed on the right and open on the left except for the lowest interval.

Notice that `image` interprets the `z` matrix as a table of `f(x[i], y[j])` values, so that the `x` axis corresponds to row number and the `y` axis to column number, with column 1 at the bottom, i.e. a 90 degree counter-clockwise rotation of the conventional printed layout of a matrix.

**Note**

Based on a function by Thomas Lumley <tlumley@u.washington.edu>.

**See Also**

`filled.contour` or `heatmap` which can look nicer (but are less modular), `contour`; The lattice equivalent of image is `levelplot`.

`heat.colors`, `topo.colors`, `terrain.colors`, `rainbow`, `hsv`, `par`.

**Examples**

```
require(grDevices) # for colours
x <- y <- seq(-4*pi, 4*pi, len=27)
r <- sqrt(outer(x^2, y^2, "+"))
image(z = z <- cos(r^2)*exp(-r/6), col=gray((0:32)/32))
image(z, axes = FALSE, main = "Math can be beautiful ...",
      xlab = expression(cos(r^2) * e^{-r/6}))
contour(z, add = TRUE, drawlabels = FALSE)

# Volcano data visualized as matrix. Need to transpose and flip
# matrix horizontally.
image(t(volcano)[ncol(volcano):1,])

# A prettier display of the volcano
x <- 10*(1:nrow(volcano))
y <- 10*(1:ncol(volcano))
image(x, y, volcano, col = terrain.colors(100), axes = FALSE)
contour(x, y, volcano, levels = seq(90, 200, by = 5),
        add = TRUE, col = "peru")
axis(1, at = seq(100, 800, by = 100))
axis(2, at = seq(100, 600, by = 100))
box()
title(main = "Maunga Whau Volcano", font.main = 4)
```

---

 layout

*Specifying Complex Plot Arrangements*


---

**Description**

`layout` divides the device up into as many rows and columns as there are in matrix `mat`, with the column-widths and the row-heights specified in the respective arguments.

**Usage**

```
layout(mat, widths = rep(1, ncol(mat)),
       heights = rep(1, nrow(mat)), respect = FALSE)

layout.show(n = 1)
lcm(x)
```

**Arguments**

`mat` a matrix object specifying the location of the next  $N$  figures on the output device. Each value in the matrix must be 0 or a positive integer. If  $N$  is the largest positive integer in the matrix, then the integers  $\{1, \dots, N-1\}$  must also appear at least once in the matrix.



<code>widths</code>	a vector of values for the widths of columns on the device. Relative widths are specified with numeric values. Absolute widths (in centimetres) are specified with the <code>lcm()</code> function (see examples).
<code>heights</code>	a vector of values for the heights of rows on the device. Relative and absolute heights can be specified, see <code>widths</code> above.
<code>respect</code>	either a logical value or a matrix object. If the latter, then it must have the same dimensions as <code>mat</code> and each value in the matrix must be either 0 or 1.
<code>n</code>	number of figures to plot.
<code>x</code>	a dimension to be interpreted as a number of centimetres.

### Details

Figure  $i$  is allocated a region composed from a subset of these rows and columns, based on the rows and columns in which  $i$  occurs in `mat`.

The `respect` argument controls whether a unit column-width is the same physical measurement on the device as a unit row-height.

There is a limit (currently 50) for the numbers of rows and columns in the layout, and also for the total number of cells (500).

`layout.show(n)` plots (part of) the current layout, namely the outlines of the next  $n$  figures.

`lcm` is a trivial function, to be used as *the* interface for specifying absolute dimensions for the `widths` and `heights` arguments of `layout()`.

### Value

`layout` returns the number of figures,  $N$ , see above.

### Warnings

These functions are totally incompatible with the other mechanisms for arranging plots on a device: `par(mfrow)`, `par(mfcol)` and `split.screen`.

### Author(s)

Paul R. Murrell

### References

Murrell, P. R. (1999) Layouts: A mechanism for arranging plots on a page. *Journal of Computational and Graphical Statistics*, **8**, 121-134.

Chapter 5 of Paul Murrell's Ph.D. thesis.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

### See Also

`par` with arguments `mfrow`, `mfcol`, or `mfg`.

**Examples**

```

def.par <- par(no.readonly = TRUE) # save default, for resetting...

## divide the device into two rows and two columns
## allocate figure 1 all of row 1
## allocate figure 2 the intersection of column 2 and row 2
layout(matrix(c(1,1,0,2), 2, 2, byrow = TRUE))
## show the regions that have been allocated to each plot
layout.show(2)

## divide device into two rows and two columns
## allocate figure 1 and figure 2 as above
## respect relations between widths and heights
nf <- layout(matrix(c(1,1,0,2), 2, 2, byrow=TRUE), respect=TRUE)
layout.show(nf)

## create single figure which is 5cm square
nf <- layout(matrix(1), widths=lcm(5), heights=lcm(5))
layout.show(nf)

##-- Create a scatterplot with marginal histograms -----

x <- pmin(3, pmax(-3, stats::rnorm(50)))
y <- pmin(3, pmax(-3, stats::rnorm(50)))
xhist <- hist(x, breaks=seq(-3,3,0.5), plot=FALSE)
yhist <- hist(y, breaks=seq(-3,3,0.5), plot=FALSE)
top <- max(c(xhist$counts, yhist$counts))
xrange <- c(-3,3)
yrange <- c(-3,3)
nf <- layout(matrix(c(2,0,1,3),2,2,byrow=TRUE), c(3,1), c(1,3), TRUE)
layout.show(nf)

par(mar=c(3,3,1,1))
plot(x, y, xlim=xrange, ylim=yrange, xlab="", ylab="")
par(mar=c(0,3,1,1))
barplot(xhist$counts, axes=FALSE, ylim=c(0, top), space=0)
par(mar=c(3,0,1,1))
barplot(yhist$counts, axes=FALSE, xlim=c(0, top), space=0, horiz=TRUE)

par(def.par)#- reset to default

```

---

legend

*Add Legends to Plots*


---

**Description**

This function can be used to add legends to plots. Note that a call to the function `locator(1)` can be used in place of the `x` and `y` arguments.

**Usage**

```

legend(x, y = NULL, legend, fill = NULL, col = par("col"),
       border="black", lty, lwd, pch,

```

```

angle = 45, density = NULL, bty = "o", bg = par("bg"),
box.lwd = par("lwd"), box.lty = par("lty"), box.col = par("fg"),
pt.bg = NA, cex = 1, pt.cex = cex, pt.lwd = lwd,
xjust = 0, yjust = 1, x.intersp = 1, y.intersp = 1,
adj = c(0, 0.5), text.width = NULL, text.col = par("col"),
merge = do.lines && has.pch, trace = FALSE,
plot = TRUE, ncol = 1, horiz = FALSE, title = NULL,
inset = 0, xpd, title.col = text.col)

```

### Arguments

<code>x, y</code>	the x and y co-ordinates to be used to position the legend. They can be specified by keyword or in any way which is accepted by <code>xy.coords</code> : See 'Details'.
<code>legend</code>	a character or <a href="#">expression</a> vector. of length $\geq 1$ to appear in the legend. Other objects will be coerced by <code>as.graphicsAnnot</code> .
<code>fill</code>	if specified, this argument will cause boxes filled with the specified colors (or shaded in the specified colors) to appear beside the legend text.
<code>col</code>	the color of points or lines appearing in the legend.
<code>border</code>	the border color for the boxes (used only if <code>fill</code> is specified).
<code>lty, lwd</code>	the line types and widths for lines appearing in the legend. One of these two <i>must</i> be specified for line drawing.
<code>pch</code>	the plotting symbols appearing in the legend, either as vector of 1-character strings, or one (multi character) string. <i>Must</i> be specified for symbol drawing.
<code>angle</code>	angle of shading lines.
<code>density</code>	the density of shading lines, if numeric and positive. If NULL or negative or NA color filling is assumed.
<code>bty</code>	the type of box to be drawn around the legend. The allowed values are "o" (the default) and "n".
<code>bg</code>	the background color for the legend box. (Note that this is only used if <code>bty != "n"</code> .)
<code>box.lty, box.lwd, box.col</code>	the line type, width and color for the legend box (if <code>bty = "o"</code> ).
<code>pt.bg</code>	the background color for the <a href="#">points</a> , corresponding to its argument <code>bg</code> .
<code>cex</code>	character expansion factor <b>relative</b> to current <code>par("cex")</code> . Used for text, and provides the default for <code>pt.cex</code> and <code>title.cex</code> .
<code>pt.cex</code>	expansion factor(s) for the points.
<code>pt.lwd</code>	line width for the points, defaults to the one for lines, or if that is not set, to <code>par("lwd")</code> .
<code>xjust</code>	how the legend is to be justified relative to the legend x location. A value of 0 means left justified, 0.5 means centered and 1 means right justified.
<code>yjust</code>	the same as <code>xjust</code> for the legend y location.
<code>x.intersp</code>	character interspacing factor for horizontal (x) spacing.
<code>y.intersp</code>	the same for vertical (y) line distances.
<code>adj</code>	numeric of length 1 or 2; the string adjustment for legend text. Useful for y-adjustment when <code>labels</code> are <a href="#">plotmath</a> expressions.

<code>text.width</code>	the width of the legend text in <code>x</code> ("user") coordinates. (Should be positive even for a reversed <code>x</code> axis.) Defaults to the proper value computed by <code>strwidth(legend)</code> .
<code>text.col</code>	the color used for the legend text.
<code>merge</code>	logical; if <code>TRUE</code> , merge points and lines but not filled boxes. Defaults to <code>TRUE</code> if there are points and lines.
<code>trace</code>	logical; if <code>TRUE</code> , shows how <code>legend</code> does all its magical computations.
<code>plot</code>	logical. If <code>FALSE</code> , nothing is plotted but the sizes are returned.
<code>ncol</code>	the number of columns in which to set the legend items (default is 1, a vertical legend).
<code>horiz</code>	logical; if <code>TRUE</code> , set the legend horizontally rather than vertically (specifying <code>horiz</code> overrides the <code>ncol</code> specification).
<code>title</code>	a character string or length-one expression giving a title to be placed at the top of the legend. Other objects will be coerced by <code>as.graphicsAnnot</code> .
<code>inset</code>	inset distance(s) from the margins as a fraction of the plot region when legend is placed by keyword.
<code>xpd</code>	if supplied, a value of the graphical parameter <code>xpd</code> to be used while the legend is being drawn.
<code>title.col</code>	color for <code>title</code> .

### Details

Arguments `x`, `y`, `legend` are interpreted in a non-standard way to allow the coordinates to be specified *via* one or two arguments. If `legend` is missing and `y` is not numeric, it is assumed that the second argument is intended to be `legend` and that the first argument specifies the coordinates.

The coordinates can be specified in any way which is accepted by `xy.coords`. If this gives the coordinates of one point, it is used as the top-left coordinate of the rectangle containing the legend. If it gives the coordinates of two points, these specify opposite corners of the rectangle (either pair of corners, in any order).

The location may also be specified by setting `x` to a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center". This places the legend on the inside of the plot frame at the given location. Partial argument matching is used. The optional `inset` argument specifies how far the legend is inset from the plot margins. If a single value is given, it is used for both margins; if two values are given, the first is used for `x`- distance, the second for `y`-distance.

Attribute arguments such as `col`, `pch`, `lty`, etc, are recycled if necessary: `merge` is not.

Points are drawn *after* lines in order that they can cover the line with their background color `pt.bg`, if applicable.

See the examples for how to right-justify labels.

### Value

A list with list components

<code>rect</code>	a list with components <code>w</code> , <code>h</code> positive numbers giving <b>w</b> idth and <b>h</b> eight of the legend's box. <code>left</code> , <code>top</code> <code>x</code> and <code>y</code> coordinates of upper left corner of the box.
<code>text</code>	a list with components

`x`, `y` numeric vectors of length `length(legend)`, giving the `x` and `y` coordinates of the legend's text(s).

returned invisibly.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

## See Also

[plot](#), [barplot](#) which uses `legend()`, and [text](#) for more examples of math expressions.

## Examples

```
## Run the example in '?matplot' or the following:
leg.txt <- c("Setosa      Petals", "Setosa      Sepals",
            "Versicolor Petals", "Versicolor Sepals")
y.leg <- c(4.5, 3, 2.1, 1.4, .7)
cexv <- c(1.2, 1, 4/5, 2/3, 1/2)
matplot(c(1,8), c(0,4.5), type = "n", xlab = "Length", ylab = "Width",
        main = "Petal and Sepal Dimensions in Iris Blossoms")
for (i in seq(cexv)) {
  text(1, y.leg[i]-.1, paste("cex=", formatC(cexv[i])), cex=.8, adj = 0)
  legend(3, y.leg[i], leg.txt, pch = "sSvV", col = c(1, 3), cex = cexv[i])
}

## 'merge = TRUE' for merging lines & points:
x <- seq(-pi, pi, len = 65)
plot(x, sin(x), type = "l", ylim = c(-1.2, 1.8), col = 3, lty = 2)
points(x, cos(x), pch = 3, col = 4)
lines(x, tan(x), type = "b", lty = 1, pch = 4, col = 6)
title("legend(..., lty = c(2, -1, 1), pch = c(-1,3,4), merge = TRUE)",
      cex.main = 1.1)
legend(-1, 1.9, c("sin", "cos", "tan"), col = c(3,4,6),
       text.col = "green4", lty = c(2, -1, 1), pch = c(-1, 3, 4),
       merge = TRUE, bg = 'gray90')

## right-justifying a set of labels: thanks to Uwe Ligges
x <- 1:5; y1 <- 1/x; y2 <- 2/x
plot(rep(x, 2), c(y1, y2), type="n", xlab="x", ylab="y")
lines(x, y1); lines(x, y2, lty=2)
temp <- legend("topright", legend = c(" ", " "),
              text.width = strwidth("1,000,000"),
              lty = 1:2, xjust = 1, yjust = 1,
              title = "Line Types")
text(temp$rect$left + temp$rect$w, temp$text$y,
      c("1,000", "1,000,000"), pos=2)

##--- log scaled Examples -----
leg.txt <- c("a one", "a two")

par(mfrow = c(2,2))
for(ll in c("", "x", "y", "xy")) {
```

```

plot(2:10, log=11, main=paste("log = ",11,"", sep=""))
abline(1,1)
lines(2:3,3:4, col=2) #
points(2,2, col=3) #
rect(2,3,3,2, col=4)
text(c(3,3),2:3, c("rect(2,3,3,2, col=4)",
                  "text(c(3,3),2:3,\"c(rect(...)\")"), adj = c(0,.3))
legend(list(x=2,y=8), legend = leg.txt, col=2:3, pch=1:2,
        lty=1, merge=TRUE)#, trace=TRUE)
}
par(mfrow=c(1,1))

##-- Math expressions: -----
x <- seq(-pi, pi, len = 65)
plot(x, sin(x), type="l", col = 2, xlab = expression(phi),
      ylab = expression(f(phi)))
abline(h=-1:1, v=pi/2*(-6:6), col="gray90")
lines(x, cos(x), col = 3, lty = 2)
ex.cs1 <- expression(plain(sin) * phi, paste("cos", phi))# 2 ways
utils::str(legend(-3, .9, ex.cs1, lty=1:2, plot=FALSE,
                 adj = c(0, .6)))# adj y !
legend(-3, .9, ex.cs1, lty=1:2, col=2:3, adj = c(0, .6))

require(stats)
x <- rexp(100, rate = .5)
hist(x, main = "Mean and Median of a Skewed Distribution")
abline(v = mean(x), col=2, lty=2, lwd=2)
abline(v = median(x), col=3, lty=3, lwd=2)
ex12 <- expression(bar(x) == sum(over(x[i], n), i==1, n),
                  hat(x) == median(x[i], i==1,n))
utils::str(legend(4.1, 30, ex12, col = 2:3, lty=2:3, lwd=2))

## 'Filled' boxes -- for more, see example(plot.factor)
op <- par(bg="white") # to get an opaque box for the legend
plot(cut(weight, 3) ~ group, data = PlantGrowth, col = NULL,
     density = 16*(1:3))
par(op)

## Using 'ncol' :
x <- 0:64/64
matplot(x, outer(x, 1:7, function(x, k) sin(k * pi * x)),
        type = "o", col = 1:7, ylim = c(-1, 1.5), pch = "*")
op <- par(bg="antiquewhite1")
legend(0, 1.5, paste("sin(", 1:7, "pi * x)"), col=1:7, lty=1:7,
      pch = "*", ncol = 4, cex = 0.8)
legend(.8,1.2, paste("sin(", 1:7, "pi * x)"), col=1:7, lty=1:7,
      pch = "*", cex = 0.8)
legend(0, -.1, paste("sin(", 1:4, "pi * x)"), col=1:4, lty=1:4,
      ncol = 2, cex = 0.8)
legend(0, -.4, paste("sin(", 5:7, "pi * x)"), col=4:6, pch=24,
      ncol = 2, cex = 1.5, lwd = 2, pt.bg = "pink", pt.cex = 1:3)
par(op)

## point covering line :
y <- sin(3*pi*x)
plot(x, y, type="l", col="blue",
     main = "points with bg & legend(*, pt.bg)")

```

```

points(x, y, pch=21, bg="white")
legend(.4,1, "sin(c x)", pch=21, pt.bg="white", lty=1, col = "blue")

## legends with titles at different locations
plot(x, y, type='n')
legend("bottomright", "(x,y)", pch=1, title="bottomright")
legend("bottom", "(x,y)", pch=1, title="bottom")
legend("bottomleft", "(x,y)", pch=1, title="bottomleft")
legend("left", "(x,y)", pch=1, title="left")
legend("topleft", "(x,y)", pch=1, title="topleft", inset = .05,
      inset = .05)
legend("top", "(x,y)", pch=1, title="top")
legend("topright", "(x,y)", pch=1, title="topright", inset = .02,
      inset = .02)
legend("right", "(x,y)", pch=1, title="right")
legend("center", "(x,y)", pch=1, title="center")

```

---

lines

---

*Add Connected Line Segments to a Plot*


---

### Description

A generic function taking coordinates given in various ways and joining the corresponding points with line segments.

### Usage

```

lines(x, ...)

## Default S3 method:
lines(x, y = NULL, type = "l", ...)

```

### Arguments

<code>x, y</code>	coordinate vectors of points to join.
<code>type</code>	character indicating the type of plotting; actually any of the types as in <a href="#">plot.default</a> .
<code>...</code>	Further graphical parameters (see <a href="#">par</a> ) may also be supplied as arguments, particularly, line type, <code>lty</code> , line width, <code>lwd</code> , color, <code>col</code> and for <code>type = "b"</code> , <code>pch</code> . Also the line characteristics <code>lend</code> , <code>ljoin</code> and <code>lmitre</code> .

### Details

The coordinates can be passed in a plotting structure (a list with `x` and `y` components), a two-column matrix, a time series, .... See [xy.coords](#). If supplied separately, they must be of the same length.

The coordinates can contain NA values. If a point contains NA in either its `x` or `y` value, it is omitted from the plot, and lines are not drawn to or from such points. Thus missing values can be used to achieve breaks in lines.

For `type = "h"`, `col` can be a vector and will be recycled as needed.

`lwd` can be a vector: its first element will apply to lines but the whole vector to symbols (recycled as necessary).

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[points](#), particularly for `type %in% c("p", "b", "o")`, [plot](#), and the workhorse function [plot.xy](#).

[abline](#) for drawing (single) straight lines.

[par](#) for how to specify colors.

## Examples

```
# draw a smooth line through a scatter plot
plot(cars, main="Stopping Distance versus Speed")
lines(stats::lowess(cars))
```

---

locator

*Graphical Input*

---

## Description

Reads the position of the graphics cursor when the (first) mouse button is pressed.

## Usage

```
locator(n = 512, type = "n", ...)
```

## Arguments

<code>n</code>	the maximum number of points to locate. Valid values start at 1.
<code>type</code>	One of "n", "p", "l" or "o". If "p" or "o" the points are plotted; if "l" or "o" they are joined by lines.
<code>...</code>	additional graphics parameters used if <code>type != "n"</code> for plotting the locations.

## Details

`locator` is only supported on screen devices such as `X11`, `windows` and `quartz`. On other devices the call will do nothing.

Unless the process is terminated prematurely by the user (see below) at most `n` positions are determined.

For the usual `X11` device the identification process is terminated by pressing any mouse button other than the first. For the `quartz` device the process is terminated by pressing the ESC key.

The current graphics parameters apply just as if `plot.default` has been called with the same value of `type`. The plotting of the points and lines is subject to clipping, but locations outside the current clipping rectangle will be returned.

On most devices which support `locator`, successful selection of a point is indicated by a bell sound unless `options(locatorBell=FALSE)` has been set.



If the window is resized or hidden and then exposed before the input process has terminated, any lines or points drawn by `locator` will disappear. These will reappear once the input process has terminated and the window is resized or hidden and exposed again. This is because the points and lines drawn by `locator` are not recorded in the device's display list until the input process has terminated.

### Value

A list containing `x` and `y` components which are the coordinates of the identified points in the user coordinate system, i.e., the one specified by `par("usr")`.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[identify](#)

---

matplot

*Plot Columns of Matrices*

---

### Description

Plot the columns of one matrix against the columns of another.

### Usage

```
matplot(x, y, type = "p", lty = 1:5, lwd = 1, lend = par("lend"),
        pch = NULL,
        col = 1:6, cex = NULL, bg = NA,
        xlab = NULL, ylab = NULL, xlim = NULL, ylim = NULL,
        ..., add = FALSE, verbose = getOption("verbose"))
```

```
matpoints(x, y, type = "p", lty = 1:5, lwd = 1, pch = NULL,
          col = 1:6, ...)
```

```
matlines(x, y, type = "l", lty = 1:5, lwd = 1, pch = NULL,
         col = 1:6, ...)
```

### Arguments

<code>x, y</code>	vectors or matrices of data for plotting. The number of rows should match. If one of them are missing, the other is taken as <code>y</code> and an <code>x</code> vector of <code>1:n</code> is used. Missing values (NAs) are allowed.
<code>type</code>	character string (length 1 vector) or vector of 1-character strings indicating the type of plot for each column of <code>y</code> , see <a href="#">plot</a> for all possible types. The first character of <code>type</code> defines the first plot, the second character the second, etc. Characters in <code>type</code> are cycled through; e.g., "pl" alternately plots points and lines.

<code>lty, lwd, lend</code>	vector of line types, widths, and end styles. The first element is for the first column, the second element for the second column, etc., even if lines are not plotted for all columns. Line types will be used cyclically until all plots are drawn.
<code>pch</code>	character string or vector of 1-characters or integers for plotting characters, see <a href="#">points</a> . The first character is the plotting-character for the first plot, the second for the second, etc. The default is the digits (1 through 9, 0) then the lowercase and uppercase letters.
<code>col</code>	vector of colors. Colors are used cyclically.
<code>cex</code>	vector of character expansion sizes, used cyclically. This works as a multiple of <code>par("cex")</code> . NULL is equivalent to 1.0.
<code>bg</code>	vector of background (fill) colors for the open plot symbols given by <code>pch=21:25</code> as in <a href="#">points</a> . The default NA corresponds to the one of the underlying function <code>plot.xy</code> .
<code>xlab, ylab</code>	titles for x and y axes, as in <a href="#">plot</a> .
<code>xlim, ylim</code>	ranges of x and y axes, as in <a href="#">plot</a> .
<code>...</code>	Graphical parameters (see <a href="#">par</a> ) and any further arguments of <code>plot</code> , typically <code>plot.default</code> , may also be supplied as arguments to this function. Hence, the high-level graphics control arguments described under <a href="#">par</a> and the arguments to <a href="#">title</a> may be supplied to this function.
<code>add</code>	logical. If TRUE, plots are added to current one, using <a href="#">points</a> and <a href="#">lines</a> .
<code>verbose</code>	logical. If TRUE, write one line of what is done.

### Details

Points involving missing values are not plotted.

The first column of `x` is plotted against the first column of `y`, the second column of `x` against the second column of `y`, etc. If one matrix has fewer columns, plotting will cycle back through the columns again. (In particular, either `x` or `y` may be a vector, against which all columns of the other argument will be plotted.)

The first element of `col`, `cex`, `lty`, `lwd` is used to plot the axes as well as the first line.

Because plotting symbols are drawn with lines and because these functions may be changing the line style, you should probably specify `lty=1` when using plotting symbols.

### Side Effects

Function `matplot` generates a new plot; `matpoints` and `matlines` add to the current one.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[plot](#), [points](#), [lines](#), [matrix](#), [par](#).

**Examples**

```

require(grDevices)
matplot((-4:5)^2, main = "Quadratic") # almost identical to plot(*)
sines <- outer(1:20, 1:4, function(x, y) sin(x / 20 * pi * y))
matplot(sines, pch = 1:4, type = "o", col = rainbow(ncol(sines)))
matplot(sines, type = "b", pch = 21:23, col = 2:5, bg = 2:5,
        main = "matplot(..., pch = 21:23, bg = 2:5)")

x <- 0:50/50
matplot(x, outer(x, 1:8, function(x, k) sin(k*pi * x)),
        ylim = c(-2,2), type = "plobcsSh",
        main= "matplot(,type = \"plobcsSh\" )")
## pch & type = vector of 1-chars :
matplot(x, outer(x, 1:4, function(x, k) sin(k*pi * x)),
        pch = letters[1:4], type = c("b","p","o"))

lends <- c("round","butt","square")
matplot(matrix(1:12, 4), type="c", lty=1, lwd=10, lend=lends)
text(cbind(2.5, 2*c(1,3,5)-.4), lends, col= 1:3, cex = 1.5)

table(iris$Species) # is data.frame with 'Species' factor
iS <- iris$Species == "setosa"
iV <- iris$Species == "versicolor"
op <- par(bg = "bisque")
matplot(c(1, 8), c(0, 4.5), type= "n", xlab = "Length", ylab = "Width",
        main = "Petal and Sepal Dimensions in Iris Blossoms")
matpoints(iris[iS,c(1,3)], iris[iS,c(2,4)], pch = "sS", col = c(2,4))
matpoints(iris[iV,c(1,3)], iris[iV,c(2,4)], pch = "vV", col = c(2,4))
legend(1, 4, c("Setosa Petals", "Setosa Sepals",
              "Versicolor Petals", "Versicolor Sepals"),
      pch = "sSvV", col = rep(c(2,4), 2))

nam.var <- colnames(iris)[-5]
nam.spec <- as.character(iris[1+50*0:2, "Species"])
iris.S <- array(NA, dim = c(50,4,3),
              dimnames = list(NULL, nam.var, nam.spec))
for(i in 1:3) iris.S[,i] <- data.matrix(iris[1:50+50*(i-1), -5])

matplot(iris.S[, "Petal.Length", ], iris.S[, "Petal.Width", ], pch="SCV",
        col = rainbow(3, start = .8, end = .1),
        sub = paste(c("S", "C", "V"), dimnames(iris.S)[[3]],
                  sep = "=", collapse= " "),
        main = "Fisher's Iris Data")
par(op)

```

mosaicplot

*Mosaic Plots***Description**

Plots a mosaic on the current graphics device.

**Usage**

```
mosaicplot(x, ...)

## Default S3 method:
mosaicplot(x, main = deparse(substitute(x)),
           sub = NULL, xlab = NULL, ylab = NULL,
           sort = NULL, off = NULL, dir = NULL,
           color = NULL, shade = FALSE, margin = NULL,
           cex.axis = 0.66, las = par("las"),
           type = c("pearson", "deviance", "FT"), ...)

## S3 method for class 'formula':
mosaicplot(formula, data = NULL, ...,
           main = deparse(substitute(data)), subset,
           na.action = stats::na.omit)
```

**Arguments**

<code>x</code>	a contingency table in array form, with optional category labels specified in the <code>dimnames(x)</code> attribute. The table is best created by the <code>table()</code> command.
<code>main</code>	character string for the mosaic title.
<code>sub</code>	character string for the mosaic sub-title (at bottom).
<code>xlab, ylab</code>	x- and y-axis labels used for the plot; by default, the first and second element of <code>names(dimnames(X))</code> (i.e., the name of the first and second variable in <code>X</code> ).
<code>sort</code>	vector ordering of the variables, containing a permutation of the integers <code>1:length(dim(x))</code> (the default).
<code>off</code>	vector of offsets to determine percentage spacing at each level of the mosaic (appropriate values are between 0 and 20, and the default is 20 times the number of splits for 2-dimensional tables, and 10 otherwise. Rescaled to maximally 50, and recycled if necessary).
<code>dir</code>	vector of split directions ("v" for vertical and "h" for horizontal) for each level of the mosaic, one direction for each dimension of the contingency table. The default consists of alternating directions, beginning with a vertical split.
<code>color</code>	logical or (recycling) vector of colors for color shading, used only when <code>shade</code> is <code>FALSE</code> , or <code>NULL</code> (default). By default, grey boxes are drawn. <code>color=TRUE</code> uses a gamma-corrected grey palette. <code>color=FALSE</code> gives empty boxes with no shading.
<code>shade</code>	a logical indicating whether to produce extended mosaic plots, or a numeric vector of at most 5 distinct positive numbers giving the absolute values of the cut points for the residuals. By default, <code>shade</code> is <code>FALSE</code> , and simple mosaics are created. Using <code>shade = TRUE</code> cuts absolute values at 2 and 4.
<code>margin</code>	a list of vectors with the marginal totals to be fit in the log-linear model. By default, an independence model is fitted. See <a href="#">loglin</a> for further information.
<code>cex.axis</code>	The magnification to be used for axis annotation, as a multiple of <code>par("cex")</code> .
<code>las</code>	numeric; the style of axis labels, see <a href="#">par</a> .
<code>type</code>	a character string indicating the type of residual to be represented. Must be one of "pearson" (giving components of Pearson's $\chi^2$ ), "deviance" (giving components of the likelihood ratio $\chi^2$ ), or "FT" for the Freeman-Tukey residuals. The value of this argument can be abbreviated.

<code>formula</code>	a formula, such as $y \sim x$ .
<code>data</code>	a data frame (or list), or a contingency table from which the variables in <code>formula</code> should be taken.
<code>...</code>	further arguments to be passed to or from methods.
<code>subset</code>	an optional vector specifying a subset of observations in the data frame to be used for plotting.
<code>na.action</code>	a function which indicates what should happen when the data contains variables to be cross-tabulated, and these variables contain NAs. The default is to omit cases which have an NA in any variable. Since the tabulation will omit all cases containing missing values, this will only be useful if the <code>na.action</code> function replaces missing values.

### Details

This is a generic function. It currently has a default method (`mosaicplot.default`) and a formula interface (`mosaicplot.formula`).

Extended mosaic displays visualize standardized residuals of a loglinear model for the table by color and outline of the mosaic's tiles. (Standardized residuals are often referred to a standard normal distribution.) Negative residuals are drawn in shaded of red and with broken outlines; positive ones are drawn in blue with solid outlines.

For the formula method, if `data` is an object inheriting from classes "table" or "ftable", or an array with more than 2 dimensions, it is taken as a contingency table, and hence all entries should be nonnegative. In this case, the left-hand side of `formula` should be empty, and the variables on the right-hand side should be taken from the names of the `dimnames` attribute of the contingency table. A marginal table of these variables is computed, and a mosaic of this table is produced.

Otherwise, `data` should be a data frame or matrix, list or environment containing the variables to be cross-tabulated. In this case, after possibly selecting a subset of the data as specified by the `subset` argument, a contingency table is computed from the variables given in `formula`, and a mosaic is produced from this.

See Emerson (1998) for more information and a case study with television viewer data from Nielsen Media Research.

Missing values are not supported except via an `na.action` function when `data` contains variables to be cross-tabulated.

A more flexible and extensible implementation of mosaic plots written in the grid graphics system is provided in the function `mosaic` in the contributed package `vcd` (Meyer, Zeileis and Hornik, 2005).

### Author(s)

S-PLUS original by John Emerson <john.emerson@yale.edu>. Originally modified and enhanced for R by Kurt Hornik.

### References

- Hartigan, J.A., and Kleiner, B. (1984) A mosaic of television ratings. *The American Statistician*, **38**, 32–35.
- Emerson, J. W. (1998) Mosaic displays in S-PLUS: A general implementation and a case study. *Statistical Computing and Graphics Newsletter (ASA)*, **9**, 1, 17–23.
- Friendly, M. (1994) Mosaic displays for multi-way contingency tables. *Journal of the American Statistical Association*, **89**, 190–200.

Meyer, D., Zeileis, A., and Hornik, K. (2005) The strucplot framework: Visualizing multi-way contingency tables with vcd. *Report 22*, Department of Statistics and Mathematics, Wirtschaftsuniversität Wien, Research Report Series. [http://epub.wu-wien.ac.at/dyn/openURL?id=oai:epub.wu-wien.ac.at:epub-wu-01\\_8a1](http://epub.wu-wien.ac.at/dyn/openURL?id=oai:epub.wu-wien.ac.at:epub-wu-01_8a1)

The home page of Michael Friendly (<http://www.math.yorku.ca/SCS/friendly.html>) provides information on various aspects of graphical methods for analyzing categorical data, including mosaic plots.

### See Also

[assocplot](#), [loglin](#).

### Examples

```
require(stats)
mosaicplot(Titanic, main = "Survival on the Titanic", color = TRUE)
## Formula interface for tabulated data:
mosaicplot(~ Sex + Age + Survived, data = Titanic, color = TRUE)

mosaicplot(HairEyeColor, shade = TRUE)
## Independence model of hair and eye color and sex. Indicates that
## there are more blue eyed blonde females than expected in the case
## of independence and too few brown eyed blonde females.
## The corresponding model is:
fm <- loglin(HairEyeColor, list(1, 2, 3))
pchisq(fm$pearson, fm$df, lower.tail = FALSE)

mosaicplot(HairEyeColor, shade = TRUE, margin = list(1:2, 3))
## Model of joint independence of sex from hair and eye color. Males
## are underrepresented among people with brown hair and eyes, and are
## overrepresented among people with brown hair and blue eyes.
## The corresponding model is:
fm <- loglin(HairEyeColor, list(1:2, 3))
pchisq(fm$pearson, fm$df, lower.tail = FALSE)

## Formula interface for raw data: visualize cross-tabulation of numbers
## of gears and carburettors in Motor Trend car data.
mosaicplot(~ gear + carb, data = mtcars, color = TRUE, las = 1)
# color recycling
mosaicplot(~ gear + carb, data = mtcars, color = 2:3, las = 1)
```

---

mtext

*Write Text into the Margins of a Plot*


---

### Description

Text is written in one of the four margins of the current figure region or one of the outer margins of the device region.

### Usage

```
mtext(text, side = 3, line = 0, outer = FALSE, at = NA,
      adj = NA, padj = NA, cex = NA, col = NA, font = NA, ...)
```

## Arguments

<code>text</code>	a character or <a href="#">expression</a> vector specifying the <i>text</i> to be written. Other objects are coerced by <code>as.graphicsAnnot</code> .
<code>side</code>	on which side of the plot (1=bottom, 2=left, 3=top, 4=right).
<code>line</code>	on which MARGin line, starting at 0 counting outwards.
<code>outer</code>	use outer margins if available.
<code>at</code>	give location of each string in user coordinates. If the component of <code>at</code> corresponding to a particular text item is not a finite value (the default), the location will be determined by <code>adj</code> .
<code>adj</code>	adjustment for each string in reading direction. For strings parallel to the axes, <code>adj = 0</code> means left or bottom alignment, and <code>adj = 1</code> means right or top alignment. If <code>adj</code> is not a finite value (the default), the value of <code>par("las")</code> determines the adjustment. For strings plotted parallel to the axis the default is to centre the string.
<code>padj</code>	adjustment for each string perpendicular to the reading direction (which is controlled by <code>adj</code> ). For strings parallel to the axes, <code>padj = 0</code> means right or top alignment, and <code>padj = 1</code> means left or bottom alignment. If <code>padj</code> is not a finite value (the default), the value of <code>par("las")</code> determines the adjustment. For strings plotted perpendicular to the axis the default is to centre the string.
<code>cex</code>	character expansion factor. <code>NULL</code> and <code>NA</code> are equivalent to <code>1.0</code> . This is an absolute measure, not scaled by <code>par("cex")</code> or by setting <code>par("mfrow")</code> or <code>par("mfcol")</code> . Can be a vector.
<code>col</code>	color to use. Can be a vector. <code>NA</code> values (the default) mean use <code>par("col")</code> .
<code>font</code>	font for text. Can be a vector. <code>NA</code> values (the default) mean use <code>par("font")</code> .
<code>...</code>	Further graphical parameters (see <a href="#">par</a> ), including <code>family</code> , <code>las</code> and <code>xpd</code> . (The latter defaults to the figure region unless <code>outer = TRUE</code> , otherwise the device region. It can only be increased.)

## Details

The user coordinates in the outer margins always range from zero to one, and are not affected by the user coordinates in the figure region(s) — R differs here from other implementations of S.

All of the named arguments can be vectors, and recycling will take place to plot as many strings as the longest of the vector arguments.

Note that a vector `adj` has a different meaning from `text`. `adj = 0.5` will centre the string, but for `outer=TRUE` on the device region rather than the plot region.

Parameter `las` will determine the orientation of the string(s). For strings plotted perpendicular to the axis the default justification is to place the end of the string nearest the axis on the specified line. (Note that this differs from S, which uses `srt` if `at` is supplied and `las` if it is not. Parameter `srt` is ignored in R.)

Note that if the text is to be plotted perpendicular to the axis, `adj` determines the justification of the string *and* the position along the axis unless `at` is specified.

## Side Effects

The given text is written onto the current plot.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[title](#), [text](#), [plot](#), [par](#); [plotmath](#) for details on mathematical annotation.

**Examples**

```
plot(1:10, (-4:5)^2, main="Parabola Points", xlab="xlab")
mtext("10 of them")
for(s in 1:4)
  mtext(paste("mtext(..., line= -1, {side, col, font} = ", s,
             ", cex = ", (1+s)/2, ")"), line = -1,
        side=s, col=s, font=s, cex= (1+s)/2)
mtext("mtext(..., line= -2)", line = -2)
mtext("mtext(..., line= -2, adj = 0)", line = -2, adj = 0)
##--- log axis :
plot(1:10, exp(1:10), log='y', main="log='y'", xlab="xlab")
for(s in 1:4) mtext(paste("mtext(...,side=",s,")"), side=s)
```

---

pairs

*Scatterplot Matrices*

---

**Description**

A matrix of scatterplots is produced.

**Usage**

```
pairs(x, ...)

## S3 method for class 'formula':
pairs(formula, data = NULL, ..., subset,
      na.action = stats::na.pass)

## Default S3 method:
pairs(x, labels, panel = points, ...,
      lower.panel = panel, upper.panel = panel,
      diag.panel = NULL, text.panel = textPanel,
      label.pos = 0.5 + has.diag/3,
      cex.labels = NULL, font.labels = 1,
      rowlattice = TRUE, gap = 1)
```

**Arguments**

**x** the coordinates of points given as numeric columns of a matrix or dataframe. Logical and factor columns are converted to numeric in the same way that [data.matrix](#) does.



<code>formula</code>	a formula, such as <code>~ x + y + z</code> . Each term will give a separate variable in the pairs plot, so terms should be numeric vectors. (A response will be interpreted as another variable, but not treated specially, so it is confusing to use one.)
<code>data</code>	a <code>data.frame</code> (or list) from which the variables in <code>formula</code> should be taken.
<code>subset</code>	an optional vector specifying a subset of observations to be used for plotting.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. The default is to pass missing values on to the panel functions, but <code>na.action = na.omit</code> will cause cases with missing values in any of the variables to be omitted entirely.
<code>labels</code>	the names of the variables.
<code>panel</code>	<code>function(x, y, ...)</code> which is used to plot the contents of each panel of the display.
<code>...</code>	arguments to be passed to or from methods. Also, graphical parameters can be given as arguments to <code>plot</code> such as <code>main.par("oma")</code> will be set appropriately unless specified.
<code>lower.panel, upper.panel</code>	separate panel functions to be used below and above the diagonal respectively.
<code>diag.panel</code>	optional <code>function(x, ...)</code> to be applied on the diagonals.
<code>text.panel</code>	optional <code>function(x, y, labels, cex, font, ...)</code> to be applied on the diagonals.
<code>label.pos</code>	y position of labels in the text panel.
<code>cex.labels, font.labels</code>	graphics parameters for the text panel.
<code>rowlattice</code>	logical. Should the layout be matrix-like with row 1 at the top, or graph-like with row 1 at the bottom?
<code>gap</code>	Distance between subplots, in margin lines.

### Details

The  $ij$ th scatterplot contains  $x[, i]$  plotted against  $x[, j]$ . The scatterplot can be customised by setting panel functions to appear as something completely different. The off-diagonal panel functions are passed the appropriate columns of  $x$  as  $x$  and  $y$ : the diagonal panel function (if any) is passed a single column, and the `text.panel` function is passed a single  $(x, y)$  location and the column name.

The graphical parameters `pch` and `col` can be used to specify a vector of plotting symbols and colors to be used in the plots.

The graphical parameter `oma` will be set by `pairs.default` unless supplied as an argument.

A panel function should not attempt to start a new plot, but just plot within a given coordinate system: thus `plot` and `boxplot` are not panel functions.

By default, missing values are passed to the panel functions and will often be ignored within a panel. However, for the formula method and `na.action = na.omit`, all cases which contain a missing values for any of the variables are omitted completely (including when the scales are selected).

### Author(s)

Enhancements for R 1.0.0 contributed by Dr. Jens Oehlschlaegel-Akiyoshi and R-core members.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## Examples

```

pairs(iris[1:4], main = "Anderson's Iris Data -- 3 species",
      pch = 21, bg = c("red", "green3", "blue")[unclass(iris$Species)])

## formula method
pairs(~ Fertility + Education + Catholic, data = swiss,
      subset = Education < 20, main = "Swiss data, Education < 20")

pairs(USJudgeRatings)

## put histograms on the diagonal
panel.hist <- function(x, ...)
{
  usr <- par("usr"); on.exit(par(usr))
  par(usr = c(usr[1:2], 0, 1.5) )
  h <- hist(x, plot = FALSE)
  breaks <- h$breaks; nB <- length(breaks)
  y <- h$counts; y <- y/max(y)
  rect(breaks[-nB], 0, breaks[-1], y, col="cyan", ...)
}
pairs(USJudgeRatings[1:5], panel=panel.smooth,
      cex = 1.5, pch = 24, bg="light blue",
      diag.panel=panel.hist, cex.labels = 2, font.labels=2)

## put (absolute) correlations on the upper panels,
## with size proportional to the correlations.
panel.cor <- function(x, y, digits=2, prefix="", cex.cor, ...)
{
  usr <- par("usr"); on.exit(par(usr))
  par(usr = c(0, 1, 0, 1))
  r <- abs(cor(x, y))
  txt <- format(c(r, 0.123456789), digits=digits)[1]
  txt <- paste(prefix, txt, sep="")
  if(missing(cex.cor)) cex.cor <- 0.8/strwidth(txt)
  text(0.5, 0.5, txt, cex = cex.cor * r)
}
pairs(USJudgeRatings, lower.panel=panel.smooth, upper.panel=panel.cor)

```

---

panel.smooth

*Simple Panel Plot*

---

## Description

An example of a simple useful panel function to be used as argument in e.g., [coplot](#) or [pairs](#).

## Usage

```

panel.smooth(x, y, col = par("col"), bg = NA, pch = par("pch"),
            cex = 1, col.smooth = "red", span = 2/3, iter = 3,
            ...)

```

**Arguments**

<code>x, y</code>	numeric vectors of the same length
<code>col, bg, pch, cex</code>	numeric or character codes for the color(s), point type and size of <code>points</code> ; see also <code>par</code> .
<code>col.smooth</code>	color to be used by lines for drawing the smooths.
<code>span</code>	smoothing parameter <code>f</code> for <code>lowess</code> , see there.
<code>iter</code>	number of robustness iterations for <code>lowess</code> .
<code>...</code>	further arguments to <code>lines</code> .

**See Also**

`coplot` and `pairs` where `panel.smooth` is typically used; `lowess` which does the smoothing.

**Examples**

```
pairs(swiss, panel = panel.smooth, pch = ".")# emphasize the smooths
pairs(swiss, panel = panel.smooth, lwd = 2, cex= 1.5, col="blue")# hmm...
```

---

 par

*Set or Query Graphical Parameters*


---

**Description**

`par` can be used to set or query graphical parameters. Parameters can be set by specifying them as arguments to `par` in `tag = value` form, or by passing them as a list of tagged values.

**Usage**

```
par(..., no.readonly = FALSE)

<highlevel plot> (... , <tag> = <value>)
```

**Arguments**

<code>...</code>	arguments in <code>tag = value</code> form, or a list of tagged values. The tags must come from the graphical parameters described below.
<code>no.readonly</code>	logical; if <code>TRUE</code> and there are no other arguments, only parameters are returned which can be set by a subsequent <code>par()</code> call <i>on the same device</i> .

**Details**

Each device has its own set of graphical parameters. If the current device is the null device, `par` will open a new device before querying/setting parameters. (What device is controlled by `options("device")`.)

Parameters are queried by giving one or more character vectors to `par`.

`par()` (no arguments) or `par(no.readonly=TRUE)` is used to get *all* the graphical parameters (as a named list). Their names are currently taken from the unexported variable `.Pars`.

**R.O.** indicates *read-only arguments*: These may only be used in queries and cannot be set. ("cin", "cra", "csi", "cxy" and "din" are always read-only.)

There are several parameters can only be set by a call to `par()`:

- "ask",
- "fig", "fin",
- "lheight",
- "mai", "mar", "mex", "mfcoll", "mfrow", "mfg",
- "new",
- "oma", "omd", "omi",
- "pin", "plt", "ps", "pty",
- "usr",
- "xlog", "ylog"

The remaining parameters can also be set as arguments (often via ...) to high-level plot functions such as `plot.default`, `plot.window`, `points`, `lines`, `abline`, `axis`, `title`, `text`, `mtext`, `segments`, `symbols`, `arrows`, `polygon`, `rect`, `box`, `contour`, `filled.contour` and `image`. Such settings will be active during the execution of the function, only. However, see the comments on `bg` and `cex`, which may be taken as arguments to certain plot functions rather than as graphical parameters.

The meaning of 'character size' is not well-defined: this is set up for the device taking `pointsize` into account but often not the actual font family in use. Internally the corresponding `pars` (`cra`, `cin`, `cxy` and `csi`) are used only to set the inter-line spacing used to convert `mar` and `oma` to physical margins. (The same inter-line spacing multiplied by `lheight` is used for multi-line strings in `text` and `strheight`.)

## Value

When parameters are set, their former values are returned in an invisible named list. Such a list can be passed as an argument to `par` to restore the parameter values. Use `par(no.readonly = TRUE)` for the full list of parameters that can be restored. However, restoring all of these is not wise since they contain several ways to set the same quantities, and these can have conflicting effects if the graphics device has been resized since the parameters were saved. You will reset all of `mfrow`, `mfcoll` and `mfg` and will find `mfrow` wins.

When just one parameter is queried, the value of that parameter is returned as (atomic) vector. When two or more parameters are queried, their values are returned in a list, with the list names giving the parameters.

Note the inconsistency: setting one parameter returns a list, but querying one parameter returns a vector.

## Graphical Parameters

`adj` The value of `adj` determines the way in which text strings are justified in `text`, `mtext` and `title`. A value of 0 produces left-justified text, 0.5 (the default) centered text and 1 right-justified text. (Any value in [0, 1] is allowed, and on most devices values outside that interval will also work.) Note that the `adj` argument of `text` also allows `adj = c(x, y)` for different adjustment in x- and y- directions. Note that whereas for `text` it refers to positioning of text about a point, for `mtext` and `title` it controls placement within the plot or device region.

- ann** If set to `FALSE`, high-level plotting functions calling `plot.default` do not annotate the plots they produce with axis titles and overall titles. The default is to do annotation.
- ask** logical. If `TRUE` (and the R session is interactive) the user is asked for input, before a new figure is drawn. As this applies to the device, it also affects output by packages **grid** and **lattice**. It can be set even on non-screen devices but may have no effect there.  
This not really a graphics parameter, and its use is deprecated in favour of `devAskNewPage`.
- bg** The color to be used for the background of the device region. When called from `par()` it also sets `new=FALSE`. See section ‘Color Specification’ for suitable values. For many devices the initial value is set from the `bg` argument of the device, and for the rest it is normally `"white"`.  
Note that some graphics functions such as `plot.default` and `points` have an *argument* of this name with a different meaning.
- bty** A character string which determined the type of `box` which is drawn about plots. If `bty` is one of `"o"` (the default), `"l"`, `"7"`, `"c"`, `"u"`, or `"j"` the resulting box resembles the corresponding upper case letter. A value of `"n"` suppresses the box.
- cex** A numerical value giving the amount by which plotting text and symbols should be magnified relative to the default. Note that some graphics functions such as `plot.default` have an *argument* of this name which *multiplies* this graphical parameter, and some functions such as `points` accept a vector of values which are recycled. Other uses will take just the first value if a vector of length greater than one is supplied.  
This starts as 1 when a device is opened, and is reset when the layout is changed, e.g. by setting `mfrow`.
- cex.axis** The magnification to be used for axis annotation relative to the current setting of `cex`.
- cex.lab** The magnification to be used for x and y labels relative to the current setting of `cex`.
- cex.main** The magnification to be used for main titles relative to the current setting of `cex`.
- cex.sub** The magnification to be used for sub-titles relative to the current setting of `cex`.
- cin** **R.O.**; character size (*width*, *height*) in inches. These are the same measurements as `cra`, expressed in different units.
- col** A specification for the default plotting color. See section ‘Color Specification’. (Some functions such as `lines` accept a vector of values which are recycled. Other uses will take just the first value if a vector of length greater than one is supplied.)
- col.axis** The color to be used for axis annotation. Defaults to `"black"`.
- col.lab** The color to be used for x and y labels. Defaults to `"black"`.
- col.main** The color to be used for plot main titles. Defaults to `"black"`.
- col.sub** The color to be used for plot sub-titles. Defaults to `"black"`.
- cra** **R.O.**; size of default character (*width*, *height*) in ‘rasters’ (pixels). Some devices have no concept of pixels and so assume an arbitrary pixel size, usually 1/72 inch. These are the same measurements as `cin`, expressed in different units.
- crt** A numerical value specifying (in degrees) how single characters should be rotated. It is unwise to expect values other than multiples of 90 to work. Compare with `srt` which does string rotation.
- csi** **R.O.**; height of (default-sized) characters in inches. The same as `par("cin")[2]`.
- cxy** **R.O.**; size of default character (*width*, *height*) in user coordinate units. `par("cxy")` is `par("cin")/par("pin")` scaled to user coordinates. Note that `c(strwidth(ch), strheight(ch))` for a given string `ch` is usually much more precise.
- din** **R.O.**; the device dimensions, (*width*, *height*), in inches.

- `err` (*Unimplemented*; **R** is silent when points outside the plot region are *not* plotted.) The degree of error reporting desired.
- `family` The name of a font family for drawing text. The maximum allowed length is 200 bytes. This name gets mapped by each graphics device to a device-specific font description. The default value is "" which means that the default device fonts will be used (and what those are should be listed on the help page for the device). Standard values are "serif", "sans" and "mono", and the [Hershey](#) font families are also available. (Different devices may define others, and some devices will ignore this setting completely.) This can be specified inline for [text](#).
- `fg` The color to be used for the foreground of plots. This is the default color used for things like axes and boxes around plots. When called from `par()` this also sets parameter `col` to the same value. See section 'Color Specification'. A few devices have an argument to set the initial value, which is otherwise "black".
- `fig` A numerical vector of the form `c(x1, x2, y1, y2)` which gives the (NDC) coordinates of the figure region in the display region of the device. If you set this, unlike `S`, you start a new plot, so to add to an existing plot use `new=TRUE` as well.
- `fin` The figure region dimensions, `(width,height)`, in inches. If you set this, unlike `S`, you start a new plot.
- `font` An integer which specifies which font to use for text. If possible, device drivers arrange so that 1 corresponds to plain text (the default), 2 to bold face, 3 to italic and 4 to bold italic. Also, font 5 is expected to be the symbol font, in Adobe symbol encoding. On some devices font families can be selected by `family` to choose different sets of 5 fonts.
- `font.axis` The font to be used for axis annotation.
- `font.lab` The font to be used for x and y labels.
- `font.main` The font to be used for plot main titles.
- `font.sub` The font to be used for plot sub-titles.
- `lab` A numerical vector of the form `c(x, y, len)` which modifies the default way that axes are annotated. The values of `x` and `y` give the (approximate) number of tickmarks on the `x` and `y` axes and `len` specifies the label length. The default is `c(5, 5, 7)`. Note that this only affects the way the parameters `xaxp` and `yaxp` are set when the user coordinate system is set up, and is not consulted when axes are drawn. `len` is *unimplemented* in **R**.
- `las` numeric in {0,1,2,3}; the style of axis labels.
- 0:** always parallel to the axis [*default*],
  - 1:** always horizontal,
  - 2:** always perpendicular to the axis,
  - 3:** always vertical.
- Also supported by [mtext](#). Note that other string/character rotation (via argument `srt` to `par`) does *not* affect the axis labels.
- `lend` The line end style. This can be specified as an integer or string:
- 0 and "round" mean rounded line caps [*default*];
  - 1 and "butt" mean butt line caps;
  - 2 and "square" mean square line caps.
- `lheight` The line height multiplier. The height of a line of text (used to vertically space multi-line text) is found by multiplying the character height both by the current character expansion and by the line height multiplier. Default value is 1. Used in [text](#) and [strheight](#).
- `ljoin` The line join style. This can be specified as an integer or string:

0 and "round" mean rounded line joins [*default*];

1 and "mitre" mean mitred line joins;

2 and "bevel" mean bevelled line joins.

**lmitre** The line mitre limit. This controls when mitred line joins are automatically converted into bevelled line joins. The value must be larger than 1 and the default is 10. Not all devices will honour this setting.

**lty** The line type. Line types can either be specified as an integer (0=blank, 1=solid (default), 2=dashed, 3=dotted, 4=dotdash, 5=longdash, 6=twodash) or as one of the character strings "blank", "solid", "dashed", "dotted", "dotdash", "longdash", or "twodash", where "blank" uses 'invisible lines' (i.e., does not draw them).

Alternatively, a string of up to 8 characters (from `c(1:9, "A":"F")`) may be given, giving the length of line segments which are alternatively drawn and skipped. See section 'Line Type Specification'.

Some functions such as `lines` accept a vector of values which are recycled. Other uses will take just the first value if a vector of length greater than one is supplied.

**lwd** The line width, a *positive* number, defaulting to 1. The interpretation is device-specific, and some devices do not implement line widths less than one. (See the help on the device for details of the interpretation.)

Some functions such as `lines` accept a vector of values which are recycled. Other uses will take just the first value if a vector of length greater than one is supplied.

**mai** A numerical vector of the form `c(bottom, left, top, right)` which gives the margin size specified in inches.

**mar** A numerical vector of the form `c(bottom, left, top, right)` which gives the number of lines of margin to be specified on the four sides of the plot. The default is `c(5, 4, 4, 2) + 0.1`.

**mex** `mex` is a character size expansion factor which is used to describe coordinates in the margins of plots. Note that this does not change the font size, rather specifies the size of font (as a multiple of `csi`) used to convert between `mar` and `mai`, and between `oma` and `omi`.

This starts as 1 when the device is opened, and is reset when the layout is changed (alongside resetting `cex`).

**mfcrow, mfrow** A vector of the form `c(nr, nc)`. Subsequent figures will be drawn in an `nr`-by-`nc` array on the device by *columns* (`mfcrow`), or *rows* (`mfrow`), respectively.

In a layout with exactly two rows and columns the base value of "`cex`" is reduced by a factor of 0.83: if there are three or more of either rows or columns, the reduction factor is 0.66.

Setting a layout resets the base value of `cex` and that of `mex` to 1.

If either of these is queried it will give the current layout, so querying cannot tell you the order the array will be filled.

Consider the alternatives, `layout` and `split.screen`.

**mfg** A numerical vector of the form `c(i, j)` where `i` and `j` indicate which figure in an array of figures is to be drawn next (if setting) or is being drawn (if enquiring). The array must already have been set by `mfcrow` or `mfrow`.

For compatibility with S, the form `c(i, j, nr, nc)` is also accepted, when `nr` and `nc` should be the current number of rows and number of columns. Mismatches will be ignored, with a warning.

**mgp** The margin line (in `mex` units) for the axis title, axis labels and axis line. Note that `mgp[1]` affects `title` whereas `mgp[2:3]` affect `axis`. The default is `c(3, 1, 0)`.

**mkh** The height in inches of symbols to be drawn when the value of `pch` is an integer. *Completely ignored in R.*

- `new` logical, defaulting to `FALSE`. If set to `TRUE`, the next high-level plotting command (actually `plot.new`) should *not clean* the frame before drawing *as if it was on a new device*. It is an error (ignored with a warning) to try to use `new=TRUE` on a device that does not currently contain a high-level plot.
- `oma` A vector of the form `c(bottom, left, top, right)` giving the size of the outer margins in lines of text.
- `omd` A vector of the form `c(x1, x2, y1, y2)` giving the region *inside* outer margins in NDC (= normalized device coordinates), i.e., as fraction (in  $[0, 1]$ ) of the device region.
- `omi` A vector of the form `c(bottom, left, top, right)` giving the size of the outer margins in inches.
- `pch` Either an integer specifying a symbol or a single character to be used as the default in plotting points. See `points` for possible values and their interpretation. Note that only integers and single-character strings can be set as a graphics parameter (and not `NA` nor `NULL`).
- `pin` The current plot dimensions, `(width, height)`, in inches.
- `plt` A vector of the form `c(x1, x2, y1, y2)` giving the coordinates of the plot region as fractions of the current figure region.
- `ps` integer; the point size of text (but not symbols). Unlike the `pointsize` argument of most devices, this does not change the relationship between `mar` and `mai` (nor `oma` and `omi`).  
What is meant by ‘point size’ is device-specific, but most devices mean a multiple of 1bp, that is 1/72 of an inch.
- `pty` A character specifying the type of plot region to be used; `"s"` generates a square plotting region and `"m"` generates the maximal plotting region.
- `smo` (*Unimplemented*) a value which indicates how smooth circles and circular arcs should be.
- `srt` The string rotation in degrees. See the comment about `crt`. Only supported by `text`.
- `tck` The length of tick marks as a fraction of the smaller of the width or height of the plotting region. If `tck >= 0.5` it is interpreted as a fraction of the relevant side, so if `tck = 1` grid lines are drawn. The default setting (`tck = NA`) is to use `tcl = -0.5`.
- `tcl` The length of tick marks as a fraction of the height of a line of text. The default value is `-0.5`; setting `tcl = NA` sets `tck = -0.01` which is S’ default.
- `usr` A vector of the form `c(x1, x2, y1, y2)` giving the extremes of the user coordinates of the plotting region. When a logarithmic scale is in use (i.e., `par("xlog")` is true, see below), then the x-limits will be  $10^{\text{par}(\text{"usr"})[1:2]}$ . Similarly for the y-axis.
- `xaxp` A vector of the form `c(x1, x2, n)` giving the coordinates of the extreme tick marks and the number of intervals between tick-marks when `par("xlog")` is false. Otherwise, when *log* coordinates are active, the three values have a different meaning: For a small range, `n` is *negative*, and the ticks are as in the linear case, otherwise, `n` is in `1:3`, specifying a case number, and `x1` and `x2` are the lowest and highest power of 10 inside the user coordinates,  $10^{\text{par}(\text{"usr"})[1:2]}$ . (The `"usr"` coordinates are log10-transformed here!)
- n=1** will produce tick marks at  $10^j$  for integer `j`,
- n=2** gives marks  $k10^j$  with  $k \in \{1, 5\}$ ,
- n=3** gives marks  $k10^j$  with  $k \in \{1, 2, 5\}$ .

See `axTicks()` for a pure R implementation of this.

This parameter is reset when a user coordinate system is set up, for example by starting a new page or by calling `plot.window` or setting `par("usr"):n` is taken from `par("lab")`. It affects the default behaviour of subsequent calls to `axis` for sides 1 or 3.



- xaxs** The style of axis interval calculation to be used for the x-axis. Possible values are "r", "i", "e", "s", "d". The styles are generally controlled by the range of data or `xlim`, if given. Style "r" (regular) first extends the data range by 4 percent at each end and then finds an axis with pretty labels that fits within the extended range. Style "i" (internal) just finds an axis with pretty labels that fits within the original data range. Style "s" (standard) finds an axis with pretty labels within which the original data range fits. Style "e" (extended) is like style "s", except that it also ensures that there is room for plotting symbols within the bounding box. Style "d" (direct) specifies that the current axis should be used on subsequent plots. (*Only "r" and "i" styles are currently implemented*)
- xaxt** A character which specifies the x axis type. Specifying "n" suppresses plotting of the axis. The standard value is "s": for compatibility with S values "l" and "t" are accepted but are equivalent to "s": any value other than "n" implies plotting.
- xlog** A logical value (see `log` in `plot.default`). If TRUE, a logarithmic scale is in use (e.g., after `plot(*, log = "x")`). For a new device, it defaults to FALSE, i.e., linear scale.
- xpd** A logical value or NA. If FALSE, all plotting is clipped to the plot region, if TRUE, all plotting is clipped to the figure region, and if NA, all plotting is clipped to the device region. See also `clip`.
- yaxp** A vector of the form `c(y1, y2, n)` giving the coordinates of the extreme tick marks and the number of intervals between tick-marks unless for log coordinates, see `xaxp` above.
- yaxs** The style of axis interval calculation to be used for the y-axis. See `xaxs` above.
- yaxt** A character which specifies the y axis type. Specifying "n" suppresses plotting.
- ylog** A logical value; see `xlog` above.

### Color Specification

Colors can be specified in several different ways. The simplest way is with a character string giving the color name (e.g., "red"). A list of the possible colors can be obtained with the function `colors`. Alternatively, colors can be specified directly in terms of their RGB components with a string of the form "#RRGGBB" where each of the pairs RR, GG, BB consist of two hexadecimal digits giving a value in the range 00 to FF. Colors can also be specified by giving an index into a small table of colors, the `palette`. This provides compatibility with S. Index 0 corresponds to the background color. (Because apparently some people have been assuming it, it is also possible to specify integers as character strings, e.g. "3".)

Additionally, "transparent" or (integer) NA is *transparent*, useful for filled areas (such as the background!), and just invisible for things like lines or text. Semi-transparent colors are available for use on devices that support them.

The functions `rgb`, `hsv`, `hcl`, `gray` and `rainbow` provide additional ways of generating colors.

### Line Type Specification

Line types can either be specified by giving an index into a small built-in table of line types (1 = solid, 2 = dashed, etc, see `lty` above) or directly as the lengths of on/off stretches of line. This is done with a string of an even number (up to eight) of characters, namely *non-zero* (hexadecimal) digits which give the lengths in consecutive positions in the string. For example, the string "33" specifies three units on followed by three off and "3313" specifies three units on followed by three off followed by one on and finally three off. The 'units' here are (on most devices) proportional to `lwd`, and with `lwd = 1` are in pixels or points or 1/96 inch.

The five standard dash-dot line types (`lty = 2:6`) correspond to `c("44", "13", "1343", "73", "2262")`.

Note that NA is not a valid value for `lty`.

**Note**

The effect of restoring all the (settable) graphics parameters as in the examples is hard to predict if the device has been resized. Several of them are attempting to set the same things in different ways, and those last in the alphabet will win. In particular, the settings of `mai`, `mar`, `pin`, `plt` and `pty` interact, as do the outer margin settings, the figure layout and figure region size.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

**See Also**

`plot.default` for some high-level plotting parameters; `colors`; `clip`; `options` for other setup parameters; graphic devices `x11`, `postscript` and setting up device regions by `layout` and `split.screen`.

**Examples**

```
op <- par(mfrow = c(2, 2), # 2 x 2 pictures on one plot
         pty = "s")      # square plotting region,
                        # independent of device size

## At end of plotting, reset to previous settings:
par(op)

## Alternatively,
op <- par(no.readonly = TRUE) # the whole list of settable par's.
## do lots of plotting and par(.) calls, then reset:
par(op)
## Note this is not in general good practice

par("ylog") # FALSE
plot(1 : 12, log = "y")
par("ylog") # TRUE

plot(1:2, xaxs = "i") # 'inner axis' w/o extra space
par(c("usr", "xaxp"))

( nr.prof <-
  c(prof.pilots=16,lawyers=11,farmers=10,salesmen=9,physicians=9,
    mechanics=6,policemen=6,managers=6,engineers=5,teachers=4,
    housewives=3,students=3,armed.forces=1)
par(las = 3)
barplot(rbind(nr.prof)) # R 0.63.2: shows alignment problem
par(las = 0) # reset to default

require(grDevices) # for gray
## 'fg' use:
plot(1:12, type = "b", main="'fg' : axes, ticks and box in gray",
     fg = gray(0.7), bty="7" , sub=R.version.string)

ex <- function() {
  old.par <- par(no.readonly = TRUE) # all par settings which
```

```

                                # could be changed.
on.exit(par(old.par))
## ...
## ... do lots of par() settings and plots
## ...
invisible() #-- now, par(old.par) will be executed
}
ex()

```

---

persp

*Perspective Plots*

---

### Description

This function draws perspective plots of surfaces over the x–y plane. `persp` is a generic function.

### Usage

```

persp(x, ...)

## Default S3 method:
persp(x = seq(0, 1, length.out = nrow(z)),
      y = seq(0, 1, length.out = ncol(z)),
      z, xlim = range(x), ylim = range(y),
      zlim = range(z, na.rm = TRUE),
      xlab = NULL, ylab = NULL, zlab = NULL,
      main = NULL, sub = NULL,
      theta = 0, phi = 15, r = sqrt(3), d = 1,
      scale = TRUE, expand = 1,
      col = "white", border = NULL, ltheta = -135, lphi = 0,
      shade = NA, box = TRUE, axes = TRUE, nticks = 5,
      ticktype = "simple", ...)

```

### Arguments

<code>x</code> , <code>y</code>	locations of grid lines at which the values in <code>z</code> are measured. These must be in ascending order. By default, equally spaced values from 0 to 1 are used. If <code>x</code> is a list, its components <code>x\$x</code> and <code>x\$y</code> are used for <code>x</code> and <code>y</code> , respectively.
<code>z</code>	a matrix containing the values to be plotted (NAs are allowed). Note that <code>x</code> can be used instead of <code>z</code> for convenience.
<code>xlim</code> , <code>ylim</code> , <code>zlim</code>	<code>x</code> -, <code>y</code> - and <code>z</code> -limits. The plot is produced so that the rectangular volume defined by these limits is visible.
<code>xlab</code> , <code>ylab</code> , <code>zlab</code>	titles for the axes. N.B. These must be character strings; expressions are not accepted. Numbers will be coerced to character strings.
<code>main</code> , <code>sub</code>	main and sub title, as for <code>title</code> .
<code>theta</code> , <code>phi</code>	angles defining the viewing direction. <code>theta</code> gives the azimuthal direction and <code>phi</code> the colatitude.
<code>r</code>	the distance of the eyepoint from the centre of the plotting box.

<code>d</code>	a value which can be used to vary the strength of the perspective transformation. Values of <code>d</code> greater than 1 will lessen the perspective effect and values less and 1 will exaggerate it.
<code>scale</code>	before viewing the <code>x</code> , <code>y</code> and <code>z</code> coordinates of the points defining the surface are transformed to the interval <code>[0,1]</code> . If <code>scale</code> is <code>TRUE</code> the <code>x</code> , <code>y</code> and <code>z</code> coordinates are transformed separately. If <code>scale</code> is <code>FALSE</code> the coordinates are scaled so that aspect ratios are retained. This is useful for rendering things like DEM information.
<code>expand</code>	a expansion factor applied to the <code>z</code> coordinates. Often used with <code>0 &lt; expand &lt; 1</code> to shrink the plotting box in the <code>z</code> direction.
<code>col</code>	the color(s) of the surface facets. Transparent colours are ignored. This is recycled to the $(nx - 1)(ny - 1)$ facets.
<code>border</code>	the color of the line drawn around the surface facets. The default, <code>NULL</code> , corresponds to <code>par("fg")</code> . A value of <code>NA</code> will disable the drawing of borders: this is sometimes useful when the surface is shaded.
<code>ltheta, lphi</code>	if finite values are specified for <code>ltheta</code> and <code>lphi</code> , the surface is shaded as though it was being illuminated from the direction specified by azimuth <code>ltheta</code> and colatitude <code>lphi</code> .
<code>shade</code>	the shade at a surface facet is computed as $(1+d)/2$ <sup>shade</sup> , where <code>d</code> is the dot product of a unit vector normal to the facet and a unit vector in the direction of a light source. Values of <code>shade</code> close to one yield shading similar to a point light source model and values close to zero produce no shading. Values in the range 0.5 to 0.75 provide an approximation to daylight illumination.
<code>box</code>	should the bounding box for the surface be displayed. The default is <code>TRUE</code> .
<code>axes</code>	should ticks and labels be added to the box. The default is <code>TRUE</code> . If <code>box</code> is <code>FALSE</code> then no ticks or labels are drawn.
<code>ticktype</code>	character: <code>"simple"</code> draws just an arrow parallel to the axis to indicate direction of increase; <code>"detailed"</code> draws normal ticks as per 2D plots.
<code>nticks</code>	the (approximate) number of tick marks to draw on the axes. Has no effect if <code>ticktype</code> is <code>"simple"</code> .
<code>...</code>	additional graphical parameters (see <code>par</code> ).

## Details

The plots are produced by first transforming the coordinates to the interval `[0,1]`. The surface is then viewed by looking at the origin from a direction defined by `theta` and `phi`. If `theta` and `phi` are both zero the viewing direction is directly down the negative `y` axis. Changing `theta` will vary the azimuth and changing `phi` the colatitude.

There is a hook called `"persp"` (see `setHook`) called after the plot is completed, which is used in the testing code to annotate the plot page. The hook function(s) are called with no argument.

Notice that `persp` interprets the `z` matrix as a table of  $f(x[i], y[j])$  values, so that the `x` axis corresponds to row number and the `y` axis to column number, with column 1 at the bottom, so that with the standard rotation angles, the top left corner of the matrix is displayed at the left hand side, closest to the user.

The sizes and fonts of the axis labels and the annotations for `ticktype="detailed"` are controlled by graphics parameters `"cex.lab"/"font.lab"` and `"cex.axis"/"font.axis"` respectively. (This changed in R 2.5.0.)

**Value**

`persp()` returns the *viewing transformation matrix*, say  $VT$ , a  $4 \times 4$  matrix suitable for projecting 3D coordinates  $(x, y, z)$  into the 2D plane using homogeneous 4D coordinates  $(x, y, z, t)$ . It can be used to superimpose additional graphical elements on the 3D plot, by `lines()` or `points()`, using the simple function `trans3d()`.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`contour` and `image`; `trans3d`.

Rotatable 3D plots can be produced by package **rgl**: other ways to produce static perspective plots are available in packages **lattice** and **scatterplot3d**.

**Examples**

```
require(grDevices) # for trans3d
## More examples in demo(persp) !!
## -----

# (1) The Obligatory Mathematical surface.
#     Rotated sinc function.

x <- seq(-10, 10, length= 30)
y <- x
f <- function(x,y) { r <- sqrt(x^2+y^2); 10 * sin(r)/r }
z <- outer(x, y, f)
z[is.na(z)] <- 1
op <- par(bg = "white")
persp(x, y, z, theta = 30, phi = 30, expand = 0.5, col = "lightblue")
persp(x, y, z, theta = 30, phi = 30, expand = 0.5, col = "lightblue",
      ltheta = 120, shade = 0.75, ticktype = "detailed",
      xlab = "X", ylab = "Y", zlab = "Sinc( r )"
) -> res
round(res, 3)

# (2) Add to existing persp plot - using trans3d() :

xE <- c(-10,10); xy <- expand.grid(xE, xE)
points(trans3d(xy[,1], xy[,2], 6, pmat = res), col = 2, pch =16)
lines (trans3d(x, y=10, z= 6 + sin(x), pmat = res), col = 3)

phi <- seq(0, 2*pi, len = 201)
r1 <- 7.725 # radius of 2nd maximum
xr <- r1 * cos(phi)
yr <- r1 * sin(phi)
lines(trans3d(xr,yr, f(xr,yr), res), col = "pink", lwd = 2)
## (no hidden lines)

# (3) Visualizing a simple DEM model

z <- 2 * volcano          # Exaggerate the relief
```

```

x <- 10 * (1:nrow(z)) # 10 meter spacing (S to N)
y <- 10 * (1:ncol(z)) # 10 meter spacing (E to W)
## Don't draw the grid lines : border = NA
par(bg = "slategray")
persp(x, y, z, theta = 135, phi = 30, col = "green3", scale = FALSE,
      ltheta = -120, shade = 0.75, border = NA, box = FALSE)

# (4) Surface colours corresponding to z-values

par(bg = "white")
x <- seq(-1.95, 1.95, length = 30)
y <- seq(-1.95, 1.95, length = 35)
z <- outer(x, y, function(a,b) a*b^2)
nrz <- nrow(z)
ncz <- ncol(z)
# Create a function interpolating colors in the range of specified colors
jet.colors <- colorRampPalette( c("blue", "green") )
# Generate the desired number of colors from this palette
nbc <- 100
color <- jet.colors(nbc)
# Compute the z-value at the facet centres
zfacet <- z[-1, -1] + z[-1, -ncz] + z[-nrz, -1] + z[-nrz, -ncz]
# Recode facet z-values into color indices
facetcol <- cut(zfacet, nbc)
persp(x, y, z, col=color[facetcol], phi=30, theta=-30)

par(op)

```

---

pie

*Pie Charts*


---

## Description

Draw a pie chart.

## Usage

```

pie(x, labels = names(x), edges = 200, radius = 0.8,
    clockwise = FALSE, init.angle = if(clockwise) 90 else 0,
    density = NULL, angle = 45, col = NULL, border = NULL,
    lty = NULL, main = NULL, ...)

```

## Arguments

x	a vector of non-negative numerical quantities. The values in x are displayed as the areas of pie slices.
labels	one or more expressions or character strings giving names for the slices. Other objects are coerced by <a href="#">as.graphicsAnnot</a> . For empty or NA (after coercion to character) labels, no label nor pointing line is drawn.
edges	the circular outline of the pie is approximated by a polygon with this many edges.

radius	the pie is drawn centered in a square box whose sides range from $-1$ to $1$ . If the character strings labeling the slices are long it may be necessary to use a smaller radius.
clockwise	logical indicating if slices are drawn clockwise or counter clockwise (i.e., mathematically positive direction), the latter is default.
init.angle	number specifying the <i>starting angle</i> (in degrees) for the slices. Defaults to 0 (i.e., '3 o'clock') unless <code>clockwise</code> is true where <code>init.angle</code> defaults to 90 (degrees), (i.e., '12 o'clock').
density	the density of shading lines, in lines per inch. The default value of <code>NULL</code> means that no shading lines are drawn. Non-positive values of <code>density</code> also inhibit the drawing of shading lines.
angle	the slope of shading lines, given as an angle in degrees (counter-clockwise).
col	a vector of colors to be used in filling or shading the slices. If missing a set of 6 pastel colours is used, unless <code>density</code> is specified when <code>par("fg")</code> is used.
border, lty	(possibly vectors) arguments passed to <code>polygon</code> which draws each slice.
main	an overall title for the plot.
...	graphical parameters can be given as arguments to <code>pie</code> . They will affect the main title and labels only.

### Note

Pie charts are a very bad way of displaying information. The eye is good at judging linear measures and bad at judging relative areas. A bar chart or dot chart is a preferable way of displaying this type of data.

Cleveland (1985), page 264: "Data that can be shown by pie charts always can be shown by a dot chart. This means that judgements of position along a common scale can be made instead of the less accurate angle judgements." This statement is based on the empirical investigations of Cleveland and McGill as well as investigations by perceptual psychologists.

### References

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- Cleveland, W. S. (1985) *The elements of graphing data*. Wadsworth: Monterey, CA, USA.

### See Also

[dotchart](#).

### Examples

```
require(grDevices)
pie(rep(1, 24), col = rainbow(24), radius = 0.9)

pie.sales <- c(0.12, 0.3, 0.26, 0.16, 0.04, 0.12)
names(pie.sales) <- c("Blueberry", "Cherry",
  "Apple", "Boston Cream", "Other", "Vanilla Cream")
pie(pie.sales) # default colours
pie(pie.sales,
  col = c("purple", "violetred1", "green3", "cornsilk", "cyan", "white"))
pie(pie.sales, col = gray(seq(0.4, 1.0, length=6)))
```

```
pie(pie.sales, density = 10, angle = 15 + 10 * 1:6)
pie(pie.sales, clockwise=TRUE, main="pie(*, clockwise=TRUE)")
segments(0,0, 0,1, col= "red", lwd = 2)
text(0,1, "init.angle = 90", col= "red")

n <- 200
pie(rep(1,n), labels="", col=rainbow(n), border=NA,
    main = "pie(*, labels=\"\\\", col=rainbow(n), border=NA,..)")
```

---

plot

*Generic X-Y Plotting*


---

### Description

Generic function for plotting of R objects. For more details about the graphical parameter arguments, see [par](#).

### Usage

```
plot(x, y, ...)
```

### Arguments

**x** the coordinates of points in the plot. Alternatively, a single plotting structure, function or *any R object with a plot method* can be provided.

**y** the y coordinates of points in the plot, *optional* if **x** is an appropriate structure.

**...** Arguments to be passed to methods, such as graphical parameters (see [par](#)). Many methods will accept the following arguments:

**type** what type of plot should be drawn. Possible types are

- "p" for **p**oints,
- "l" for **l**ines,
- "b" for **b**oth,
- "c" for the lines part alone of "b",
- "o" for both 'overplotted',
- "h" for 'histogram' like (or 'high-density') vertical lines,
- "s" for stair steps,
- "S" for other steps, see 'Details' below,
- "n" for no plotting.

All other types give a warning or an error; using, e.g., `type = "punkte"` being equivalent to `type = "p"` for S compatibility. Note that some methods, e.g. [plot.factor](#), do not accept this.

**main** an overall title for the plot: see [title](#).

**sub** a sub title for the plot: see [title](#).

**xlab** a title for the x axis: see [title](#).

**ylab** a title for the y axis: see [title](#).

**asp** the *y/x* aspect ratio, see [plot.window](#).



**Details**

For simple scatter plots, `plot.default` will be used. However, there are `plot` methods for many R objects, including `functions`, `data.frames`, `density` objects, etc. Use `methods(plot)` and the documentation for these.

The two step types differ in their x-y preference: Going from  $(x_1, y_1)$  to  $(x_2, y_2)$  with  $x_1 < x_2$ , `type = "s"` moves first horizontal, then vertical, whereas `type = "S"` moves the other way around.

**See Also**

`plot.default`, `plot.formula` and other methods; `points`, `lines`, `par`.

For X-Y-Z plotting see `contour`, `persp` and `image`.

**Examples**

```
require(stats)
plot(cars)
lines(lowess(cars))

plot(sin, -pi, 2*pi)

## Discrete Distribution Plot:
plot(table(rpois(100,5)), type = "h", col = "red", lwd=10,
      main="rpois(100,lambda=5)")

## Simple quantiles/ECDF, see ecdf() {library(stats)} for a better one:
plot(x <- sort(rnorm(47)), type = "s", main = "plot(x, type = \"s\")")
points(x, cex = .5, col = "dark red")
```

---

plot.data.frame      *Plot Method for Data Frames*

---

**Description**

`plot.data.frame`, a method for the `plot` generic. It is designed for a quick look at numeric data frames.

**Usage**

```
## S3 method for class 'data.frame':
plot(x, ...)
```

**Arguments**

`x`                    object of class `data.frame`.  
`...`                further arguments to `stripchart`, `plot.default` or `pairs`.

**Details**

This is intended for data frames with *numeric* columns. For more than two columns it first calls `data.matrix` to convert the data frame to a numeric matrix and then calls `pairs` to produce a scatterplot matrix). This can fail and may well be inappropriate: for example numerical conversion of dates will lose their special meaning and a warning will be given.

For a two-column data frame it plots the second column against the first by the most appropriate method for the first column.

For a single numeric column it uses `stripchart`, and for other single-column data frames tries to find a plot method for the single column.

**See Also**

`data.frame`

**Examples**

```
plot(OrchardSprays[1], method="jitter")
plot(OrchardSprays[c(4,1)])
plot(OrchardSprays)

plot(iris)
plot(iris[5:4])
plot(women)
```

---

plot.default

*The Default Scatterplot Function*

---

**Description**

Draw a scatter plot with decorations such as axes and titles in the active graphics window.

**Usage**

```
## Default S3 method:
plot(x, y = NULL, type = "p", xlim = NULL, ylim = NULL,
     log = "", main = NULL, sub = NULL, xlab = NULL, ylab = NULL,
     ann = par("ann"), axes = TRUE, frame.plot = axes,
     panel.first = NULL, panel.last = NULL, asp = NA, ...)
```

**Arguments**

<code>x, y</code>	the <code>x</code> and <code>y</code> arguments provide the <code>x</code> and <code>y</code> coordinates for the plot. Any reasonable way of defining the coordinates is acceptable. See the function <code>xy.coords</code> for details. If supplied separately, they must be of the same length.
<code>type</code>	1-character string giving the type of plot desired. The following values are possible, for details, see <code>plot</code> : "p" for points, "l" for lines, "o" for overplotted points and lines, "b", "c") for (empty if "c") points joined by lines, "s" and "S" for stair steps and "h" for histogram-like vertical lines. Finally, "n" does not produce any points or lines.
<code>xlim</code>	the <code>x</code> limits ( <code>x1</code> , <code>x2</code> ) of the plot. Note that <code>x1 &gt; x2</code> is allowed and leads to a 'reversed axis'.

<code>ylim</code>	the y limits of the plot.
<code>log</code>	a character string which contains "x" if the x axis is to be logarithmic, "y" if the y axis is to be logarithmic and "xy" or "yx" if both axes are to be logarithmic.
<code>main</code>	a main title for the plot, see also <a href="#">title</a> .
<code>sub</code>	a sub title for the plot.
<code>xlab</code>	a label for the x axis, defaults to a description of x.
<code>ylab</code>	a label for the y axis, defaults to a description of y.
<code>ann</code>	a logical value indicating whether the default annotation (title and x and y axis labels) should appear on the plot.
<code>axes</code>	a logical value indicating whether both axes should be drawn on the plot. Use graphical parameter "xaxt" or "yaxt" to suppress just one of the axes.
<code>frame.plot</code>	a logical indicating whether a box should be drawn around the plot.
<code>panel.first</code>	an expression to be evaluated after the plot axes are set up but before any plotting takes place. This can be useful for drawing background grids or scatterplot smooths.
<code>panel.last</code>	an expression to be evaluated after plotting has taken place.
<code>asp</code>	the $y/x$ aspect ratio, see <a href="#">plot.window</a> .
<code>...</code>	other graphical parameters (see <a href="#">par</a> and section 'Details' below).

## Details

Commonly used graphical parameters are:

<code>col</code>	The colors for lines and points. Multiple colors can be specified so that each point can be given its own color. If there are fewer colors than points they are recycled in the standard fashion. Lines will all be plotted in the first colour specified.
<code>bg</code>	a vector of background colors for open plot symbols, see <a href="#">points</a> . Note: this is <b>not</b> the same setting as <a href="#">par</a> ("bg").
<code>pch</code>	a vector of plotting characters or symbols: see <a href="#">points</a> .
<code>cex</code>	a numerical vector giving the amount by which plotting characters and symbols should be scaled relative to the default. This works as a multiple of <a href="#">par</a> ("cex"). NULL and NA are equivalent to 1.0. Note that this does not affect annotation: see below.
<code>lty</code>	the line type, see <a href="#">par</a> .
<code>cex.main, col.lab, font.sub, etc</code>	settings for main- and sub-title and axis annotation, see <a href="#">title</a> and <a href="#">par</a> .
<code>lwd</code>	the line width, see <a href="#">par</a> .

## References

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- Cleveland, W. S. (1985) *The Elements of Graphing Data*. Monterey, CA: Wadsworth.
- Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

## See Also

[plot](#), [plot.window](#), [xy.coords](#).

**Examples**

```

Speed <- cars$speed
Distance <- cars$dist
plot(Speed, Distance, panel.first = grid(8,8),
     pch = 0, cex = 1.2, col = "blue")
plot(Speed, Distance,
     panel.first = lines(stats::lowess(Speed, Distance), lty = "dashed"),
     pch = 0, cex = 1.2, col = "blue")

## Show the different plot types
x <- 0:12
y <- sin(pi/5 * x)
op <- par(mfrow = c(3,3), mar = .1+ c(2,2,3,1))
for (tp in c("p","l","b", "c","o","h", "s","S","n")) {
  plot(y ~ x, type = tp,
       main = paste("plot(*, type = \"",tp,"\"",sep=""))
  if(tp == "S") {
    lines(x,y, type = "s", col = "red", lty = 2)
    mtext("lines(*, type = \"s\", ...)", col = "red", cex=.8)
  }
}
par(op)

##--- Log-Log Plot with custom axes
lx <- seq(1,5, length=41)
yl <- expression(e^{-frac(1,2) * {log[10](x)}^2})
y <- exp(-.5*lx^2)
op <- par(mfrow=c(2,1), mar=par("mar")+c(0,1,0,0))
plot(10^lx, y, log="xy", type="l", col="purple",
     main="Log-Log plot", ylab=yl, xlab="x")
plot(10^lx, y, log="xy", type="o", pch='.', col="forestgreen",
     main="Log-Log plot with custom axes", ylab=yl, xlab="x",
     axes = FALSE, frame.plot = TRUE)
my.at <- 10^(1:5)
axis(1, at = my.at, labels = formatC(my.at, format="fg"))
at.y <- 10^(-5:-1)
axis(2, at = at.y, labels = formatC(at.y, format="fg"), col.axis="red")
par(op)

```

plot.design

*Plot Univariate Effects of a 'Design' or Model***Description**

Plot univariate effects of one or more [factors](#), typically for a designed experiment as analyzed by [aov\(\)](#). Further, in S this a method of the [plot](#) generic function for [design](#) objects.

**Usage**

```

plot.design(x, y = NULL, fun = mean, data = NULL, ...,
           ylim = NULL, xlab = "Factors", ylab = NULL,
           main = NULL, ask = NULL, xaxt = par("xaxt"),
           axes = TRUE, xtack = FALSE)

```

**Arguments**

x	either a data frame containing the design factors and optionally the response, or a <code>formula</code> or <code>terms</code> object.
y	the response, if not given in x.
fun	a function (or name of one) to be applied to each subset. It must return one number for a numeric (vector) input.
data	data frame containing the variables referenced by x when that is formula like.
...	graphical arguments such as <code>col</code> , see <code>par</code> .
ylim	range of y values, as in <code>plot.default</code> .
xlab	x axis label, see <code>title</code> .
ylab	y axis label with a ‘smart’ default.
main	main title, see <code>title</code> .
ask	logical indicating if the user should be asked before a new page is started – in the case of multiple y’s.
xaxt	character giving the type of x axis.
axes	logical indicating if axes should be drawn.
xtick	logical indicating if ticks (one per factor) should be drawn on the x axis.

**Details**

The supplied function will be called once for each level of each factor in the design and the plot will show these summary values. The levels of a particular factor are shown along a vertical line, and the overall value of `fun()` for the response is drawn as a horizontal line.

This is a new R implementation which will not be completely compatible to the earlier S implementations. This is not a bug but might still change.

**Note**

A big effort was taken to make this closely compatible to the S version. However, `col` (and `fg`) specification has different effects.

**Author(s)**

Roberto Frisullo and Martin Maechler

**References**

Chambers, J. M. and Hastie, T. J. eds (1992) *Statistical Models in S*. Chapman & Hall, London, **the white book**, pp. 546–7 (and 163–4).

Freeny, A. E. and Landwehr, J. M. (1990) Displays for data from large designed experiments; Computer Science and Statistics: Proc.\ 22nd Symp\ Interface, 117–126, Springer Verlag.

**See Also**

`interaction.plot` for a ‘standard graphic’ of designed experiments.

**Examples**

```

require(stats)
plot.design(warpbreaks)# automatic for data frame with one numeric var.

Form <- breaks ~ wool + tension
summary(fml <- aov(Form, data = warpbreaks))
plot.design(      Form, data = warpbreaks, col = 2)# same as above

## More than one y :
utils::str(esoph)
plot.design(esoph) ## two plots; if interactive you are "ask"ed

## or rather, compare mean and median:
op <- par(mfcol = 1:2)
plot.design(ncases/ncontrols ~ ., data = esoph, ylim = c(0, 0.8))
plot.design(ncases/ncontrols ~ ., data = esoph, ylim = c(0, 0.8),
            fun = median)
par(op)

```

---

plot.factor

*Plotting Factor Variables*


---

**Description**

This functions implements a scatterplot method for [factor](#) arguments of the *generic* [plot](#) function.

If *y* is missing [barplot](#) is produced. For numeric *y* a [boxplot](#) is used, and for a factor *y* a [spineplot](#) is shown. For any other type of *y* the next [plot](#) method is called, normally [plot.default](#).

**Usage**

```

## S3 method for class 'factor':
plot(x, y, legend.text = NULL, ...)

```

**Arguments**

<i>x</i> , <i>y</i>	numeric or factor. <i>y</i> may be missing.
<i>legend.text</i>	character vector for annotation of <i>y</i> axis in the case of a factor <i>y</i> : defaults to <code>levels(y)</code> . This sets the <code>yaxlabels</code> argument of <a href="#">spineplot</a> .
<i>...</i>	Further arguments to <a href="#">barplot</a> , <a href="#">boxplot</a> , <a href="#">spineplot</a> or <a href="#">plot</a> as appropriate. All of these accept graphical parameters, see <a href="#">par</a> , annotation arguments passed to <a href="#">title</a> and <code>axes = FALSE</code> . None accept <code>type</code> .

**See Also**

[plot.default](#), [plot.formula](#), [barplot](#), [boxplot](#), [spineplot](#).

**Examples**

```
require(grDevices)

plot(weight ~ group, data = PlantGrowth)           # numeric vector ~ factor
plot(cut(weight, 2) ~ group, data = PlantGrowth) # factor ~ factor
## passing "." to spineplot() eventually:
plot(cut(weight, 3) ~ group, data = PlantGrowth,
      col = hcl(c(0, 120, 240), 50, 70))

plot(PlantGrowth$group, axes=FALSE, main="no axes")# extremely silly
```

plot.formula

*Formula Notation for Scatterplots***Description**

Specify a scatterplot or add points or lines via a formula.

**Usage**

```
## S3 method for class 'formula':
plot(formula, data = parent.frame(), ..., subset,
      ylab = varnames[response], ask = dev.interactive())

## S3 method for class 'formula':
points(formula, data = parent.frame(), ..., subset)

## S3 method for class 'formula':
lines(formula, data = parent.frame(), ..., subset)
```

**Arguments**

formula	a <a href="#">formula</a> , such as $y \sim x$ .
data	a <code>data.frame</code> (or list) from which the variables in <code>formula</code> should be taken.
...	Arguments to be passed to or from other methods. <code>horizontal = TRUE</code> is also accepted.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
ylab	the y label of the plot(s).
ask	logical, see <a href="#">par</a> .

**Details**

Both the terms in the formula and the ... arguments are evaluated in `data` enclosed in `parent.frame()` if `data` is a list or a data frame. The terms of the formula and those arguments in ... that are of the same length as `data` are subjected to the subsetting specified in `subset`. If the formula in `plot.formula` contains more than one non-response term, a series of plots of  $y$  against each term is given. A plot against the running index can be specified as `plot(y ~ 1)`.

Missing values are not considered in these methods, and in particular cases with missing values are not removed.

If `y` is an object (i.e. has a `class` attribute) then `plot.formula` looks for a plot method for that class first. Otherwise, the class of `x` will determine the type of the plot. For factors this will be a parallel boxplot, and argument `horizontal = TRUE` can be used (see `boxplot`).

### Value

These functions are invoked for their side effect of drawing in the active graphics device.

### See Also

`plot.default`, `points`, `lines`, `plot.factor`.

### Examples

```
op <- par(mfrow=c(2,1))
plot(Ozone ~ Wind, data = airquality, pch=as.character(Month))
plot(Ozone ~ Wind, data = airquality, pch=as.character(Month),
      subset = Month != 7)
par(op)
```

---

plot.histogram      *Plot Histograms*

---

### Description

These are methods for objects of class "histogram", typically produced by `hist`.

### Usage

```
## S3 method for class 'histogram':
plot(x, freq = equidist, density = NULL, angle = 45,
      col = NULL, border = par("fg"), lty = NULL,
      main = paste("Histogram of",
                   paste(x$xname, collapse="\n")),
      sub = NULL, xlab = x$xname, ylab,
      xlim = range(x$breaks), ylim = NULL,
      axes = TRUE, labels = FALSE, add = FALSE, ann = TRUE, ...)

## S3 method for class 'histogram':
lines(x, ...)
```

### Arguments

<code>x</code>	a histogram object, or a list with components <code>density</code> , <code>mid</code> , etc, see <code>hist</code> for information about the components of <code>x</code> .
<code>freq</code>	logical; if <code>TRUE</code> , the histogram graphic is to present a representation of frequencies, i.e. <code>x\$counts</code> ; if <code>FALSE</code> , <i>relative</i> frequencies (probabilities), i.e., <code>x\$density</code> , are plotted. The default is true for equidistant breaks and false otherwise.



col	a colour to be used to fill the bars. The default of NULL yields unfilled bars.
border	the color of the border around the bars.
angle, density	select shading of bars by lines: see <a href="#">rect</a> .
lty	the line type used for the bars, see also <a href="#">lines</a> .
main, sub, xlab, ylab	these arguments to <code>title</code> have useful defaults here.
xlim, ylim	the range of x and y values with sensible defaults.
axes	logical, indicating if axes should be drawn.
labels	logical or character. Additionally draw labels on top of bars, if not FALSE; if TRUE, draw the counts or rounded densities; if labels is a character, draw itself.
add	logical. If TRUE, only the bars are added to the current plot. This is what <code>lines.histogram(*)</code> does.
ann	logical. Should annotations (titles and axis titles) be plotted?
...	further graphical parameters to <code>title</code> and <code>axis</code> .

### Details

`lines.histogram(*)` is the same as `plot.histogram(*, add = TRUE)`.

### See Also

[hist](#), [stem](#), [density](#).

### Examples

```
(wwt <- hist(women$weight, nclass = 7, plot = FALSE))
plot(wwt, labels = TRUE) # default main & xlab using wwt$xname
plot(wwt, border = "dark blue", col = "light blue",
      main = "Histogram of 15 women's weights", xlab = "weight [pounds]")

## Fake "lines" example, using non-default labels:
w2 <- wwt; w2$counts <- w2$counts - 1
lines(w2, col = "Midnight Blue", labels = ifelse(w2$counts, "> 1", "1"))
```

---

plot.table

*Plot Methods for 'table' Objects*

---

### Description

This is a method of the generic `plot` function for (contingency) `table` objects. Whereas for two- and more dimensional tables, a `mosaicplot` is drawn, one-dimensional ones are plotted as bars.

### Usage

```
## S3 method for class 'table':
plot(x, type = "h", ylim = c(0, max(x)), lwd = 2,
      xlab = NULL, ylab = NULL, frame.plot = is.num, ...)
```

**Arguments**

x	a <a href="#">table</a> (like) object.
type	plotting type.
ylim	range of y-axis.
lwd	line width for bars when <code>type = "h"</code> is used in the 1D case.
xlab, ylab	x- and y-axis labels.
frame.plot	logical indicating if a frame ( <a href="#">box</a> ) should be drawn in the 1D case. Defaults to true when x has <a href="#">dimnames</a> coerce-able to numbers.
...	further graphical arguments, see <a href="#">plot.default</a> .

**See Also**

[plot.factor](#), the [plot](#) method for factors.

**Examples**

```
## 1-d tables
(Poiss.tab <- table(N = stats::rpois(200, lambda = 5)))
plot(Poiss.tab, main = "plot(table(rpois(200, lambda = 5)))")

plot(table(state.division))

## 4-D :
plot(Titanic, main = "plot(Titanic, main= *)")
```

---

plot.window

*Set up World Coordinates for Graphics Window*


---

**Description**

This function sets up the world coordinate system for a graphics window. It is called by higher level functions such as [plot.default](#) (after [plot.new](#)).

**Usage**

```
plot.window(xlim, ylim, log = "", asp = NA, ...)
```

**Arguments**

xlim, ylim	numeric vectors of length 2, giving the x and y coordinates ranges.
log	character; indicating which axes should be in log scale.
asp	numeric, giving the <b>aspect</b> ratio y/x, see below.
...	further graphical parameters as in <a href="#">par</a> . The relevant ones are <code>xaxs</code> , <code>yaxs</code> and <code>lab</code> .

## Details

**asp:** If `asp` is a finite positive value then the window is set up so that one data unit in the x direction is equal in length to `asp × one data unit in the y direction`.

Note that in this case, `par("usr")` is no longer determined by, e.g., `par("xaxs")`, but rather by `asp` and the device's aspect ratio. (See what happens if you interactively resize the plot device after running the example below!)

The special case `asp == 1` produces plots where distances between points are represented accurately on screen. Values with `asp > 1` can be used to produce more accurate maps when using latitude and longitude.

To reverse an axis, use `xlim` or `ylim` of the form `c(hi, lo)`.

The function attempts to produce a plausible set of scales if one or both of `xlim` and `ylim` is of length one or the two values given are identical, but it is better to avoid that case.

Usually, one should rather use the higher level functions such as `plot`, `hist`, `image`, ..., instead and refer to their help pages for explanation of the arguments.

A side-effect of the call is to set up the `usr`, `xaxp` and `yaxp` graphical parameters. (It is for the latter two that `lab` is used.)

## See Also

[xy.coords](#), [plot.xy](#), [plot.default](#).

## Examples

```
##--- An example for the use of 'asp' :
require(stats) # normally loaded
loc <- cmdscale(eurodist)
rx <- range(x <- loc[,1])
ry <- range(y <- -loc[,2])
plot(x, y, type="n", asp=1, xlab="", ylab="")
abline(h = pretty(rx, 10), v = pretty(ry, 10), col = "lightgray")
text(x, y, labels(eurodist), cex=0.8)
```

---

plot.xy

*Basic Internal Plot Function*

---

## Description

This is *the* internal function that does the basic plotting of points and lines. Usually, one should rather use the higher level functions instead and refer to their help pages for explanation of the arguments.

## Usage

```
plot.xy(xy, type, pch = par("pch"), lty = par("lty"),
        col = par("col"), bg = NA,
        cex = 1, lwd = par("lwd"), ...)
```

**Arguments**

<code>xy</code>	A four-element list as results from <code>xy.coords</code> .
<code>type</code>	1 character code: see <code>plot.default</code> . NULL is accepted as a synonym for "p".
<code>pch</code>	character or integer code for kind of points, see <code>points.default</code> .
<code>lty</code>	line type code, see <code>lines</code> .
<code>col</code>	color code or name, see <code>colors</code> , <code>palette</code> . Here NULL means colour 0.
<code>bg</code>	background (fill) color for the open plot symbols 21:25: see <code>points.default</code> .
<code>cex</code>	character expansion.
<code>lwd</code>	line width, also used for (non-filled) plot symbols, see <code>lines</code> and <code>points</code> .
<code>...</code>	further graphical parameters such as <code>xpd</code> , <code>lend</code> , <code>ljoin</code> and <code>lmitre</code> .

**Details**

The arguments `pch`, `col`, `bg`, `cex`, `lwd` may be vectors and may be recycled, depending on `type`: see `points` and `lines` for specifics. In particular note that `lwd` is treated as a vector for points and as a single (first) value for lines.

`cex` is a numeric factor in addition to `par("cex")` which affects symbols and characters as drawn by type "p", "o", "b" and "c".

**See Also**

`plot`, `plot.default`, `points`, `lines`.

**Examples**

```
points.default # to see how it calls "plot.xy(xy.coords(x, y), ...)"
```

---

`points` *Add Points to a Plot*

---

**Description**

`points` is a generic function to draw a sequence of points at the specified coordinates. The specified character(s) are plotted, centered at the coordinates.

**Usage**

```
points(x, ...)

## Default S3 method:
points(x, y = NULL, type = "p", ...)
```

**Arguments**

<code>x, y</code>	coordinate vectors of points to plot.
<code>type</code>	character indicating the type of plotting; actually any of the types as in <code>plot.default</code> .
<code>...</code>	Further graphical parameters may also be supplied as arguments. See 'Details'.

## Details

The coordinates can be passed in a plotting structure (a list with `x` and `y` components), a two-column matrix, a time series, ... See `xy.coords`. If supplied separately, they must be of the same length.

Graphical parameters commonly used are

`pch` plotting 'character', i.e., symbol to use. This can either be a single character or an integer code for one of a set of graphics symbols. The full set of S symbols is available with `pch=0:18`, see the examples below. (NB: R uses circles instead of the octagons used in S.)

Value `pch="."` (equivalently `pch = 46`) is handled specially. It is a rectangle of side 0.01 inch (scaled by `cex`). In addition, if `cex = 1` (the default), each side is at least one pixel (1/72 inch on the `pdf`, `postscript` and `xfig` devices).

For other text symbols, `cex = 1` corresponds to the default fontsize of the device, often specified by an argument `pointsize`. For `pch` in `0:25` the default size is about 75% of the character height (see `par("cin")`).

`col` color code or name, see `par`.

`bg` background (fill) color for the open plot symbols given by `pch=21:25`.

`cex` character (or symbol) expansion: a numerical vector. This works as a multiple of `par("cex")`.

`lwd` line width for drawing symbols see `par`.

Others less commonly used are `lty` and `lwd` for types such as "b" and "l".

Graphical parameters `pch`, `col`, `bg`, `cex` and `lwd` can be vectors (which will be recycled as needed) giving a value for each point plotted. If lines are to be plotted (e.g. for `type = "b"/` the first element of `lwd` is used).

Points whose `x`, `y`, `pch`, `col` or `cex` value is NA are omitted from the plot.

## 'pch' values

Values of `pch` are stored internally as integers. The interpretation is

- `NA_integer_`: no symbol.
- `0:18`: S-compatible vector symbols.
- `19:25`: further R vector symbols.
- `26:31`: unused (and ignored).
- `32:127`: ASCII characters.
- `128:255` native characters *only in a single-byte locale and for the symbol font*. (`128:159` are only used on Windows.)
- `-32 ...` Unicode point (where supported).

Note that unlike S (which uses octagons), symbols 1, 10, 13 and 16 use circles. The filled shapes `15:18` do not include a border.

The following R plotting symbols are can be obtained with `pch=19:25`: those with `21:25` can be colored and filled with different colors: `col` gives the border color and `bg` the background color.

- `pch=19`: solid circle,
- `pch=20`: bullet (smaller solid circle, 2/3 the size of 19),
- `pch=21`: filled circle,
- `pch=22`: filled square,

- `pch=23`: filled diamond,
- `pch=24`: filled triangle point-up,
- `pch=25`: filled triangle point down.

Note that all of these both fill the shape and draw a border. Some care in interpretation is needed when semi-transparent colours are used for both fill and border (and the result might be device-specific and even viewer-specific for [pdf](#)).

The difference between `pch=16` and `pch=19` is that the latter uses a border and so is perceptibly larger when `lty` is large relative to `cex`.

Values `pch=26:31` are currently unused and `pch=32:127` give the ASCII characters. In a single-byte locale `pch=128:255` give the corresponding character (if any) in the locale's character set. Where supported by the OS, negative values specify a Unicode point, so e.g. `-0x2642L` is a 'male sign' and `-0x20ACL` is the Euro.

A character string consisting of a single character is converted to an integer: `32:127` for ASCII characters, and usually to the Unicode point number otherwise. (In non-Latin-1 single-byte locales, `128:255` will be used for 8-bit characters.)

If `pch` supplied is a logical, integer or character NA or an empty character string the point is omitted from the plot.

If `pch` is NULL or otherwise of length 0, `par("pch")` is used.

If the symbol font (`par(font = 5)`) is used, numerical values should be used for `pch`: the range is `c(32:126, 160:254)` in all locales (but 240 is not defined (used for 'apple' on Mac OS) and 160, Euro, may not be present).

### Note

A single-byte encoding may include the characters in `pch=128:255`, and if it does, a font may not include all (or even any) of them.

Not all negative numbers are valid as Unicode points, and no check is done. A display device is likely to use a rectangle for (or omit) Unicode points that do not exist or which it does not have a glyph.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[plot](#), [lines](#), and the underlying workhorse function [plot.xy](#).

### Examples

```
require(stats) # for rnorm
plot(-4:4, -4:4, type = "n")# setting up coord. system
points(rnorm(200), rnorm(200), col = "red")
points(rnorm(100)/2, rnorm(100)/2, col = "blue", cex = 1.5)

op <- par(bg = "light blue")
x <- seq(0, 2*pi, len=51)
## something "between type='b' and type='o'":
plot(x, sin(x), type="o", pch=21, bg=par("bg"), col = "blue", cex=.6,
     main='plot(..., type="o", pch=21, bg=par("bg"))')
```

```

par(op)

##----- Showing all the extra & some char graphics symbols -----
pchShow <-
  function(extras = c("*", ".", "o", "O", "0", "+", "-", "|", "%", "#"),
           cex = 3, ## good for both .Device=="postscript" and "x11"
           col = "red3", bg = "gold", coltext = "brown", cextext = 1.2,
           main = paste("plot symbols : points (... pch = *, cex =",
                        cex, ")"))
  {
    nex <- length(extras)
    np <- 26 + nex
    ipch <- 0:(np-1)
    k <- floor(sqrt(np))
    dd <- c(-1,1)/2
    rx <- dd + range(ix <- ipch %% k)
    ry <- dd + range(iy <- 3 + (k-1) - ipch %% k)
    pch <- as.list(ipch) # list with integers & strings
    if(nex > 0) pch[26+ 1:nex] <- as.list(extras)
    plot(rx, ry, type="n", axes = FALSE, xlab = "", ylab = "",
         main = main)
    abline(v = ix, h = iy, col = "lightgray", lty = "dotted")
    for(i in 1:np) {
      pc <- pch[[i]]
      ## 'col' symbols with a 'bg'-colored interior (where available) :
      points(ix[i], iy[i], pch = pc, col = col, bg = bg, cex = cex)
      if(cextext > 0)
        text(ix[i] - 0.3, iy[i], pc, col = coltext, cex = cextext)
    }
  }

pchShow()
pchShow(c("o", "O", "0"), cex = 2.5)
pchShow(NULL, cex = 4, cextext = 0, main = NULL)

## ----- test code for various pch specifications -----
# Try this in various font families (including Hershey)
# and locales. Use sign=-1 asserts we want Latin-1.
# Standard cases in a MBCS locale will not plot the top half.
TestChars <- function(sign=1, font=1, ...)
{
  if(font == 5) { sign <- 1; r <- c(32:126, 160:254)
  } else if (l10n_info()$MBCS) r <- 32:126 else r <- 32:255
  if (sign == -1) r <- c(32:126, 160:255)
  par(pty="s")
  plot(c(-1,16), c(-1,16), type="n", xlab="", ylab="",
        xaxs="i", yaxs="i")
  grid(17, 17, lty=1)
  for(i in r) try(points(i%%16, i%%16, pch=sign*i, font=font,...))
}
TestChars()
try(TestChars(sign=-1)) # needs MBCS support
TestChars(font=5) # Euro might be at 160. Mac OS has apple at 240.

```

---

 polygon

*Polygon Drawing*


---

**Description**

`polygon` draws the polygons whose vertices are given in `x` and `y`.

**Usage**

```

polygon(x, y = NULL, density = NULL, angle = 45,
        border = NULL, col = NA, lty = par("lty"),
        ..., fillOddEven = FALSE)

```

**Arguments**

<code>x, y</code>	vectors containing the coordinates of the vertices of the polygon.
<code>density</code>	the density of shading lines, in lines per inch. The default value of <code>NULL</code> means that no shading lines are drawn. A zero value of <code>density</code> means no shading nor filling whereas negative values (and <code>NA</code> ) suppress shading (and so allow color filling).
<code>angle</code>	the slope of shading lines, given as an angle in degrees (counter-clockwise).
<code>col</code>	the color for filling the polygon. The default, <code>NA</code> , is to leave polygons unfilled, unless <code>density</code> is specified. (For back-compatibility, <code>NULL</code> is equivalent to <code>NA</code> .) If <code>density</code> is specified with a positive value this gives the color of the shading lines.
<code>border</code>	the color to draw the border. The default, <code>NULL</code> , means to use <code>par("fg")</code> . Use <code>border = NA</code> to omit borders.  For compatibility with <code>S</code> , <code>border</code> can also be logical, in which case <code>FALSE</code> is equivalent to <code>NA</code> (borders omitted) and <code>TRUE</code> is equivalent to <code>NULL</code> (use the foreground colour),
<code>lty</code>	the line type to be used, as in <code>par</code> .
<code>...</code>	graphical parameters such as <code>xpd</code> , <code>lend</code> , <code>ljoin</code> and <code>lmitre</code> can be given as arguments.
<code>fillOddEven</code>	logical controlling the polygon fill mode: see below for details. Default <code>FALSE</code> .

**Details**

The coordinates can be passed in a plotting structure (a list with `x` and `y` components), a two-column matrix, .... See [xy.coords](#).

It is assumed that the polygon is to be closed by joining the last point to the first point.

The coordinates can contain missing values. The behaviour is similar to that of [lines](#), except that instead of breaking a line into several lines, `NA` values break the polygon into several complete polygons (including closing the last point to the first point). See the examples below.

When multiple polygons are produced, the values of `density`, `angle`, `col`, `border`, and `lty` are recycled in the usual manner.



**Bugs**

Self-intersecting polygons may be filled using either the “odd-even” or “non-zero” rule. These fill a region if the polygon border encircles it an odd or non-zero number of times, respectively. Shading lines are handled internally by R according to the `fillOddEven` argument, but device-based solid fills depend on the graphics device. The `pdf` and `postscript` devices have their own `fillOddEven` argument to control this.

**Author(s)**

The code implementing `polygon` shading was donated by Kevin Buhr <buhr@stat.wisc.edu>.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

**See Also**

`segments` for even more flexibility, `lines`, `rect`, `box`, `abline`.

`par` for how to specify colors.

**Examples**

```
x <- c(1:9, 8:1)
y <- c(1, 2*(5:3), 2, -1, 17, 9, 8, 2:9)
op <- par(mfcol=c(3,1))
for(xpd in c(FALSE, TRUE, NA)) {
  plot(1:10, main = paste("xpd =", xpd))
  box("figure", col = "pink", lwd=3)
  polygon(x, y, xpd=xpd, col="orange", lty=2, lwd=2, border="red")
}
par(op)

n <- 100
xx <- c(0:n, n:0)
yy <- c(c(0, cumsum(stats::rnorm(n))), rev(c(0, cumsum(stats::rnorm(n)))))
plot(xx, yy, type="n", xlab="Time", ylab="Distance")
polygon(xx, yy, col="gray", border = "red")
title("Distance Between Brownian Motions")

# Multiple polygons from NA values
# and recycling of col, border, and lty
op <- par(mfrow=c(2,1))
plot(c(1,9), 1:2, type="n")
polygon(1:9, c(2,1,2,1,1,2,1,2,1),
  col=c("red", "blue"),
  border=c("green", "yellow"),
  lwd=3, lty=c("dashed", "solid"))
plot(c(1,9), 1:2, type="n")
polygon(1:9, c(2,1,2,1,NA,2,1,2,1),
  col=c("red", "blue"),
  border=c("green", "yellow"),
  lwd=3, lty=c("dashed", "solid"))
```

```

par(op)

# Line-shaded polygons
plot(c(1,9), 1:2, type="n")
polygon(1:9, c(2,1,2,1,NA,2,1,2,1),
        density=c(10, 20), angle=c(-45, 45))

```

---

rasterImage

*Draw One or More Raster Images*


---

## Description

`rasterImage` draws a raster image at the given locations and sizes.

## Usage

```

rasterImage(image,
            xleft, ybottom, xright, ytop,
            angle = 0, interpolate = TRUE, ...)

```

## Arguments

<code>image</code>	a raster object, or an object that can be coerced to one.
<code>xleft</code>	a vector (or scalar) of left x positions.
<code>ybottom</code>	a vector (or scalar) of bottom y positions.
<code>xright</code>	a vector (or scalar) of right x positions.
<code>ytop</code>	a vector (or scalar) of top y positions.
<code>angle</code>	angle of rotation (in degrees, anti-clockwise from positive x-axis, about the bottom-left corner).
<code>interpolate</code>	a logical vector (or scalar) indicating whether to apply linear interpolation to the image when drawing.
<code>...</code>	graphical parameters.

## Details

The positions supplied, i.e., `xleft`, `...`, are relative to the current plotting region. If the x-axis goes from 100 to 200 then `xleft` should be larger than 100 and `xright` should be less than 200. The position vectors will be recycled to the length of the longest.

## See Also

[rect](#), [polygon](#), and [segments](#) and others for flexible ways to draw shapes.

**Examples**

```

require(grDevices)
## set up the plot region:
op <- par(bg = "thistle")
plot(c(100, 250), c(300, 450), type = "n", xlab="", ylab="")
image <- as.raster(matrix(0:1, ncol=5, nrow=3))
rasterImage(image, 100, 300, 150, 350, interpolate=FALSE)
rasterImage(image, 100, 400, 150, 450)
rasterImage(image, 200, 300, 200 + xinch(.5), 300 + yinch(.3),
            interpolate=FALSE)
rasterImage(image, 200, 400, 250, 450, angle=15, interpolate=FALSE)
par(op)

```

rect

*Draw One or More Rectangles***Description**

rect draws a rectangle (or sequence of rectangles) with the given coordinates, fill and border colors.

**Usage**

```

rect(xleft, ybottom, xright, ytop, density = NULL, angle = 45,
     col = NA, border = NULL, lty = par("lty"), lwd = par("lwd"),
     ...)

```

**Arguments**

xleft	a vector (or scalar) of left x positions.
ybottom	a vector (or scalar) of bottom y positions.
xright	a vector (or scalar) of right x positions.
ytop	a vector (or scalar) of top y positions.
density	the density of shading lines, in lines per inch. The default value of NULL means that no shading lines are drawn. A zero value of density means no shading lines whereas negative values (and NA) suppress shading (and so allow color filling).
angle	angle (in degrees) of the shading lines.
col	color(s) to fill or shade the rectangle(s) with. The default NA (or also NULL) means do not fill, i.e., draw transparent rectangles, unless density is specified.
border	color for rectangle border(s). The default means par("fg"). Use border = NA to omit borders. If there are shading lines, border = TRUE means use the same colour for the border as for the shading lines.
lty	line type for borders and shading; defaults to "solid".
lwd	line width for borders and shading.
...	graphical parameters such as xpd, lend, ljoin and lmitre can be given as arguments.

## Details

The positions supplied, i.e., `xleft`, . . . , are relative to the current plotting region. If the x-axis goes from 100 to 200 then `xleft` must be larger than 100 and `xright` must be less than 200. The position vectors will be recycled to the length of the longest.

It is a graphics primitive used in [hist](#), [barplot](#), [legend](#), etc.

## See Also

[box](#) for the standard box around the plot; [polygon](#) and [segments](#) for flexible line drawing.

[par](#) for how to specify colors.

## Examples

```
require(grDevices)
## set up the plot region:
op <- par(bg = "thistle")
plot(c(100, 250), c(300, 450), type = "n", xlab="", ylab="",
      main = "2 x 11 rectangles; 'rect(100+i,300+i, 150+i,380+i)'" )
i <- 4*(0:10)
## draw rectangles with bottom left (100, 300)+i
## and top right (150, 380)+i
rect(100+i, 300+i, 150+i, 380+i, col=rainbow(11, start=.7,end=.1))
rect(240-i, 320+i, 250-i, 410+i, col=heat.colors(11), lwd=i/5)
## Background alternating ( transparent / "bg" ) :
j <- 10*(0:5)
rect(125+j, 360+j, 141+j, 405+j/2, col = c(NA,0),
     border = "gold", lwd = 2)
rect(125+j, 296+j/2, 141+j, 331+j/5, col = c(NA,"midnightblue"))
mtext("+ 2 x 6 rect(*, col = c(NA,0)) and col = c(NA,\"m..blue\")")

## an example showing colouring and shading
plot(c(100, 200), c(300, 450), type= "n", xlab="", ylab="")
rect(100, 300, 125, 350) # transparent
rect(100, 400, 125, 450, col="green", border="blue") # coloured
rect(115, 375, 150, 425, col=par("bg"), border="transparent")
rect(150, 300, 175, 350, density=10, border="red")
rect(150, 400, 175, 450, density=30, col="blue",
     angle=-30, border="transparent")

legend(180, 450, legend=1:4, fill=c(NA, "green", par("fg"), "blue"),
       density=c(NA, NA, 10, 30), angle=c(NA, NA, 30, -30))

par(op)
```

## Description

Adds a *rug* representation (1-d plot) of the data to the plot.

## Usage

```
rug(x, ticksize = 0.03, side = 1, lwd = 0.5, col = par("fg"),
    quiet = getOption("warn") < 0, ...)
```

## Arguments

<code>x</code>	A numeric vector
<code>ticksize</code>	The length of the ticks making up the ‘rug’. Positive lengths give inwards ticks.
<code>side</code>	On which side of the plot box the rug will be plotted. Normally 1 (bottom) or 3 (top).
<code>lwd</code>	The line width of the ticks. Some devices will round the default width up to 1.
<code>col</code>	The colour the ticks are plotted in.
<code>quiet</code>	logical indicating if there should be a warning about clipped values.
<code>...</code>	further arguments, passed to <code>axis</code> , such as <code>line</code> or <code>pos</code> for specifying the location of the rug.

## Details

Because of the way `rug` is implemented, only values of `x` that fall within the plot region are included. There will be a warning if any finite values are omitted, but non-finite values are omitted silently.

Prior to R 2.8.0 `rug` re-drew the axis like: it no longer does so.

## References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

## See Also

`jitter` which you may want for ties in `x`.

## Examples

```
require(stats)# both 'density' and its default method
with(faithful, {
  plot(density(eruptions, bw = 0.15))
  rug(eruptions)
  rug(jitter(eruptions, amount = 0.01), side = 3, col = "light blue")
})
```

## Description

`split.screen` defines a number of regions within the current device which can, to some extent, be treated as separate graphics devices. It is useful for generating multiple plots on a single device. Screens can themselves be split, allowing for quite complex arrangements of plots.

`screen` is used to select which screen to draw in.

`erase.screen` is used to clear a single screen, which it does by filling with the background colour.

`close.screen` removes the specified screen definition(s).

## Usage

```
split.screen(figs, screen, erase = TRUE)
screen(n = , new = TRUE)
erase.screen(n = )
close.screen(n, all.screens = FALSE)
```

## Arguments

<code>figs</code>	A two-element vector describing the number of rows and the number of columns in a screen matrix <i>or</i> a matrix with 4 columns. If a matrix, then each row describes a screen with values for the left, right, bottom, and top of the screen (in that order) in NDC units, that is 0 at the lower left corner of the device surface, and 1 at the upper right corner.
<code>screen</code>	A number giving the screen to be split. It defaults to the current screen if there is one, otherwise the whole device region.
<code>erase</code>	logical: should selected screen be cleared?
<code>n</code>	A number indicating which screen to prepare for drawing ( <code>screen</code> ), erase ( <code>erase.screen</code> ), or close ( <code>close.screen</code> ). ( <code>close.screen</code> will accept a vector of screen numbers.)
<code>new</code>	A logical value indicating whether the screen should be erased as part of the preparation for drawing in the screen.
<code>all.screens</code>	A logical value indicating whether all of the screens should be closed.

## Details

The first call to `split.screen` places R into split-screen mode. The other split-screen functions only work within this mode. While in this mode, certain other commands should be avoided (see the Warnings section below). Split-screen mode is exited by the command `close.screen(all = TRUE)`.

If the current screen is closed, `close.screen` sets the current screen to be the next larger screen number if there is one, otherwise to the first available screen.

## Value

`split.screen` returns a vector of screen numbers for the newly-created screens. With no arguments, `split.screen` returns a vector of valid screen numbers.

`screen` invisibly returns the number of the selected screen. With no arguments, `screen` returns the number of the current screen.

`close.screen` returns a vector of valid screen numbers.

`screen`, `erase.screen`, and `close.screen` all return `FALSE` if `R` is not in split-screen mode.

### Warnings

The recommended way to use these functions is to completely draw a plot and all additions (i.e. points and lines) to the base plot, prior to selecting and plotting on another screen. The behavior associated with returning to a screen to add to an existing plot is unpredictable and may result in problems that are not readily visible.

These functions are totally incompatible with the other mechanisms for arranging plots on a device: `par(mfrow)`, `par(mfcol)` and `layout()`.

The functions are also incompatible with some plotting functions, such as `coplot`, which make use of these other mechanisms.

`erase.screen` will appear not to work if the background colour is transparent (as it is by default on most devices).

### References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

### See Also

`par`, `layout`, `Devices`, `dev.*`

### Examples

```
if (interactive()) {
  par(bg = "white")           # default is likely to be transparent
  split.screen(c(2,1))       # split display into two screens
  split.screen(c(1,3), screen = 2) # now split the bottom half into 3
  screen(1) # prepare screen 1 for output
  plot(10:1)
  screen(4) # prepare screen 4 for output
  plot(10:1)
  close.screen(all = TRUE)   # exit split-screen mode

  split.screen(c(2,1))       # split display into two screens
  split.screen(c(1,2), 2)    # split bottom half in two
  plot(1:10)                 # screen 3 is active, draw plot
  erase.screen()             # forgot label, erase and redraw
  plot(1:10, ylab= "ylab 3")
  screen(1)                  # prepare screen 1 for output
  plot(1:10)
  screen(4)                  # prepare screen 4 for output
  plot(1:10, ylab="ylab 4")
  screen(1, FALSE)          # return to screen 1, but do not clear
  plot(10:1, axes=FALSE, lty=2, ylab="") # overlay second plot
  axis(4)                   # add tic marks to right-hand axis
  title("Plot 1")
  close.screen(all = TRUE)   # exit split-screen mode
}
```

---

 segments

*Add Line Segments to a Plot*


---

### Description

Draw line segments between pairs of points.

### Usage

```
segments(x0, y0, x1 = x0, y1 = y0,
         col = par("fg"), lty = par("lty"), lwd = par("lwd"),
         ...)
```

### Arguments

`x0`, `y0` coordinates of points **from** which to draw.

`x1`, `y1` coordinates of points **to** which to draw. At least one must be supplied.

`col`, `lty`, `lwd` graphical parameters as in [par](#), possibly vectors. NA values in `col` cause the segment to be omitted.

... further graphical parameters (from [par](#)), such as `xpd` and the line characteristics `lend`, `ljoin` and `lmitre`.

### Details

For each `i`, a line segment is drawn between the point  $(x0[i], y0[i])$  and the point  $(x1[i], y1[i])$ . The coordinate vectors will be recycled to the length of the longest.

The graphical parameters `col`, `lty` and `lwd` can be vectors of length greater than one and will be recycled if necessary.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[arrows](#), [polygon](#) for slightly easier and less flexible line drawing, and [lines](#) for the usual polygons.

### Examples

```
x <- stats::runif(12); y <- stats::rnorm(12)
i <- order(x,y); x <- x[i]; y <- y[i]
plot(x, y, main="arrows(.) and segments(.)")
## draw arrows from point to point :
s <- seq(length(x)-1)# one shorter than data
arrows(x[s], y[s], x[s+1], y[s+1], col= 1:3)
s <- s[-length(s)]
segments(x[s], y[s], x[s+2], y[s+2], col= 'pink')
```



## Description

`smoothScatter` produces a smoothed color density representation of the scatterplot, obtained through a kernel density estimate. `densCols` produces a vector containing colors which encode the local densities at each point in a scatterplot.

## Usage

```
smoothScatter(x, y = NULL, nbin = 128, bandwidth,
              colramp = colorRampPalette(c("white", blues9)),
              nrpoints = 100, pch = ".", cex = 1, col = "black",
              transformation = function(x) x^.25,
              postPlotHook = box,
              xlab = NULL, ylab = NULL, xlim, ylim,
              xaxs = par("xaxs"), yaxs = par("yaxs"), ...)
```

## Arguments

<code>x, y</code>	the <code>x</code> and <code>y</code> arguments provide the <code>x</code> and <code>y</code> coordinates for the plot. Any reasonable way of defining the coordinates is acceptable. See the function <a href="#">xy.coords</a> for details. If supplied separately, they must be of the same length.
<code>nbin</code>	numeric vector of length one (for both directions) or two (for <code>x</code> and <code>y</code> separately) specifying the number of equally spaced grid points for the density estimation; directly used as <code>gridsize</code> in <a href="#">bkde2D()</a> .
<code>bandwidth</code>	numeric vector (length 1 or 2) of smoothing bandwidth(s). If missing, a more or less useful default is used. <code>bandwidth</code> is subsequently passed to function <a href="#">bkde2D</a> .
<code>colramp</code>	function accepting an integer <code>n</code> as an argument and returning <code>n</code> colors.
<code>nrpoints</code>	number of points to be superimposed on the density image. The first <code>nrpoints</code> points from those areas of lowest regional densities will be plotted. Adding points to the plot allows for the identification of outliers. If all points are to be plotted, choose <code>nrpoints = Inf</code> .
<code>pch, cex, col</code>	arguments passed to <a href="#">points</a> , when <code>nrpoints &gt; 0</code> : point symbol, character expansion factor and color, see also <a href="#">par</a> .
<code>transformation</code>	function mapping the density scale to the color scale.
<code>postPlotHook</code>	either <code>NULL</code> or a function which will be called (with no arguments) after <a href="#">image</a> .
<code>xlab, ylab</code>	character strings to be used as axis labels, passed to <a href="#">image</a> .
<code>xlim, ylim</code>	numeric vectors of length 2 specifying axis limits.
<code>xaxs, yaxs, ...</code>	further arguments, passed to <a href="#">image</a> .

**Details**

`smoothScatter` produces a smoothed version of a scatter plot. Two dimensional (kernel density) smoothing is performed by `bkde2D` from package **KernSmooth**. See the examples for how to use this function together with `pairs`.

**Author(s)**

Florian Hahne at FHCRC, originally

**See Also**

`bkde2D` from package **KernSmooth**; `densCols` which uses the same smoothing computations and `blues9` in package **grDevices**.

`scatter.smooth` adds a `loess` regression smoother to a scatter plot.

**Examples**

```
## A largish data set
n <- 10000
x1 <- matrix(rnorm(n), ncol=2)
x2 <- matrix(rnorm(n, mean=3, sd=1.5), ncol=2)
x <- rbind(x1,x2)

oldpar <- par(mfrow=c(2,2))
smoothScatter(x, nrpoints=0)
smoothScatter(x)

## a different color scheme:
Lab.palette <- colorRampPalette(c("blue", "orange", "red"), space = "Lab")
smoothScatter(x, colramp = Lab.palette)

## somewhat similar, using identical smoothing computations,
## but considerably *less* efficient for really large data:
plot(x, col = densCols(x), pch=20)

## use with pairs:
par(mfrow=c(1,1))
y <- matrix(rnorm(40000), ncol=4) + 3*rnorm(10000)
y[, c(2,4)] <- -y[, c(2,4)]
pairs(y, panel=function(...) {par(new=TRUE);smoothScatter(..., nrpoints=0)})

par(oldpar)
```

**Description**

Spine plots are a special cases of mosaic plots, and can be seen as a generalization of stacked (or highlighted) bar plots. Analogously, spinograms are an extension of histograms.

**Usage**

```

spineplot(x, ...)

## Default S3 method:
spineplot(x, y = NULL,
          breaks = NULL, tol.ylab = 0.05, off = NULL,
          ylevels = NULL, col = NULL,
          main = "", xlab = NULL, ylab = NULL,
          xaxlabels = NULL, yaxlabels = NULL,
          xlim = NULL, ylim = c(0, 1), axes = TRUE, ...)

## S3 method for class 'formula':
spineplot(formula, data = list(),
          breaks = NULL, tol.ylab = 0.05, off = NULL,
          ylevels = NULL, col = NULL,
          main = "", xlab = NULL, ylab = NULL,
          xaxlabels = NULL, yaxlabels = NULL,
          xlim = NULL, ylim = c(0, 1), axes = TRUE, ...,
          subset = NULL)

```

**Arguments**

<code>x</code>	an object, the default method expects either a single variable (interpreted to be the explanatory variable) or a 2-way table. See details.
<code>y</code>	a "factor" interpreted to be the dependent variable
<code>formula</code>	a "formula" of type $y \sim x$ with a single dependent "factor" and a single explanatory variable.
<code>data</code>	an optional data frame.
<code>breaks</code>	if the explanatory variable is numeric, this controls how it is discretized. <code>breaks</code> is passed to <code>hist</code> and can be a list of arguments.
<code>tol.ylab</code>	convenience tolerance parameter for y-axis annotation. If the distance between two labels drops under this threshold, they are plotted equidistantly.
<code>off</code>	vertical offset between the bars (in per cent). It is fixed to 0 for spinograms and defaults to 2 for spine plots.
<code>ylevels</code>	a character or numeric vector specifying in which order the levels of the dependent variable should be plotted.
<code>col</code>	a vector of fill colors of the same length as <code>levels(y)</code> . The default is to call <code>gray.colors</code> .
<code>main, xlab, ylab</code>	character strings for annotation
<code>xaxlabels, yaxlabels</code>	character vectors for annotation of x and y axis. Default to <code>levels(y)</code> and <code>levels(x)</code> , respectively for the spine plot. For <code>xaxlabels</code> in the spinogram, the <code>breaks</code> are used.
<code>xlim, ylim</code>	the range of x and y values with sensible defaults.
<code>axes</code>	logical. If <code>FALSE</code> all axes (including those giving level names) are suppressed.
<code>...</code>	additional arguments passed to <code>rect</code> .
<code>subset</code>	an optional vector specifying a subset of observations to be used for plotting.

## Details

`spineplot` creates either a spinogram or a spine plot. It can be called via `spineplot(x, y)` or `spineplot(y ~ x)` where `y` is interpreted to be the dependent variable (and has to be categorical) and `x` the explanatory variable. `x` can be either categorical (then a spine plot is created) or numerical (then a spinogram is plotted). Additionally, `spineplot` can also be called with only a single argument which then has to be a 2-way table, interpreted to correspond to `table(x, y)`.

Both, spine plots and spinograms, are essentially mosaic plots with special formatting of spacing and shading. Conceptually, they plot  $P(y|x)$  against  $P(x)$ . For the spine plot (where both  $x$  and  $y$  are categorical), both quantities are approximated by the corresponding empirical relative frequencies. For the spinogram (where  $x$  is numerical),  $x$  is first discretized (by calling `hist` with `breaks` argument) and then empirical relative frequencies are taken.

Thus, spine plots can also be seen as a generalization of stacked bar plots where not the heights but the widths of the bars corresponds to the relative frequencies of  $x$ . The heights of the bars then correspond to the conditional relative frequencies of  $y$  in every  $x$  group. Analogously, spinograms extend stacked histograms.

## Value

The table visualized is returned invisibly.

## Author(s)

Achim Zeileis <Achim.Zeileis@R-project.org>

## References

- Friendly, M. (1994), Mosaic displays for multi-way contingency tables. *Journal of the American Statistical Association*, **89**, 190–200.
- Hartigan, J.A., and Kleiner, B. (1984), A mosaic of television ratings. *The American Statistician*, **38**, 32–35.
- Hofmann, H., Theus, M. (2005), *Interactive graphics for visualizing conditional distributions*, Unpublished Manuscript.
- Hummel, J. (1996), Linked bar charts: Analysing categorical data graphically. *Computational Statistics*, **11**, 23–33.

## See Also

`mosaicplot`, `hist`, `cdplot`

## Examples

```
## treatment and improvement of patients with rheumatoid arthritis
treatment <- factor(rep(c(1, 2), c(43, 41)), levels = c(1, 2),
                  labels = c("placebo", "treated"))
improved <- factor(rep(c(1, 2, 3, 1, 2, 3), c(29, 7, 7, 13, 7, 21)),
                 levels = c(1, 2, 3),
                 labels = c("none", "some", "marked"))

## (dependence on a categorical variable)
(spineplot(improved ~ treatment))

## applications and admissions by department at UC Berkeley
```

```
## (two-way tables)
(spineplot(margin.table(UCBAdmissions, c(3, 2)),
           main = "Applications at UCB"))
(spineplot(margin.table(UCBAdmissions, c(3, 1)),
           main = "Admissions at UCB"))

## NASA space shuttle o-ring failures
fail <- factor(c(2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 2, 1, 2, 1,
                1, 1, 1, 2, 1, 1, 1, 1, 1),
              levels = c(1, 2), labels = c("no", "yes"))
temperature <- c(53, 57, 58, 63, 66, 67, 67, 67, 68, 69, 70, 70,
                70, 70, 72, 73, 75, 75, 76, 76, 78, 79, 81)

## (dependence on a numerical variable)
(spineplot(fail ~ temperature))
(spineplot(fail ~ temperature, breaks = 3))
(spineplot(fail ~ temperature, breaks = quantile(temperature)))

## highlighting for failures
spineplot(fail ~ temperature, ylevels = 2:1)
```

stars

*Star (Spider/Radar) Plots and Segment Diagrams***Description**

Draw star plots or segment diagrams of a multivariate data set. With one single location, also draws ‘spider’ (or ‘radar’) plots.

**Usage**

```
stars(x, full = TRUE, scale = TRUE, radius = TRUE,
      labels = dimnames(x)[[1]], locations = NULL,
      nrow = NULL, ncol = NULL, len = 1,
      key.loc = NULL, key.labels = dimnames(x)[[2]],
      key.xpd = TRUE,
      xlim = NULL, ylim = NULL, flip.labels = NULL,
      draw.segments = FALSE,
      col.segments = 1:n.seg, col.stars = NA,
      axes = FALSE, frame.plot = axes,
      main = NULL, sub = NULL, xlab = "", ylab = "",
      cex = 0.8, lwd = 0.25, lty = par("lty"), xpd = FALSE,
      mar = pmin(par("mar"),
                 1.1+ c(2*axes+ (xlab != ""),
                       2*axes+ (ylab != ""), 1,0)),
      add = FALSE, plot = TRUE, ...)
```

**Arguments**

**x** matrix or data frame of data. One star or segment plot will be produced for each row of **x**. Missing values (NA) are allowed, but they are treated as if they were 0 (after scaling, if relevant).

<code>full</code>	logical flag: if <code>TRUE</code> , the segment plots will occupy a full circle. Otherwise, they occupy the (upper) semicircle only.
<code>scale</code>	logical flag: if <code>TRUE</code> , the columns of the data matrix are scaled independently so that the maximum value in each column is 1 and the minimum is 0. If <code>FALSE</code> , the presumption is that the data have been scaled by some other algorithm to the range $[0, 1]$ .
<code>radius</code>	logical flag: in <code>TRUE</code> , the radii corresponding to each variable in the data will be drawn.
<code>labels</code>	vector of character strings for labeling the plots. Unlike the S function <code>stars</code> , no attempt is made to construct labels if <code>labels = NULL</code> .
<code>locations</code>	Either two column matrix with the x and y coordinates used to place each of the segment plots; or numeric of length 2 when all plots should be superimposed (for a 'spider plot'). By default, <code>locations = NULL</code> , the segment plots will be placed in a rectangular grid.
<code>nrow, ncol</code>	integers giving the number of rows and columns to use when <code>locations</code> is <code>NULL</code> . By default, <code>nrow == ncol</code> , a square layout will be used.
<code>len</code>	scale factor for the length of radii or segments.
<code>key.loc</code>	vector with x and y coordinates of the unit key.
<code>key.labels</code>	vector of character strings for labeling the segments of the unit key. If omitted, the second component of <code>dimnames(x)</code> is used, if available.
<code>key.xpd</code>	clipping switch for the unit key (drawing and labeling), see <code>par("xpd")</code> .
<code>xlim</code>	vector with the range of x coordinates to plot.
<code>ylim</code>	vector with the range of y coordinates to plot.
<code>flip.labels</code>	logical indicating if the label locations should flip up and down from diagram to diagram. Defaults to a somewhat smart heuristic.
<code>draw.segments</code>	logical. If <code>TRUE</code> draw a segment diagram.
<code>col.segments</code>	color vector (integer or character, see <code>par</code> ), each specifying a color for one of the segments (variables). Ignored if <code>draw.segments = FALSE</code> .
<code>col.stars</code>	color vector (integer or character, see <code>par</code> ), each specifying a color for one of the stars (cases). Ignored if <code>draw.segments = TRUE</code> .
<code>axes</code>	logical flag: if <code>TRUE</code> axes are added to the plot.
<code>frame.plot</code>	logical flag: if <code>TRUE</code> , the plot region is framed.
<code>main</code>	a main title for the plot.
<code>sub</code>	a sub title for the plot.
<code>xlab</code>	a label for the x axis.
<code>ylab</code>	a label for the y axis.
<code>cex</code>	character expansion factor for the labels.
<code>lwd</code>	line width used for drawing.
<code>lty</code>	line type used for drawing.
<code>xpd</code>	logical or NA indicating if clipping should be done, see <code>par(xpd = .)</code> .
<code>mar</code>	argument to <code>par(mar = *)</code> , typically choosing smaller margins than by default.
<code>...</code>	further arguments, passed to the first call of <code>plot()</code> , see <code>plot.default</code> and to <code>box()</code> if <code>frame.plot</code> is true.
<code>add</code>	logical, if <code>TRUE</code> <i>add</i> stars to current plot.
<code>plot</code>	logical, if <code>FALSE</code> , nothing is plotted.

**Details**

Missing values are treated as 0.

Each star plot or segment diagram represents one row of the input `x`. Variables (columns) start on the right and wind counterclockwise around the circle. The size of the (scaled) column is shown by the distance from the center to the point on the star or the radius of the segment representing the variable.

Only one page of output is produced.

**Value**

Returns the locations of the plots in a two column matrix, invisibly when `plot=TRUE`.

**Note**

This code started life as spatial star plots by David A. Andrews. See <http://www.udallas.edu:8080/~andrews/software/software.html>.

Prior to 1.4.1, scaling only shifted the maximum to 1, although documented as here.

**Author(s)**

Thomas S. Dye

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[symbols](#) for another way to draw stars and other symbols.

**Examples**

```
require(grDevices)
stars(mtcars[, 1:7], key.loc = c(14, 2),
      main = "Motor Trend Cars : stars(*, full = F)", full = FALSE)
stars(mtcars[, 1:7], key.loc = c(14, 1.5),
      main = "Motor Trend Cars : full stars()", flip.labels=FALSE)

## 'Spider' or 'Radar' plot:
stars(mtcars[, 1:7], locations = c(0,0), radius = FALSE,
      key.loc=c(0,0), main="Motor Trend Cars", lty = 2)

## Segment Diagrams:
palette(rainbow(12, s = 0.6, v = 0.75))
stars(mtcars[, 1:7], len = 0.8, key.loc = c(12, 1.5),
      main = "Motor Trend Cars", draw.segments = TRUE)
stars(mtcars[, 1:7], len = 0.6, key.loc = c(1.5, 0),
      main = "Motor Trend Cars", draw.segments = TRUE,
      frame.plot=TRUE, nrow = 4, cex = .7)

## scale linearly (not affinely) to [0, 1]
USJudge <- apply(USJudgeRatings, 2, function(x) x/max(x))
Jnam <- row.names(USJudgeRatings)
```

```

Snam <- abbreviate(substring(Jnam,1,regexpr("[,\\.]",Jnam) - 1), 7)
stars(USJudge, labels = Jnam, scale = FALSE,
      key.loc = c(13, 1.5), main = "Judge not ...", len = 0.8)
stars(USJudge, labels = Snam, scale = FALSE,
      key.loc = c(13, 1.5), radius = FALSE)

loc <- stars(USJudge, labels = NULL, scale = FALSE,
            radius = FALSE, frame.plot = TRUE,
            key.loc = c(13, 1.5), main = "Judge not ...", len = 1.2)
text(loc, Snam, col = "blue", cex = 0.8, xpd = TRUE)

## 'Segments':
stars(USJudge, draw.segments = TRUE, scale = FALSE, key.loc = c(13,1.5))

## 'Spider':
stars(USJudgeRatings, locations=c(0,0), scale=FALSE,radius = FALSE,
      col.stars=1:10, key.loc = c(0,0), main="US Judges rated")
## 'Radar-Segments'
stars(USJudgeRatings[1:10,], locations = 0:1, scale=FALSE,
      draw.segments = TRUE, col.segments=0, col.stars=1:10,key.loc= 0:1,
      main="US Judges 1-10 ")
palette("default")
stars(cbind(1:16,10*(16:1)),draw.segments=TRUE,
      main = "A Joke -- do *not* use symbols on 2D data!")

```

stem

*Stem-and-Leaf Plots***Description**

stem produces a stem-and-leaf plot of the values in x. The parameter scale can be used to expand the scale of the plot. A value of scale=2 will cause the plot to be roughly twice as long as the default.

**Usage**

```
stem(x, scale = 1, width = 80, atom = 1e-08)
```

**Arguments**

x	a numeric vector.
scale	This controls the plot length.
width	The desired width of plot.
atom	a tolerance.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**Examples**

```

stem(islands)
stem(log10(islands))

```



stripchart

*1-D Scatter Plots***Description**

stripchart produces one dimensional scatter plots (or dot plots) of the given data. These plots are a good alternative to `boxplots` when sample sizes are small.

**Usage**

```
stripchart(x, ...)

## S3 method for class 'formula':
stripchart(x, data = NULL, dlab = NULL, ...,
           subset, na.action = NULL)

## Default S3 method:
stripchart(x, method = "overplot", jitter = 0.1, offset = 1/3,
           vertical = FALSE, group.names, add = FALSE,
           at = NULL, xlim = NULL, ylim = NULL,
           ylab=NULL, xlab=NULL, dlab="", glab="",
           log = "", pch = 0, col = par("fg"), cex = par("cex"),
           axes = TRUE, frame.plot = axes, ...)
```

**Arguments**

<code>x</code>	the data from which the plots are to be produced. In the default method the data can be specified as a single numeric vector, or as list of numeric vectors, each corresponding to a component plot. In the <code>formula</code> method, a symbolic specification of the form $y \sim g$ can be given, indicating the observations in the vector <code>y</code> are to be grouped according to the levels of the factor <code>g</code> . NAs are allowed in the data.
<code>data</code>	a data.frame (or list) from which the variables in <code>x</code> should be taken.
<code>subset</code>	an optional vector specifying a subset of observations to be used for plotting.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. The default is to ignore missing values in either the response or the group.
<code>...</code>	additional parameters passed to the default method, or by it to <code>plot</code> , <code>points</code> , <code>axis</code> and <code>title</code> to control the appearance of the plot.
<code>method</code>	the method to be used to separate coincident points. The default method "overplot" causes such points to be overplotted, but it is also possible to specify "jitter" to jitter the points, or "stack" have coincident points stacked. The last method only makes sense for very granular data.
<code>jitter</code>	when <code>method="jitter"</code> is used, <code>jitter</code> gives the amount of jittering applied.
<code>offset</code>	when stacking is used, points are stacked this many line-heights (symbol widths) apart.
<code>vertical</code>	when <code>vertical</code> is TRUE the plots are drawn vertically rather than the default horizontal.

`group.names` group labels which will be printed alongside (or underneath) each plot.  
`add` logical, if true *add* the chart to the current plot.  
`at` numeric vector giving the locations where the charts should be drawn, particularly when `add = TRUE`; defaults to `1:n` where `n` is the number of boxes.  
`ylab, xlab` labels: see [title](#).  
`dlab, glab` alternate way to specify axis labels: see ‘Details’.  
`xlim, ylim` plot limits: see [plot.window](#).  
`log` on which axes to use a log scale: see [plot.default](#)  
`pch, col, cex` Graphical parameters: see [par](#).  
`axes, frame.plot` Axis control: see [plot.default](#)

### Details

Extensive examples of the use of this kind of plot can be found in Box, Hunter and Hunter or Seber and Wild.

The `dlab` and `glab` labels may be used instead of `xlab` and `ylab` if those are not specified. `dlab` applies to the continuous data axis (the X axis unless `vertical` is `TRUE`), `glab` to the group axis.

### Examples

```

x <- stats::rnorm(50)
xr <- round(x, 1)
stripchart(x) ; m <- mean(par("usr")[1:2])
text(m, 1.04, "stripchart(x, \"overplot\")")
stripchart(xr, method = "stack", add = TRUE, at = 1.2)
text(m, 1.35, "stripchart(round(x,1), \"stack\")")
stripchart(xr, method = "jitter", add = TRUE, at = 0.7)
text(m, 0.85, "stripchart(round(x,1), \"jitter\")")

stripchart(decrease ~ treatment,
  main = "stripchart(OrchardSprays)",
  vertical = TRUE, log = "y", data = OrchardSprays)

stripchart(decrease ~ treatment, at = c(1:8)^2,
  main = "stripchart(OrchardSprays)",
  vertical = TRUE, log = "y", data = OrchardSprays)

```

### Description

These functions compute the width or height, respectively, of the given strings or mathematical expressions `s[i]` on the current plotting device in *user* coordinates, *inches* or as fraction of the figure width `par("fin")`.

**Usage**

```
strwidth(s, units = "user", cex = NULL, font = NULL, vfont = NULL, ...)
strheight(s, units = "user", cex = NULL, font = NULL, vfont = NULL, ...)
```

**Arguments**

**s** a character or [expression](#) vector whose dimensions are to be determined. Other objects are coerced by [as.graphicsAnnot](#).

**units** character indicating in which units **s** is measured; should be one of "user", "inches", "figure"; partial matching is performed.

**cex** numeric character **expansion** factor; multiplied by [par\("cex"\)](#) yields the final character size; the default NULL is equivalent to 1.

**font, vfont, ...** additional information about the font, possibly including the graphics parameter "family": see [text](#).

**Details**

Where an element of **s** is a multi-line string (that is, contains newlines '\n'), the width and height are of an enclosing rectangle of the string as plotted by [text](#). The inter-line spacing is controlled by **cex**, [par\("lheight"\)](#) and the 'point size' (but not the actual font in use).

Measurements in "user" units (the default) are only available after [plot.new](#) has been called – otherwise an error is thrown.

**Value**

Numeric vector with the same length as **s**, giving the width or height for each **s[i]**. NA strings are given width and height 0 (as they are not plotted).

**See Also**

[text](#), [nchar](#)

**Examples**

```
str.ex <- c("W", "w", "I", ".", "WwI.")
op <- par(pty='s'); plot(1:100, 1:100, type="n")
sw <- strwidth(str.ex); sw
all.equal(sum(sw[1:4]), sw[5])
#- since the last string contains the others

sw.i <- strwidth(str.ex, "inches"); 25.4 * sw.i # width in [mm]
unique(sw / sw.i)
# constant factor: 1 value
mean(sw.i / strwidth(str.ex, "fig")) / par('fin')[1] # = 1: are the same

## See how letters fall in classes
## -- depending on graphics device and font!
all.lett <- c(letters, LETTERS)
shL <- strheight(all.lett, units = "inches") * 72 # 'big points'
table(shL) # all have same heights ...
mean(shL)/par("cin")[2] # around 0.6
```

```
(swL <- strwidth(all.lett, units="inches") * 72) # 'big points'
split(all.lett, factor(round(swL, 2)))

sumex <- expression(sum(x[i], i=1,n), e^{i * pi} == -1)
strwidth(sumex)
strheight(sumex)

par(op)#- reset to previous setting
```

sunflowerplot

*Produce a Sunflower Scatter Plot***Description**

Multiple points are plotted as ‘sunflowers’ with multiple leaves (‘petals’) such that overplotting is visualized instead of accidental and invisible.

**Usage**

```
sunflowerplot(x, y = NULL, number, log = "", digits = 6,
              xlab = NULL, ylab = NULL, xlim = NULL, ylim = NULL,
              add = FALSE, rotate = FALSE,
              pch = 16, cex = 0.8, cex.fact = 1.5,
              col = par("col"), bg = NA, size = 1/8, seg.col = 2,
              seg.lwd = 1.5, ...)
```

**Arguments**

x	numeric vector of x-coordinates of length n, say, or another valid plotting structure, as for <code>plot.default</code> , see also <code>xy.coords</code> .
y	numeric vector of y-coordinates of length n.
number	integer vector of length n. <code>number[i]</code> = number of replicates for <code>(x[i], y[i])</code> , may be 0. Default ( <code>missing(number)</code> ): compute the exact multiplicity of the points <code>x[], y[]</code> , via <code>xyTable()</code> .
log	character indicating log coordinate scale, see <code>plot.default</code> .
digits	when <code>number</code> is computed (i.e., not specified), <code>x</code> and <code>y</code> are rounded to <code>digits</code> significant digits before multiplicities are computed.
xlab, ylab	character label for x-, or y-axis, respectively.
xlim, ylim	<code>numeric(2)</code> limiting the extents of the x-, or y-axis.
add	logical; should the plot be added on a previous one? Default is <code>FALSE</code> .
rotate	logical; if <code>TRUE</code> , randomly rotate the sunflowers (preventing artefacts).
pch	plotting character to be used for points ( <code>number[i]==1</code> ) and center of sunflowers.
cex	numeric; character size expansion of center points (s. <code>pch</code> ).
cex.fact	numeric <i>shrinking</i> factor to be used for the center points <i>when there are flower leaves</i> , i.e., <code>cex / cex.fact</code> is used for these.
col, bg	colors for the plot symbols, passed to <code>plot.default</code> .

size	of sunflower leaves in inches, 1[in] := 2.54[cm]. Default: 1/8", approximately 3.2mm.
seg.col	color to be used for the <b>segments</b> which make the sunflowers leaves, see <code>par(col=)</code> ; <code>col = "gold"</code> reminds of real sunflowers.
seg.lwd	numeric; the line width for the leaves' segments.
...	further arguments to <code>plot</code> [if <code>add=FALSE</code> ].

### Details

For `number[i]==1`, a (slightly enlarged) usual plotting symbol (`pch`) is drawn. For `number[i] > 1`, a small plotting symbol is drawn and `number[i]` equi-angular 'rays' emanate from it.

If `rotate=TRUE` and `number[i] >= 2`, a random direction is chosen (instead of the y-axis) for the first ray. The goal is to `jitter` the orientations of the sunflowers in order to prevent artefactual visual impressions.

### Value

A list with three components of same length,

x	x coordinates
y	y coordinates
number	number

Use `xyTable()` (from package **grDevices**) if you are only interested in this return value.

### Side Effects

A scatter plot is drawn with 'sunflowers' as symbols.

### Author(s)

Andreas Ruckstuhl, Werner Stahel, Martin Maechler, Tim Hesterberg, 1989–1993. Port to R by Martin Maechler <maechler@stat.math.ethz.ch>.

### References

Chambers, J. M., Cleveland, W. S., Kleiner, B. and Tukey, P. A. (1983) *Graphical Methods for Data Analysis*. Wadsworth.

Schilling, M. F. and Watkins, A. E. (1994) A suggestion for sunflower plots. *The American Statistician*, **48**, 303–305.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

### See Also

`density`, `xyTable`

**Examples**

```

require(stats)
require(grDevices)

## 'number' is computed automatically:
sunflowerplot(iris[, 3:4])
## Imitating Chambers et al., p.109, closely:
sunflowerplot(iris[, 3:4], cex=.2, cex.fact=1, size=.035, seg.lwd=.8)

sunflowerplot(x=sort(2*round(rnorm(100))), y= round(rnorm(100),0),
              main = "Sunflower Plot of Rounded N(0,1)")
## Similarly using a "xyTable" argument:
xyT <- xyTable(x=sort(2*round(rnorm(100))), y= round(rnorm(100),0),
              digits=3)
utils::str(xyT, vec.len=20)
sunflowerplot(xyT, main = "2nd Sunflower Plot of Rounded N(0,1)")

## A 'marked point process' {explicit 'number' argument}:
sunflowerplot(rnorm(100), rnorm(100), number = rpois(n=100,lambda=2),
              main="Sunflower plot (marked point process)",
              rotate=TRUE, col = "blue4")

```

symbols

---

*Draw Symbols (Circles, Squares, Stars, Thermometers, Boxplots) on a Plot*

---

**Description**

This function draws symbols on a plot. One of six symbols; *circles*, *squares*, *rectangles*, *stars*, *thermometers*, and *boxplots*, can be plotted at a specified set of x and y coordinates. Specific aspects of the symbols, such as relative size, can be customized by additional parameters.

**Usage**

```

symbols(x, y = NULL, circles, squares, rectangles, stars,
        thermometers, boxplots, inches = TRUE, add = FALSE,
        fg = par("col"), bg = NA,
        xlab = NULL, ylab = NULL, main = NULL,
        xlim = NULL, ylim = NULL, ...)

```

**Arguments**

<code>x, y</code>	the x and y co-ordinates for the centres of the symbols. They can be specified in any way which is accepted by <code>xy.coords</code> .
<code>circles</code>	a vector giving the radii of the circles.
<code>squares</code>	a vector giving the length of the sides of the squares.
<code>rectangles</code>	a matrix with two columns. The first column gives widths and the second the heights of rectangles.
<code>stars</code>	a matrix with three or more columns giving the lengths of the rays from the center of the stars. NA values are replaced by zeroes.

<code>thermometers</code>	a matrix with three or four columns. The first two columns give the width and height of the thermometer symbols. If there are three columns, the third is taken as a proportion: the thermometers are filled (using colour <code>fg</code> ) from their base to this proportion of their height. If there are four columns, the third and fourth columns are taken as proportions and the thermometers are filled between these two proportions of their heights. The part of the box not filled in <code>fg</code> will be filled in the background colour (default transparent) given by <code>bg</code> .
<code>boxplots</code>	a matrix with five columns. The first two columns give the width and height of the boxes, the next two columns give the lengths of the lower and upper whiskers and the fifth the proportion (with a warning if not in <code>[0,1]</code> ) of the way up the box that the median line is drawn.
<code>inches</code>	TRUE, FALSE or a positive number. See ‘Details’.
<code>add</code>	if <code>add</code> is TRUE, the symbols are added to an existing plot, otherwise a new plot is created.
<code>fg</code>	colour(s) the symbols are to be drawn in.
<code>bg</code>	if specified, the symbols are filled with colour(s), the vector <code>bg</code> being recycled to the number of symbols. The default is to leave the symbols unfilled.
<code>xlab</code>	the x label of the plot if <code>add</code> is not true. Defaults to the <code>deparsed</code> expression used for <code>x</code> .
<code>ylab</code>	the y label of the plot. Unused if <code>add = TRUE</code> .
<code>main</code>	a main title for the plot. Unused if <code>add = TRUE</code> .
<code>xlim</code>	numeric vector of length 2 giving the x limits for the plot. Unused if <code>add = TRUE</code> .
<code>ylim</code>	numeric vector of length 2 giving the y limits for the plot. Unused if <code>add = TRUE</code> .
<code>...</code>	graphics parameters can also be passed to this function, as can the plot aspect ratio <code>asp</code> (see <code>plot.window</code> ).

### Details

Observations which have missing coordinates or missing size parameters are not plotted. The exception to this is `stars`. In that case, the length of any ray which is NA is reset to zero.

Argument `inches` controls the sizes of the symbols. If TRUE (the default), the symbols are scaled so that the largest dimension of any symbol is one inch. If a positive number is given the symbols are scaled to make largest dimension this size in inches (so TRUE and 1 are equivalent). If `inches` is FALSE, the units are taken to be those of the appropriate axes. (For circles, squares and stars the units of the x axis are used. For boxplots, the lengths of the whiskers are regarded as dimensions alongside width and height when scaling by `inches`, and are otherwise interpreted in the units of the y axis.)

Circles of radius zero are plotted at radius one pixel (which is device-dependent).

### References

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- W. S. Cleveland (1985) *The Elements of Graphing Data*. Monterey, California: Wadsworth.
- Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

**See Also**

[stars](#) for drawing *stars* with a bit more flexibility.

If you are thinking about doing ‘bubble plots’ by symbols (\*, circles=\*), you should *really* consider using [sunflowerplot](#) instead.

**Examples**

```
require(stats); require(grDevices)
x <- 1:10
y <- sort(10*runif(10))
z <- runif(10)
z3 <- cbind(z, 2*runif(10), runif(10))
symbols(x, y, thermometers=cbind(.5, 1, z), inches=.5, fg = 1:10)
symbols(x, y, thermometers = z3, inches=FALSE)
text(x,y, apply(format(round(z3, digits=2)), 1, paste, collapse = ","),
      adj = c(-.2,0), cex = .75, col = "purple", xpd=NA)

## Note that example(trees) shows more sensible plots!
N <- nrow(trees)
with(trees, {
  ## Girth is diameter in inches
  symbols(Height, Volume, circles=Girth/24, inches=FALSE,
          main="Trees' Girth")# xlab and ylab automatically
  ## Colours too:
  palette(rainbow(N, end = 0.9))
  symbols(Height, Volume, circles=Girth/16, inches=FALSE, bg = 1:N,
          fg="gray30", main="symbols(*, circles=Girth/16, bg = 1:N)")
  palette("default")
})
```

---

text

*Add Text to a Plot*


---

**Description**

`text` draws the strings given in the vector `labels` at the coordinates given by `x` and `y`. `y` may be missing since `xy.coords(x, y)` is used for construction of the coordinates.

**Usage**

```
text(x, ...)

## Default S3 method:
text(x, y = NULL, labels = seq_along(x), adj = NULL,
      pos = NULL, offset = 0.5, vfont = NULL,
      cex = 1, col = NULL, font = NULL, ...)
```

**Arguments**

`x`, `y` numeric vectors of coordinates where the text labels should be written. If the length of `x` and `y` differs, the shorter one is recycled.



labels	a character vector or <a href="#">expression</a> specifying the <i>text</i> to be written. An attempt is made to coerce other language objects (names and calls) to expressions, and vectors and other classed objects to character vectors by <a href="#">as.character</a> . If labels is longer than x and y, the coordinates are recycled to the length of labels.
adj	one or two values in $[0, 1]$ which specify the x (and optionally y) adjustment of the labels. On most devices values outside that interval will also work.
pos	a position specifier for the text. If specified this overrides any adj value given. Values of 1, 2, 3 and 4, respectively indicate positions below, to the left of, above and to the right of the specified coordinates.
offset	when pos is specified, this value gives the offset of the label from the specified coordinate in fractions of a character width.
vfont	NULL for the current font family, or a character vector of length 2 for Hershey vector fonts. The first element of the vector selects a typeface and the second element selects a style. Ignored if labels is an expression.
cex	numeric character expansion factor; multiplied by <a href="#">par</a> ("cex") yields the final character size. NULL and NA are equivalent to 1.0.
col, font	the color and (if vfont = NULL) font to be used, possibly vectors. These default to the values of the global graphical parameters in <a href="#">par</a> ().
...	further graphical parameters (from <a href="#">par</a> ), such as srt, family and xpd.

### Details

labels must be of type [character](#) or [expression](#) (or be coercible to such a type). In the latter case, quite a bit of mathematical notation is available such as sub- and superscripts, greek letters, fractions, etc.

adj allows *adjustment* of the text with respect to  $(x, y)$ . Values of 0, 0.5, and 1 specify left/bottom, middle and right/top alignment, respectively. The default is for centered text, i.e., `adj = c(0.5, 0.5)`. Accurate vertical centering needs character metric information on individual characters which is only available on some devices. Vertical alignment is done slightly differently for character strings and for expressions: `adj=c(0, 0)` means to left-justify and to align on the baseline for strings but on the bottom of the bounding box for expressions. This also affects vertical centering: for strings the centering excludes any descenders whereas for expressions it includes them.

The pos and offset arguments can be used in conjunction with values returned by [identify](#) to recreate an interactively labelled plot.

Text can be rotated by using graphical parameters srt (see [par](#)); this rotates about the centre set by adj.

Graphical parameters col, cex and font can be vectors and will then be applied cyclically to the labels (and extra values will be ignored). NA values of font are replaced by `par("font")`.

Labels whose x, y, labels, cex or col value is NA are omitted from the plot.

What happens when font = 5 (the symbol font) is selected can be both device- and locale-dependent. Most often labels will be interpreted in the Adobe symbol encoding, so e.g. "d" is delta, and "\300" is aleph.

### Euro symbol

The Euro symbol was introduced relatively recently and may not be available in older fonts. In recent versions of Adobe symbol fonts it is character 160, so `text(x, y, "\xA0", font =`

5) may work. People using Western European locales on Unix-alikes can probably select ISO-8895-15 (Latin-9) which has the Euro as character 165: this can also be used for `postscript` and `pdf`. It is `'\u20ac'` in Unicode, which can be used in UTF-8 locales.

The Euro should be rendered correctly by `X11` in UTF-8 locales, but the corresponding single-byte encoding in `postscript` and `pdf` will need to be selected as `ISOLatin9.enc`.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

## See Also

`mtext`, `title`, `Hershey` for details on Hershey vector fonts, `plotmath` for details and more examples on mathematical annotation.

## Examples

```
plot(-1:1,-1:1, type = "n", xlab = "Re", ylab = "Im")
K <- 16; text(exp(1i * 2 * pi * (1:K) / K), col = 2)

## The following two examples use latin1 characters: these may not
## appear correctly (or be omitted entirely).
plot(1:10, 1:10, main = "text(...) examples\n~~~~~",
     sub = "R is GNU @, but not @ ...")
mtext("«Latin-1 accented chars»: éè øØ å<Å æ<Æ", side=3)
points(c(6,2), c(2,1), pch = 3, cex = 4, col = "red")
text(6, 2, "the text is CENTERED around (x,y) = (6,2) by default",
     cex = .8)
text(2, 1, "or Left/Bottom - JUSTIFIED at (2,1) by 'adj = c(0,0)'",
     adj = c(0,0))
text(4, 9, expression(hat(beta) == (X^t * X)^{-1} * X^t * y))
text(4, 8.4, "expression(hat(beta) == (X^t * X)^{-1} * X^t * y)",
     cex = .75)
text(4, 7, expression(bar(x) == sum(frac(x[i], n), i==1, n)))

## Two more latin1 examples
text(5,10.2,
     "Le français, c'est facile: Règles, Liberté, Egalité, Fraternité...")
text(5,9.8,
     "Jetzt no chli züritüütsch: (noch ein bißchen Zürcher deutsch)")
```

---

title

*Plot Annotation*

---

## Description

This function can be used to add labels to a plot. Its first four principal arguments can also be used as arguments in most high-level plotting functions. They must be of type `character` or `expression`. In the latter case, quite a bit of mathematical notation is available such as sub- and superscripts, greek letters, fractions, etc: see `plotmath`

**Usage**

```
title(main = NULL, sub = NULL, xlab = NULL, ylab = NULL,
      line = NA, outer = FALSE, ...)
```

**Arguments**

<code>main</code>	The main title (on top) using font and size (character expansion) <code>par("font.main")</code> and color <code>par("col.main")</code> .
<code>sub</code>	Sub-title (at bottom) using font and size <code>par("font.sub")</code> and color <code>par("col.sub")</code> .
<code>xlab</code>	X axis label using font and character expansion <code>par("font.lab")</code> and color <code>par("col.lab")</code> .
<code>ylab</code>	Y axis label, same font attributes as <code>xlab</code> .
<code>line</code>	specifying a value for <code>line</code> overrides the default placement of labels, and places them this many lines outwards from the plot edge.
<code>outer</code>	a logical value. If <code>TRUE</code> , the titles are placed in the outer margins of the plot.
<code>...</code>	further graphical parameters from <code>par</code> . Use e.g., <code>col.main</code> or <code>cex.sub</code> instead of just <code>col</code> or <code>cex</code> . <code>adj</code> controls the justification of the titles. <code>xpd</code> can be used to set the clipping region: this defaults to the figure region unless <code>outer = TRUE</code> , otherwise the device region and can only be increased. <code>mgp</code> controls the default placing of the axis titles.

**Details**

The labels passed to `title` can be character strings or language objects (names, calls or expressions), or a list containing the string to be plotted, and a selection of the optional modifying graphical parameters `cex=`, `col=` and `font=`. Other objects will be coerced by `as.graphicsAnnot`.

The position of `main` defaults to being vertically centered in (outer) margin 3 and justified horizontally according to `par("adj")` on the plot region (device region for `outer=TRUE`).

The positions of `xlab`, `ylab` and `sub` are `line` (default for `xlab` and `ylab` being `par("mgp")[1]` and increased by 1 for `sub`) lines (of height `par("mex")`) into the appropriate margin, justified in the text direction according to `par("adj")` on the plot/device region.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[mtext](#), [text](#); [plotmath](#) for details on mathematical annotation.

**Examples**

```
plot(cars, main = "") # here, could use main directly
title(main = "Stopping Distance versus Speed")

plot(cars, main = "")
title(main = list("Stopping Distance versus Speed", cex=1.5,
                 col="red", font=3))
```

```
## Specifying "...":
plot(1, col.axis = "sky blue", col.lab = "thistle")
title("Main Title", sub = "sub title",
      cex.main = 2, font.main = 4, col.main = "blue",
      cex.sub = 0.75, font.sub = 3, col.sub = "red")

x <- seq(-4, 4, len = 101)
y <- cbind(sin(x), cos(x))
matplot(x, y, type = "l", xaxt = "n",
        main = expression(paste(plain(sin) * phi, " and ",
                                plain(cos) * phi)),
        ylab = expression("sin" * phi, "cos" * phi), # only 1st is taken
        xlab = expression(paste("Phase Angle ", phi)),
        col.main = "blue")
axis(1, at = c(-pi, -pi/2, 0, pi/2, pi),
     labels = expression(-pi, -pi/2, 0, pi/2, pi))
abline(h = 0, v = pi/2 * c(-1,1), lty = 2, lwd = .1, col = "gray70")
```

units

*Graphical Units***Description**

`xinch` and `yinch` convert the specified number of inches given as their arguments into the correct units for plotting with graphics functions. Usually, this only makes sense when normal coordinates are used, i.e., *no* log scale (see the `log` argument to `par`).

`xyinch` does the same for a pair of numbers `xy`, simultaneously.

**Usage**

```
xinch(x = 1, warn.log = TRUE)
yinch(y = 1, warn.log = TRUE)
xyinch(xy = 1, warn.log = TRUE)
```

**Arguments**

<code>x, y</code>	numeric vector
<code>xy</code>	numeric of length 1 or 2.
<code>warn.log</code>	logical; if TRUE, a warning is printed in case of active log scale.

**Examples**

```
all(c(xinch(),yinch()) == xyinch()) # TRUE
xyinch()
xyinch #- to see that is really delta{"usr"} / "pin"

## plot labels offset 0.12 inches to the right
## of plotted symbols in a plot
with(mtcars, {
  plot(mpg, disp, pch=19, main= "Motor Trend Cars")
  text(mpg + xinch(0.12), disp, row.names(mtcars),
       adj = 0, cex = .7, col = 'blue')
})
```

xspline

*Draw an X-spline***Description**

Draw an X-spline, a curve drawn relative to control points.

**Usage**

```
xspline(x, y = NULL, shape = 0, open = TRUE, repEnds = TRUE, draw = TRUE,
        border = par("fg"), col = NA, ...)
```

**Arguments**

<code>x, y</code>	vectors containing the coordinates of the vertices of the polygon. See <a href="#">xy.coords</a> for alternatives.
<code>shape</code>	A numeric vector of values between -1 and 1, which control the shape of the spline relative to the control points.
<code>open</code>	A logical value indicating whether the spline is an open or a closed shape.
<code>repEnds</code>	For open X-splines, a logical value indicating whether the first and last control points should be replicated for drawing the curve. Ignored for closed X-splines.
<code>draw</code>	logical: should the X-spline be drawn? If false, a set of line segments to draw the curve is returned, and nothing is drawn.
<code>border</code>	the color to draw the curve. Use <code>border = NA</code> to omit borders.
<code>col</code>	the color for filling the shape. The default, <code>NA</code> , is to leave unfilled.
<code>...</code>	graphical parameters such as <code>lty</code> , <code>xpd</code> , <code>lend</code> , <code>ljoin</code> and <code>lmitre</code> can be given as arguments.

**Details**

An X-spline is a line drawn relative to control points. For each control point, the line may pass through (interpolate) the control point or it may only approach (approximate) the control point; the behaviour is determined by a shape parameter for each control point.

If the shape parameter is greater than zero, the spline approximates the control points (and is very similar to a cubic B-spline when the shape is 1). If the shape parameter is less than zero, the spline interpolates the control points (and is very similar to a Catmull-Rom spline when the shape is -1). If the shape parameter is 0, the spline forms a sharp corner at that control point.

For open X-splines, the start and end control points must have a shape of 0 (and non-zero values are silently converted to zero).

For open X-splines, by default the start and end control points are replicated before the curve is drawn. A curve is drawn between (interpolating or approximating) the second and third of each set of four control points, so this default behaviour ensures that the resulting curve starts at the first control point you have specified and ends at the last control point. The default behaviour can be turned off via the `repEnds` argument.

**Value**

If `draw = TRUE`, `NULL` otherwise a list with elements `x` and `y` which could be passed to `lines`, `polygon` and so on.

Invisible in both cases.

**Note**

Two-dimensional splines need to be created in an isotropic coordinate system. Device coordinates are used (with an anisotropy correction if needed.)

**References**

Blanc, C. and Schlick, C. (1995), *X-splines : A Spline Model Designed for the End User*, in *Proceedings of SIGGRAPH 95*, pp. 377–386. <http://dept-info.labri.fr/~schlick/DOC/sigl.html>

**See Also**

`polygon`.

`par` for how to specify colors.

**Examples**

```
## based on examples in ?grid.xspline

xsplineTest <- function(s, open = TRUE,
                        x = c(1,1,3,3)/4,
                        y = c(1,3,3,1)/4, ...) {
  plot(c(0,1), c(0,1), type="n", axes=FALSE, xlab="", ylab="")
  points(x, y, pch=19)
  xspline(x, y, s, open, ...)
  text(x+0.05*c(-1,-1,1,1), y+0.05*c(-1,1,1,-1), s)
}

op <- par(mfrow=c(3,3), mar=rep(0,4), oma=c(0,0,2,0))
xsplineTest(c(0, -1, -1, 0))
xsplineTest(c(0, -1, 0, 0))
xsplineTest(c(0, -1, 1, 0))
xsplineTest(c(0, 0, -1, 0))
xsplineTest(c(0, 0, 0, 0))
xsplineTest(c(0, 0, 1, 0))
xsplineTest(c(0, 1, -1, 0))
xsplineTest(c(0, 1, 0, 0))
xsplineTest(c(0, 1, 1, 0))
title("Open X-splines", outer=TRUE)

par(mfrow=c(3,3), mar=rep(0,4), oma=c(0,0,2,0))
xsplineTest(c(0, -1, -1, 0), FALSE, col="grey80")
xsplineTest(c(0, -1, 0, 0), FALSE, col="grey80")
xsplineTest(c(0, -1, 1, 0), FALSE, col="grey80")
xsplineTest(c(0, 0, -1, 0), FALSE, col="grey80")
xsplineTest(c(0, 0, 0, 0), FALSE, col="grey80")
xsplineTest(c(0, 0, 1, 0), FALSE, col="grey80")
xsplineTest(c(0, 1, -1, 0), FALSE, col="grey80")
xsplineTest(c(0, 1, 0, 0), FALSE, col="grey80")
xsplineTest(c(0, 1, 1, 0), FALSE, col="grey80")
```

```
title("Closed X-splines", outer=TRUE)

par(op)

x <- sort(stats::rnorm(5))
y <- sort(stats::rnorm(5))
plot(x, y, pch=19)
res <- xspline(x, y, 1, draw=FALSE)
lines(res)
## the end points may be very close together,
## so use last few for direction
nr <- length(res$x)
arrows(res$x[1], res$y[1], res$x[4], res$y[4], code=1, length=0.1)
arrows(res$x[nr-3], res$y[nr-3], res$x[nr], res$y[nr],
       code = 2, length = 0.1)
```

## Chapter 5

# The `grid` package

---

`grid-package`

*The Grid Graphics Package*

---

### Description

A rewrite of the graphics layout capabilities, plus some support for interaction.

### Details

This package contains a graphics system which supplements S-style graphics (see the **graphics** package).

Further information is available in the following [vignettes](#):

<code>grid</code>	Introduction to <code>grid</code> ( <a href="#">../doc/grid.pdf</a> )
<code>displaylist</code>	Display Lists in <code>grid</code> ( <a href="#">../doc/displaylist.pdf</a> )
<code>frame</code>	Frames and packing grobs ( <a href="#">../doc/frame.pdf</a> )
<code>grobs</code>	Working with <code>grid</code> grobs ( <a href="#">../doc/grobs.pdf</a> )
<code>interactive</code>	Editing <code>grid</code> Graphics ( <a href="#">../doc/interactive.pdf</a> )
<code>locndimn</code>	Locations versus Dimensions ( <a href="#">../doc/locndimn.pdf</a> )
<code>moveline</code>	Demonstrating move-to and line-to ( <a href="#">../doc/moveline.pdf</a> )
<code>nonfinite</code>	How <code>grid</code> responds to non-finite values ( <a href="#">../doc/nonfinite.pdf</a> )
<code>plotexample</code>	Writing <code>grid</code> Code ( <a href="#">../doc/plotexample.pdf</a> )
<code>rotated</code>	Rotated Viewports ( <a href="#">../doc/rotated.pdf</a> )
<code>saveload</code>	Persistent representations ( <a href="#">../doc/saveload.pdf</a> )
<code>sharing</code>	Modifying multiple grobs simultaneously ( <a href="#">../doc/sharing.pdf</a> )
<code>viewports</code>	Working with <code>grid</code> viewports ( <a href="#">../doc/viewports.pdf</a> )

For a complete list of functions with individual help pages, use `library(help="grid")`.

### Author(s)

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Maintainer: R Core Team <[R-core@r-project.org](mailto:R-core@r-project.org)>



## References

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

---

absolute.size	<i>Absolute Size of a Grob</i>
---------------	--------------------------------

---

## Description

This function converts a unit object into absolute units. Absolute units are unaffected, but non-absolute units are converted into "null" units.

## Usage

```
absolute.size(unit)
```

## Arguments

unit            An object of class "unit".

## Details

Absolute units are things like "inches", "cm", and "lines". Non-absolute units are "npc" and "native".

This function is designed to be used in `widthDetails` and `heightDetails` methods.

## Value

An object of class "unit".

## Author(s)

Paul Murrell

## See Also

[widthDetails](#) and [heightDetails](#) methods.

---

 arrow
 

---



---

*Describe arrows to add to a line.*


---

**Description**

Produces a description of what arrows to add to a line. The result can be passed to a function that draws a line, e.g., `grid.lines`.

**Usage**

```
arrow(angle = 30, length = unit(0.25, "inches"),
      ends = "last", type = "open")
```

**Arguments**

angle	The angle of the arrow head in degrees (smaller numbers produce narrower, pointier arrows). Essentially describes the width of the arrow head.
length	A unit specifying the length of the arrow head (from tip to base).
ends	One of "last", "first", or "both", indicating which ends of the line to draw arrow heads.
type	One of "open" or "closed" indicating whether the arrow head should be a closed triangle.

**Examples**

```
arrow()
```

---

 convertNative
 

---



---

*Convert a Unit Object to Native units*


---

**Description**

**This function is deprecated in grid version 0.8 and will be made defunct in grid version 1.9**

You should use the `convertUnit()` function or one of its close allies instead.

This function returns a numeric vector containing the specified x or y locations or dimensions, converted to "user" or "data" units, relative to the current viewport.

**Usage**

```
convertNative(unit, dimension="x", type="location")
```

**Arguments**

unit	A unit object.
dimension	Either "x" or "y".
type	Either "location" or "dimension".

**Value**

A numeric vector.

**WARNING**

If you draw objects based on output from these conversion functions, then resize your device, the objects will be drawn incorrectly – the base R display list will not recalculate these conversions. This means that you can only rely on the results of these calculations if the size of your device is fixed.

**Author(s)**

Paul Murrell

**See Also**

[grid.convert](#), [unit](#)

**Examples**

```
grid.newpage()
pushViewport(viewport(width=unit(.5, "npc"),
                      height=unit(.5, "npc")))

grid.rect()
w <- convertNative(unit(1, "inches"))
h <- convertNative(unit(1, "inches"), "y")
# This rectangle starts off life as 1in square, but if you
# resize the device it will no longer be 1in square
grid.rect(width=unit(w, "native"), height=unit(h, "native"),
          gp=gpar(col="red"))
popViewport(1)

# How to use grid.convert(), etc instead
convertNative(unit(1, "inches")) ==
  convertX(unit(1, "inches"), "native", valueOnly=TRUE)
convertNative(unit(1, "inches"), "y", "dimension") ==
  convertHeight(unit(1, "inches"), "native", valueOnly=TRUE)
```

---

dataViewport

*Create a Viewport with Scales based on Data*

---

**Description**

This is a convenience function for producing a viewport with x- and/or y-scales based on numeric values passed to the function.

**Usage**

```
dataViewport(xData = NULL, yData = NULL, xscale = NULL,
            yscale = NULL, extension = 0.05, ...)
```

**Arguments**

xData	A numeric vector of data.
yData	A numeric vector of data.
xscale	A numeric vector (length 2).
yscale	A numeric vector (length 2).
extension	A numeric. If length greater than 1, then first value is used to extend the xscale and second value is used to extend the yscale.
...	All other arguments will be passed to a call to the <code>viewport()</code> function.

**Details**

If `xscale` is not specified then the values in `x` are used to generate an x-scale based on the range of `x`, extended by the proportion specified in `extension`. Similarly for the y-scale.

**Value**

A grid viewport object.

**Author(s)**

Paul Murrell

**See Also**

[viewport](#) and [plotViewport](#).

---

drawDetails

*Customising grid Drawing*

---

**Description**

These generic hook functions are called whenever a grid grob is drawn. They provide an opportunity for customising the drawing of a new class derived from grob (or gTree).

**Usage**

```
drawDetails(x, recording)
draw.details(x, recording)
preDrawDetails(x)
postDrawDetails(x)
```

**Arguments**

x	A grid grob.
recording	A logical value indicating whether a grob is being added to the display list or redrawn from the display list.

## Details

These functions are called by the `grid.draw` methods for grobs and `gTrees`.

`preDrawDetails` is called first during the drawing of a grob. This is where any additional viewports should be pushed (see, for example, `grid::preDrawDetails.frame`). Note that the default behaviour for grobs is to push any viewports in the `vp` slot, and for `gTrees` is to also push and up any viewports in the `childrenvp` slot so there is typically nothing to do here.

`drawDetails` is called next and is where any additional calculations and graphical output should occur (see, for example, `grid::drawDetails.xaxis`). Note that the default behaviour for `gTrees` is to draw all grobs in the `children` slot so there is typically nothing to do here.

`postDrawDetails` is called last and should reverse anything done in `preDrawDetails` (i.e., `pop` or `up` any viewports that were pushed; again, see, for example, `grid::postDrawDetails.frame`). Note that the default behaviour for grobs is to `pop` any viewports that were pushed so there is typically nothing to do here.

Note that `preDrawDetails` and `postDrawDetails` are also called in the calculation of "grobwidth" and "grobheight" units.

## Value

None of these functions are expected to return a value.

## Author(s)

Paul Murrell

## See Also

[grid.draw](#)

---

editDetails

*Customising grid Editing*

---

## Description

This generic hook function is called whenever a `grid` grob is edited via `grid.edit` or `editGrob`. This provides an opportunity for customising the editing of a new class derived from `grob` (or `gTree`).

## Usage

```
editDetails(x, specs)
```

## Arguments

<code>x</code>	A <code>grid</code> grob.
<code>specs</code>	A list of named elements. The names indicate the grob slots to modify and the values are the new values for the slots.

**Details**

This function is called by `grid.edit` and `editGrob`. A method should be written for classes derived from `grob` or `gTree` if a change in a slot has an effect on other slots in the `grob` or children of a `gTree` (e.g., see `grid:::editDetails.xaxis`).

Note that the slot already has the new value.

**Value**

The function **MUST** return the modified `grob`.

**Author(s)**

Paul Murrell

**See Also**

[grid.edit](#)

---

gEdit

*Create and Apply Edit Objects*

---

**Description**

The functions `gEdit` and `gEditList` create objects representing an edit operation (essentially a list of arguments to `editGrob`).

The functions `applyEdit` and `applyEdits` apply one or more edit operations to a graphical object.

These functions are most useful for developers creating new graphical functions and objects.

**Usage**

```
gEdit(...)
gEditList(...)
applyEdit(x, edit)
applyEdits(x, edits)
```

**Arguments**

<code>...</code>	one or more arguments to the <code>editGrob</code> function (for <code>gEdit</code> ) or one or more "gEdit" objects (for <code>gEditList</code> ).
<code>x</code>	a <code>grob</code> (grid graphical object).
<code>edit</code>	a "gEdit" object.
<code>edits</code>	either a "gEdit" object or a "gEditList" object.

**Value**

`gEdit` returns an object of class "gEdit".

`gEditList` returns an object of class "gEditList".

`applyEdit` and `applyEditList` return the modified `grob`.

**Author(s)**

Paul Murrell

**See Also**[grob editGrob](#)**Examples**

```
grid.rect(gp=gpar(col="red"))
# same thing, but more verbose
grid.draw(applyEdit(rectGrob(), gEdit(gp=gpar(col="red"))))
```

---

getNames

*List the names of grobs on the display list*


---

**Description**

Returns a character vector containing the names of all top-level grobs on the display list.

**Usage**

```
getNames()
```

**Value**

A character vector.

**Author(s)**

Paul Murrell

**Examples**

```
grid.grill()
getNames()
```

---

gpar

*Handling Grid Graphical Parameters*


---

**Description**

`gpar()` should be used to create a set of graphical parameter settings. It returns an object of class "gpar". This is basically a list of name-value pairs.

`get.gpar()` can be used to query the current graphical parameter settings.

**Usage**

```
gpar(...)
get.gpar(names = NULL)
```

**Arguments**

...	Any number of named arguments.
names	A character vector of valid graphical parameter names.

**Details**

All grid viewports and (predefined) graphical objects have a slot called `gp`, which contains a "gpar" object. When a viewport is pushed onto the viewport stack and when a graphical object is drawn, the settings in the "gpar" object are enforced. In this way, the graphical output is modified by the `gp` settings until the graphical object has finished drawing, or until the viewport is popped off the viewport stack, or until some other viewport or graphical object is pushed or begins drawing.

Valid parameter names are:

<code>col</code>	Colour for lines and borders.
<code>fill</code>	Colour for filling rectangles, polygons, ...
<code>alpha</code>	Alpha channel for transparency
<code>lty</code>	Line type
<code>lwd</code>	Line width
<code>lex</code>	Multiplier applied to line width
<code>lineend</code>	Line end style (round, butt, square)
<code>linejoin</code>	Line join style (round, mitre, bevel)
<code>linemitre</code>	Line mitre limit (number greater than 1)
<code>fontsize</code>	The size of text (in points)
<code>cex</code>	Multiplier applied to fontsize
<code>fontfamily</code>	The font family
<code>fontface</code>	The font face (bold, italic, ...)
<code>lineheight</code>	The height of a line as a multiple of the size of text
<code>font</code>	Font face (alias for fontface; for backward compatibility)

Colours can be specified in one of the forms returned by `rgb`, as a name (see `colors`) or as a positive integer index into the current `palette` (with zero or negative values being taken as transparent).

The `alpha` setting is combined with the alpha channel for individual colours by multiplying (with both alpha settings normalised to the range 0 to 1).

The size of text is `fontsize*cex`. The size of a line is `fontsize*cex*lineheight`.

The `cex` setting is cumulative; if a viewport is pushed with a `cex` of 0.5 then another viewport is pushed with a `cex` of 0.5, the effective `cex` is 0.25.

The `alpha` and `lex` settings are also cumulative.

Changes to the `fontfamily` may be ignored by some devices, but is supported by PostScript, PDF, X11, Windows, and Quartz. The `fontfamily` may be used to specify one of the Hershey Font families (e.g., `HersheySerif`) and this specification will be honoured on all devices.

The specification of `fontface` can be an integer or a string. If an integer, then it follows the R base graphics standard: 1 = plain, 2 = bold, 3 = italic, 4 = bold italic. If a string, then valid values are: "plain", "bold", "italic", "oblique", and "bold.italic". For the special case of the `HersheySerif` font family, "cyrillic", "cyrillic.oblique", and "EUC" are also available.

All parameter values can be vectors of multiple values. (This will not always make sense – for example, viewports will only take notice of the first parameter value.)



The `gamma` parameter is defunct since R 2.7.0.

`get.gpar()` returns all current graphical parameter settings.

### Value

An object of class "gpar".

### Author(s)

Paul Murrell

### See Also

[Hershey](#).

### Examples

```
gp <- get.gpar()
utils::str(gp)
## These *do* nothing but produce a "gpar" object:
gpar(col = "red")
gpar(col = "blue", lty = "solid", lwd = 3, fontsize = 16)
get.gpar(c("col", "lty"))
grid.newpage()
vp <- viewport(w = .8, h = .8, gp = gpar(col="blue"))
grid.draw(gTree(children=gList(rectGrob(gp = gpar(col="red")),
                               textGrob(paste("The rect is its own colour (red)",
                                               "but this text is the colour",
                                               "set by the gTree (green)",
                                               sep = "\n"))),
            gp = gpar(col="green"), vp = vp))
grid.text("This text is the colour set by the viewport (blue)",
          y = 1, just = c("center", "bottom"),
          gp = gpar(fontsize=20), vp = vp)
grid.newpage()
## example with multiple values for a parameter
pushViewport(viewport())
grid.points(1:10/11, 1:10/11, gp = gpar(col=1:10))
popViewport()
```

---

gPath

*Concatenate Grob Names*

---

### Description

This function can be used to generate a grob path for use in `grid.edit` and friends.

A grob path is a list of nested grob names.

### Usage

```
gPath(...)
```

**Arguments**

... Character values which are grob names.

**Details**

Grob names must only be unique amongst grobs which share the same parent in a gTree.

This function can be used to generate a specification for a grob that includes the grob's parent's name (and the name of its parent and so on).

For interactive use, it is possible to directly specify a path, but it is strongly recommended that this function is used otherwise in case the path separator is changed in future versions of grid.

**Value**

A `gPath` object.

**See Also**

[grob](#), [editGrob](#), [addGrob](#), [removeGrob](#), [getGrob](#), [setGrob](#)

**Examples**

```
gPath("g1", "g2")
```

---

Grid

*Grid Graphics*

---

**Description**

General information about the grid graphics package.

**Details**

Grid graphics provides an alternative to the standard R graphics. The user is able to define arbitrary rectangular regions (called *viewports*) on the graphics device and define a number of coordinate systems for each region. Drawing can be specified to occur in any viewport using any of the available coordinate systems.

Grid graphics and standard R graphics do not mix!

Type `library(help = grid)` to see a list of (public) Grid graphics functions.

**Author(s)**

Paul Murrell

**See Also**

[viewport](#), [grid.layout](#), and [unit](#).

**Examples**

```
## Diagram of a simple layout
grid.show.layout(grid.layout(4,2,
    heights=unit(rep(1, 4),
        c("lines", "lines", "lines", "null")),
    widths=unit(c(1, 1), "inches")))
## Diagram of a sample viewport
grid.show.viewport(viewport(x=0.6, y=0.6,
    w=unit(1, "inches"), h=unit(1, "inches")))
## A flash plotting example
grid.multipanel(vp=viewport(0.5, 0.5, 0.8, 0.8))
```

Grid Viewports

*Create a Grid Viewport***Description**

These functions create viewports, which describe rectangular regions on a graphics device and define a number of coordinate systems within those regions.

**Usage**

```
viewport(x = unit(0.5, "npc"), y = unit(0.5, "npc"),
    width = unit(1, "npc"), height = unit(1, "npc"),
    default.units = "npc", just = "centre",
    gp = gpar(), clip = "inherit",
    xscale = c(0, 1), yscale = c(0, 1),
    angle = 0,
    layout = NULL,
    layout.pos.row = NULL, layout.pos.col = NULL,
    name = NULL)
vpList(...)
vpStack(...)
vpTree(parent, children)
```

**Arguments**

<code>x</code>	A numeric vector or unit object specifying x-location.
<code>y</code>	A numeric vector or unit object specifying y-location.
<code>width</code>	A numeric vector or unit object specifying width.
<code>height</code>	A numeric vector or unit object specifying height.
<code>default.units</code>	A string indicating the default units to use if <code>x</code> , <code>y</code> , <code>width</code> , or <code>height</code> are only given as numeric vectors.
<code>just</code>	A string or numeric vector specifying the justification of the viewport relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". For numeric values, 0 means left alignment and 1 means right alignment.

<code>gp</code>	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
<code>clip</code>	One of "on", "inherit", or "off", indicating whether to clip to the extent of this viewport, inherit the clipping region from the parent viewport, or turn clipping off altogether. For back-compatibility, a logical value of TRUE corresponds to "on" and FALSE corresponds to "inherit".
<code>xscale</code>	A numeric vector of length two indicating the minimum and maximum on the x-scale.
<code>yscale</code>	A numeric vector of length two indicating the minimum and maximum on the y-scale.
<code>angle</code>	A numeric value indicating the angle of rotation of the viewport. Positive values indicate the amount of rotation, in degrees, anticlockwise from the positive x-axis.
<code>layout</code>	A Grid layout object which splits the viewport into subregions.
<code>layout.pos.row</code>	A numeric vector giving the rows occupied by this viewport in its parent's layout.
<code>layout.pos.col</code>	A numeric vector giving the columns occupied by this viewport in its parent's layout.
<code>name</code>	A character value to uniquely identify the viewport once it has been pushed onto the viewport tree.
<code>...</code>	Any number of grid viewport objects.
<code>parent</code>	A grid viewport object.
<code>children</code>	A <code>vpList</code> object.

### Details

The location and size of a viewport are relative to the coordinate systems defined by the viewport's parent (either a graphical device or another viewport). The location and size can be specified in a very flexible way by specifying them with unit objects. When specifying the location of a viewport, specifying both `layout.pos.row` and `layout.pos.col` as `NULL` indicates that the viewport ignores its parent's layout and specifies its own location and size (via its `locn`). If only one of `layout.pos.row` and `layout.pos.col` is `NULL`, this means occupy ALL of the appropriate row(s)/column(s). For example, `layout.pos.row = 1` and `layout.pos.col = NULL` means occupy all of row 1. Specifying non-NULL values for both `layout.pos.row` and `layout.pos.col` means occupy the intersection of the appropriate rows and columns. If a vector of length two is specified for `layout.pos.row` or `layout.pos.col`, this indicates a range of rows or columns to occupy. For example, `layout.pos.row = c(1, 3)` and `layout.pos.col = c(2, 4)` means occupy cells in the intersection of rows 1, 2, and 3, and columns, 2, 3, and 4.

Clipping obeys only the most recent viewport clip setting. For example, if you clip to viewport1, then clip to viewport2, the clipping region is determined wholly by viewport2, the size and shape of viewport1 is irrelevant (until viewport2 is popped of course).

If a viewport is rotated (because of its own `angle` setting or because it is within another viewport which is rotated) then the `clip` flag is ignored.

Viewport names need not be unique. When pushed, viewports sharing the same parent must have unique names, which means that if you push a viewport with the same name as an existing viewport, the existing viewport will be replaced in the viewport tree. A viewport name can be any string, but

grid uses the reserved name "ROOT" for the top-level viewport. Also, when specifying a viewport name in `downViewport` and `seekViewport`, it is possible to provide a viewport path, which consists of several names concatenated using the separator (currently `: :`). Consequently, it is not advisable to use this separator in viewport names.

The viewports in a `vpList` are pushed in parallel. The viewports in a `vpStack` are pushed in series. When a `vpTree` is pushed, the parent is pushed first, then the children are pushed in parallel.

### Value

An R object of class `viewport`.

### Author(s)

Paul Murrell

### See Also

[Grid](#), [pushViewport](#), [popViewport](#), [downViewport](#), [seekViewport](#), [upViewport](#), [unit](#), [grid.layout](#), [grid.show.layout](#).

### Examples

```
# Diagram of a sample viewport
grid.show.viewport(viewport(x=0.6, y=0.6,
                           w=unit(1, "inches"), h=unit(1, "inches")))
# Demonstrate viewport clipping
clip.demo <- function(i, j, clip1, clip2) {
  pushViewport(viewport(layout.pos.col=i,
                        layout.pos.row=j))
  pushViewport(viewport(width=0.6, height=0.6, clip=clip1))
  grid.rect(gp=gpar(fill="white"))
  grid.circle(r=0.55, gp=gpar(col="red", fill="pink"))
  popViewport()
  pushViewport(viewport(width=0.6, height=0.6, clip=clip2))
  grid.polygon(x=c(0.5, 1.1, 0.6, 1.1, 0.5, -0.1, 0.4, -0.1),
              y=c(0.6, 1.1, 0.5, -0.1, 0.4, -0.1, 0.5, 1.1),
              gp=gpar(col="blue", fill="light blue"))
  popViewport(2)
}

grid.newpage()
grid.rect(gp=gpar(fill="grey"))
pushViewport(viewport(layout=grid.layout(2, 2)))
clip.demo(1, 1, FALSE, FALSE)
clip.demo(1, 2, TRUE, FALSE)
clip.demo(2, 1, FALSE, TRUE)
clip.demo(2, 2, TRUE, TRUE)
popViewport()
# Demonstrate turning clipping off
grid.newpage()
pushViewport(viewport(w=.5, h=.5, clip="on"))
grid.rect()
grid.circle(r=.6, gp=gpar(lwd=10))
pushViewport(viewport(clip="inherit"))
grid.circle(r=.6, gp=gpar(lwd=5, col="grey"))
```

```

pushViewport(viewport(clip="off"))
grid.circle(r=.6)
popViewport(3)
# Demonstrate vpList, vpStack, and vpTree
grid.newpage()
tree <- vpTree(viewport(w=0.8, h=0.8, name="A"),
               vpList(vpStack(viewport(x=0.1, y=0.1, w=0.5, h=0.5,
                                     just=c("left", "bottom"), name="B"),
                           viewport(x=0.1, y=0.1, w=0.5, h=0.5,
                                     just=c("left", "bottom"), name="C"),
                           viewport(x=0.1, y=0.1, w=0.5, h=0.5,
                                     just=c("left", "bottom"), name="D")),
                       viewport(x=0.5, w=0.4, h=0.9,
                                just="left", name="E")))
pushViewport(tree)
for (i in LETTERS[1:5]) {
  seekViewport(i)
  grid.rect()
  grid.text(current.vpTree(FALSE),
            x=unit(1, "mm"), y=unit(1, "npc") - unit(1, "mm"),
            just=c("left", "top"),
            gp=gpar(fontsize=8))
}

```

---

grid.add

*Add a Grid Graphical Object*


---

## Description

Add a grob to a gTree or a descendant of a gTree.

## Usage

```

grid.add(gPath, child, strict = FALSE, grep = FALSE,
         global = FALSE, allDevices = FALSE, redraw = TRUE)

addGrob(gTree, child, gPath = NULL, strict = FALSE, grep = FALSE,
        global = FALSE, warn = TRUE)

setChildren(x, children)

```

## Arguments

gTree, x	A gTree object.
gPath	A gPath object. For grid.add this specifies a gTree on the display list. For addGrob this specifies a descendant of the specified gTree.
child	A grob object.
children	A gList object.
strict	A boolean indicating whether the gPath must be matched exactly.
grep	A boolean indicating whether the gPath should be treated as a regular expression. Values are recycled across elements of the gPath (e.g., c(TRUE, FALSE) means that every odd element of the gPath will be treated as a regular expression).

global	A boolean indicating whether the function should affect just the first match of the <code>gPath</code> , or whether all matches should be affected.
warn	A logical to indicate whether failing to find the specified <code>gPath</code> should trigger an error.
allDevices	A boolean indicating whether all open devices should be searched for matches, or just the current device. NOT YET IMPLEMENTED.
redraw	A logical value to indicate whether to redraw the grob.

### Details

`addGrob` copies the specified grob and returns a modified grob.

`grid.add` destructively modifies a grob on the display list. If `redraw` is TRUE it then redraws everything to reflect the change.

`setChildren` is a basic function for setting all children of a `gTree` at once (instead of repeated calls to `addGrob`).

### Value

`addGrob` returns a grob object; `grid.add` returns NULL.

### Author(s)

Paul Murrell

### See Also

[grob](#), [getGrob](#), [addGrob](#), [removeGrob](#).

---

grid.arrows

*Draw Arrows*

---

### Description

Functions to create and draw arrows at either end of a line, or at either end of a `line.to`, `lines`, or `segments` grob.

These functions have been deprecated in favour of `arrow` arguments to the line-related primitives.

### Usage

```
grid.arrows(x = c(0.25, 0.75), y = 0.5, default.units = "npc",
            grob = NULL,
            angle = 30, length = unit(0.25, "inches"),
            ends = "last", type = "open", name = NULL,
            gp = gpar(), draw = TRUE, vp = NULL)
```

```
arrowsGrob(x = c(0.25, 0.75), y = 0.5, default.units = "npc",
            grob = NULL,
            angle = 30, length = unit(0.25, "inches"),
            ends = "last", type = "open", name = NULL,
            gp = gpar(), vp = NULL)
```

**Arguments**

<code>x</code>	A numeric vector or unit object specifying x-values.
<code>y</code>	A numeric vector or unit object specifying y-values.
<code>default.units</code>	A string indicating the default units to use if <code>x</code> or <code>y</code> are only given as numeric vectors.
<code>grob</code>	A grob to add arrows to; currently can only be a <code>line.to</code> , <code>lines</code> , or <code>segments</code> grob.
<code>angle</code>	A numeric specifying (half) the width of the arrow head (in degrees).
<code>length</code>	A unit object specifying the length of the arrow head.
<code>ends</code>	One of "first", "last", or "both", indicating which end of the line to add arrow heads.
<code>type</code>	Either "open" or "closed" to indicate the type of arrow head.
<code>name</code>	A character identifier.
<code>gp</code>	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
<code>draw</code>	A logical value indicating whether graphics output should be produced.
<code>vp</code>	A Grid viewport object (or NULL).

**Details**

Both functions create an arrows grob (a graphical object describing arrows), but only `grid.arrows()` draws the arrows (and then only if `draw` is TRUE).

If the `grob` argument is specified, this overrides any `x` and/or `y` arguments.

**Value**

An arrows grob. `grid.arrows()` returns the value invisibly.

**Author(s)**

Paul Murrell

**See Also**

[Grid](#), [viewport](#), [grid.line.to](#), [grid.lines](#), [grid.segments](#)

**Examples**

```
## Not run: ## to avoid lots of deprecation warnings
pushViewport(viewport(layout=grid.layout(2, 4)))
pushViewport(viewport(layout.pos.col=1,
                      layout.pos.row=1))
grid.rect(gp=gpar(col="grey"))
grid.arrows()
popViewport()
pushViewport(viewport(layout.pos.col=2,
                      layout.pos.row=1))
grid.rect(gp=gpar(col="grey"))
grid.arrows(angle=15, type="closed")
popViewport()
```



```

pushViewport (viewport (layout.pos.col=3,
                        layout.pos.row=1))
grid.rect (gp=gpar (col="grey"))
grid.arrows (angle=5, length=unit (0.1, "npc"),
            type="closed", gp=gpar (fill="white"))
popViewport ()
pushViewport (viewport (layout.pos.col=4,
                        layout.pos.row=1))
grid.rect (gp=gpar (col="grey"))
grid.arrows (x=unit (0:80/100, "npc"),
            y=unit (1 - (0:80/100)^2, "npc"))
popViewport ()
pushViewport (viewport (layout.pos.col=1,
                        layout.pos.row=2))
grid.rect (gp=gpar (col="grey"))
grid.arrows (ends="both")
popViewport ()
pushViewport (viewport (layout.pos.col=2,
                        layout.pos.row=2))
grid.rect (gp=gpar (col="grey"))
# Recycling arguments
grid.arrows (x=unit (1:10/11, "npc"), y=unit (1:3/4, "npc"))
popViewport ()
pushViewport (viewport (layout.pos.col=3,
                        layout.pos.row=2))
grid.rect (gp=gpar (col="grey"))
# Drawing arrows on a segments grob
gs <- segmentsGrob (x0=unit (1:4/5, "npc"),
                   x1=unit (1:4/5, "npc"))
grid.arrows (grob=gs, length=unit (0.1, "npc"),
            type="closed", gp=gpar (fill="white"))
popViewport ()
pushViewport (viewport (layout.pos.col=4,
                        layout.pos.row=2))
grid.rect (gp=gpar (col="grey"))
# Arrows on a lines grob
# Name these because going to grid.edit them later
gl <- linesGrob (name="curve", x=unit (0:80/100, "npc"),
                y=unit ((0:80/100)^2, "npc"))
grid.arrows (name="arrowOnLine", grob=gl, angle=15, type="closed",
            gp=gpar (fill="black"))
popViewport ()
pushViewport (viewport (layout.pos.col=1,
                        layout.pos.row=2))
grid.move.to (x=0.5, y=0.8)
popViewport ()
pushViewport (viewport (layout.pos.col=4,
                        layout.pos.row=1))
# Arrows on a line.to grob
glt <- lineToGrob (x=0.5, y=0.2, gp=gpar (lwd=3))
grid.arrows (grob=glt, ends="first", gp=gpar (lwd=3))
popViewport (2)
grid.edit (gPath ("arrowOnLine", "curve"), y=unit ((0:80/100)^3, "npc"))

## End (Not run)

```

---

`grid.cap`*Capture a raster image*

---

**Description**

Capture the current contents of a graphics device as a raster (bitmap) image.

**Usage**

```
grid.cap()
```

**Details**

This function is only implemented for on-screen graphics devices.

**Value**

A matrix of R colour names.

**Author(s)**

Paul Murrell

**See Also**

[grid.raster](#)

**Examples**

```
## Not run:
dev.new(width=.5, height=.5)
grid.rect()
grid.text("hi")
cap <- grid.cap()
dev.off()

grid.raster(cap, width=.5, height=.5, interpolate=FALSE)

## End(Not run)
```

---

`grid.circle`*Draw a Circle*

---

**Description**

Functions to create and draw a circle.

**Usage**

```
grid.circle(x=0.5, y=0.5, r=0.5, default.units="npc", name=NULL,
            gp=gpar(), draw=TRUE, vp=NULL)
circleGrob(x=0.5, y=0.5, r=0.5, default.units="npc", name=NULL,
            gp=gpar(), vp=NULL)
```

**Arguments**

<code>x</code>	A numeric vector or unit object specifying x-locations.
<code>y</code>	A numeric vector or unit object specifying y-locations.
<code>r</code>	A numeric vector or unit object specifying radii.
<code>default.units</code>	A string indicating the default units to use if <code>x</code> , <code>y</code> , <code>width</code> , or <code>height</code> are only given as numeric vectors.
<code>name</code>	A character identifier.
<code>gp</code>	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
<code>draw</code>	A logical value indicating whether graphics output should be produced.
<code>vp</code>	A Grid viewport object (or <code>NULL</code> ).

**Details**

Both functions create a circle grob (a graphical object describing a circle), but only `grid.circle()` draws the circle (and then only if `draw` is `TRUE`).

The radius may be given in any units; if the units are *relative* (e.g., "npc" or "native") then the radius will be different depending on whether it is interpreted as a width or as a height. In such cases, the smaller of these two values will be the result. To see the effect, type `grid.circle()` and adjust the size of the window.

**Value**

A circle grob. `grid.circle()` returns the value invisibly.

**Warning**

Negative values for the radius are silently converted to their absolute value.

**Author(s)**

Paul Murrell

**See Also**

[Grid](#), [viewport](#)

grid.clip

*Set the Clipping Region***Description**

These functions set the clipping region within the current viewport *without* altering the current coordinate system.

**Usage**

```
grid.clip(...)
clipGrob(x = unit(0.5, "npc"), y = unit(0.5, "npc"),
         width = unit(1, "npc"), height = unit(1, "npc"),
         just = "centre", hjust = NULL, vjust = NULL,
         default.units = "npc", name = NULL, vp = NULL)
```

**Arguments**

<code>x</code>	A numeric vector or unit object specifying x-location.
<code>y</code>	A numeric vector or unit object specifying y-location.
<code>width</code>	A numeric vector or unit object specifying width.
<code>height</code>	A numeric vector or unit object specifying height.
<code>just</code>	The justification of the clip rectangle relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". For numeric values, 0 means left alignment and 1 means right alignment.
<code>hjust</code>	A numeric vector specifying horizontal justification. If specified, overrides the <code>just</code> setting.
<code>vjust</code>	A numeric vector specifying vertical justification. If specified, overrides the <code>just</code> setting.
<code>default.units</code>	A string indicating the default units to use if <code>x</code> , <code>y</code> , <code>width</code> , or <code>height</code> are only given as numeric vectors.
<code>name</code>	A character identifier.
<code>vp</code>	A Grid viewport object (or NULL).
<code>...</code>	Arguments passed to <code>clipGrob</code> .

**Details**

Both functions create a clip rectangle (a graphical object describing a clip rectangle), but only `grid.clip` enforces the clipping.

Pushing or popping a viewport *always* overrides the clip region set by a clip grob, regardless of whether that viewport explicitly enforces a clipping region.

**Value**

`clipGrob` returns a clip grob.

**Author(s)**

Paul Murrell

**See Also**[Grid](#), [viewport](#)**Examples**

```
# draw across entire viewport, but clipped
grid.clip(x = 0.3, width = 0.1)
grid.lines(gp=gpar(col="green", lwd=5))
# draw across entire viewport, but clipped (in different place)
grid.clip(x = 0.7, width = 0.1)
grid.lines(gp=gpar(col="red", lwd=5))
# Viewport sets new clip region
pushViewport(viewport(width=0.5, height=0.5, clip=TRUE))
grid.lines(gp=gpar(col="grey", lwd=3))
# Return to original viewport; get
# clip region from previous grid.clip()
# (NOT from previous viewport clip region)
popViewport()
grid.lines(gp=gpar(col="black"))
```

---

grid.collection      *Create a Coherent Group of Grid Graphical Objects*

---

**Description**

This function is deprecated; please use `gTree`.

This function creates a graphical object which contains several other graphical objects. When it is drawn, it draws all of its children.

It may be convenient to name the elements of the collection.

**Usage**

```
grid.collection(..., gp=gpar(), draw=TRUE, vp=NULL)
```

**Arguments**

...	Zero or more objects of class "grob".
gp	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
draw	A logical value to indicate whether to produce graphical output.
vp	A Grid viewport object (or <code>NULL</code> ).

**Value**

A collection `grob`.

**Author(s)**

Paul Murrell

**See Also**[grid.grob.](#)

grid.convert

*Convert Between Different grid Coordinate Systems***Description**

These functions take a unit object and convert it to an equivalent unit object in a different coordinate system.

**Usage**

```

convertX(x, unitTo, valueOnly = FALSE)
convertY(x, unitTo, valueOnly = FALSE)
convertWidth(x, unitTo, valueOnly = FALSE)
convertHeight(x, unitTo, valueOnly = FALSE)
convertUnit(x, unitTo,
            axisFrom = "x", typeFrom = "location",
            axisTo = axisFrom, typeTo = typeFrom,
            valueOnly = FALSE)
grid.convertX(x, unitTo, valueOnly = FALSE)
grid.convertY(x, unitTo, valueOnly = FALSE)
grid.convertWidth(x, unitTo, valueOnly = FALSE)
grid.convertHeight(x, unitTo, valueOnly = FALSE)
grid.convert(x, unitTo,
            axisFrom = "x", typeFrom = "location",
            axisTo = axisFrom, typeTo = typeFrom,
            valueOnly = FALSE)

```

**Arguments**

x	A unit object.
unitTo	The coordinate system to convert the unit to. See the <a href="#">unit</a> function for valid coordinate systems.
axisFrom	Either "x" or "y" to indicate whether the unit object represents a value in the x- or y-direction.
typeFrom	Either "location" or "dimension" to indicate whether the unit object represents a location or a length.
axisTo	Same as axisFrom, but applies to the unit object that is to be created.
typeTo	Same as typeFrom, but applies to the unit object that is to be created.
valueOnly	A logical indicating. If TRUE then the function does not return a unit object, but rather only the converted numeric values.

**Details**

The `convertUnit` function allows for general-purpose conversions. The other four functions are just more convenient front-ends to it for the most common conversions.

The conversions occur within the current viewport.

It is not currently possible to convert to all valid coordinate systems (e.g., "strwidth" or "grob-width"). I'm not sure if all of these are impossible, they just seem implausible at this stage.

In normal usage of `grid`, these functions should not be necessary. If you want to express a location or dimension in inches rather than user coordinates then you should simply do something like `unit(1, "inches")` rather than something like `unit(0.134, "native")`.

In some cases, however, it is necessary for the user to perform calculations on a unit value and this function becomes necessary. In such cases, please take note of the warning below.

The `grid.*` versions are just previous incarnations which have been deprecated.

**Value**

A unit object in the specified coordinate system (unless `valueOnly` is `TRUE` in which case the returned value is a numeric).

**Warning**

The conversion is only valid for the current device size. If the device is resized then at least some conversions will become invalid. For example, suppose that I create a unit object as follows: `oneinch <- convertUnit(unit(1, "inches"), "native")`. Now if I resize the device, the unit object in `oneinch` no longer corresponds to a physical length of 1 inch.

**Author(s)**

Paul Murrell

**See Also**

[unit](#)

**Examples**

```
## A tautology
convertX(unit(1, "inches"), "inches")
## The physical units
convertX(unit(2.54, "cm"), "inches")
convertX(unit(25.4, "mm"), "inches")
convertX(unit(72.27, "points"), "inches")
convertX(unit(1/12*72.27, "picas"), "inches")
convertX(unit(72, "bigpts"), "inches")
convertX(unit(1157/1238*72.27, "dida"), "inches")
convertX(unit(1/12*1157/1238*72.27, "cicero"), "inches")
convertX(unit(65536*72.27, "scaledpts"), "inches")
convertX(unit(1/2.54, "inches"), "cm")
convertX(unit(1/25.4, "inches"), "mm")
convertX(unit(1/72.27, "inches"), "points")
convertX(unit(1/(1/12*72.27), "inches"), "picas")
convertX(unit(1/72, "inches"), "bigpts")
convertX(unit(1/(1157/1238*72.27), "inches"), "dida")
convertX(unit(1/(1/12*1157/1238*72.27), "inches"), "cicero")
```

```
convertX(unit(1/(65536*72.27), "inches"), "scaledpts")

pushViewport(viewport(width=unit(1, "inches"),
                      height=unit(2, "inches"),
                      xscale=c(0, 1),
                      yscale=c(1, 3)))

## Location versus dimension
convertY(unit(2, "native"), "inches")
convertHeight(unit(2, "native"), "inches")
## From "x" to "y" (the conversion is via "inches")
convertUnit(unit(1, "native"), "native",
            axisFrom="x", axisTo="y")
## Convert several values at once
convertX(unit(c(0.5, 2.54), c("npc", "cm")),
        c("inches", "native"))
popViewport()
## Convert a complex unit
convertX(unit(1, "strwidth", "Hello"), "native")
```

---

grid.copy

*Make a Copy of a Grid Graphical Object*

---

## Description

This function is redundant and will disappear in future versions.

## Usage

```
grid.copy(grob)
```

## Arguments

grob            A grob object.

## Value

A copy of the grob object.

## Author(s)

Paul Murrell

## See Also

[grid.grob.](#)



grid.curve

*Draw a Curve Between Locations***Description**

These functions create and draw a curve from one location to another.

**Usage**

```
grid.curve(...)
curveGrob(x1, y1, x2, y2, default.units = "npc",
          curvature = 1, angle = 90, ncp = 1, shape = 0.5,
          square = TRUE, squareShape = 1,
          inflect = FALSE, arrow = NULL, open = TRUE,
          debug = FALSE,
          name = NULL, gp = gpar(), vp = NULL)
arcCurvature(theta)
```

**Arguments**

x1	A numeric vector or unit object specifying the x-location of the start point.
y1	A numeric vector or unit object specifying the y-location of the start point.
x2	A numeric vector or unit object specifying the x-location of the end point.
y2	A numeric vector or unit object specifying the y-location of the end point.
default.units	A string indicating the default units to use if x1, y1, x2 or y2 are only given as numeric values.
curvature	A numeric value giving the amount of curvature. Negative values produce left-hand curves, positive values produce right-hand curves, and zero produces a straight line.
angle	A numeric value between 0 and 180, giving an amount to skew the control points of the curve. Values less than 90 skew the curve towards the start point and values greater than 90 skew the curve towards the end point.
ncp	The number of control points used to draw the curve. More control points creates a smoother curve.
shape	A numeric vector of values between -1 and 1, which control the shape of the curve relative to its control points. See <code>grid.xspline</code> for more details.
square	A logical value that controls whether control points for the curve are created city-block fashion or obliquely. When <code>ncp</code> is 1 and <code>angle</code> is 90, this is typically <code>TRUE</code> , otherwise this should probably be set to <code>FALSE</code> (see Examples below).
squareShape	A shape value to control the behaviour of the curve relative to any additional control point that is inserted if <code>square</code> is <code>TRUE</code> .
inflect	A logical value specifying whether the curve should be cut in half and inverted (see Examples below).
arrow	A list describing arrow heads to place at either end of the curve, as produced by the <code>arrow</code> function.

open	A logical value indicating whether to close the curve (connect the start and end points).
debug	A logical value indicating whether debugging information should be drawn.
name	A character identifier.
gp	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or NULL).
...	Arguments to be passed to <code>curveGrob</code> .
theta	An angle (in degrees).

### Details

Both functions create a curve grob (a graphical object describing an curve), but only `grid.curve` draws the curve.

The `arcCurvature` function can be used to calculate a `curvature` such that control points are generated on an arc corresponding to angle `theta`. This is typically used in conjunction with a large `ncp` to produce a curve corresponding to the desired arc.

### Value

A grob object.

### See Also

[Grid](#), [viewport](#), [grid.xspline](#), [arrow](#)

### Examples

```
curveTest <- function(i, j, ...) {
  pushViewport(viewport(layout.pos.col=j, layout.pos.row=i))
  do.call("grid.curve", c(list(x1=.25, y1=.25, x2=.75, y2=.75), list(...)))
  grid.text(sub("list\\((.*)\\)", "\\1",
               deparse(substitute(list(...)))),
            y=unit(1, "npc"))
  popViewport()
}
# grid.newpage()
pushViewport(plotViewport(c(0, 0, 1, 0),
                          layout=grid.layout(2, 1, heights=c(2, 1))))
pushViewport(viewport(layout.pos.row=1,
                      layout=grid.layout(3, 3, respect=TRUE)))
curveTest(1, 1)
curveTest(1, 2, inflect=TRUE)
curveTest(1, 3, angle=135)
curveTest(2, 1, arrow=arrow())
curveTest(2, 2, ncp=8)
curveTest(2, 3, shape=0)
curveTest(3, 1, curvature=-1)
curveTest(3, 2, square=FALSE)
curveTest(3, 3, debug=TRUE)
popViewport()
pushViewport(viewport(layout.pos.row=2,
                      layout=grid.layout(3, 3)))
```

```
curveTest(1, 1)
curveTest(1, 2, inflect=TRUE)
curveTest(1, 3, angle=135)
curveTest(2, 1, arrow=arrow())
curveTest(2, 2, ncp=8)
curveTest(2, 3, shape=0)
curveTest(3, 1, curvature=-1)
curveTest(3, 2, square=FALSE)
curveTest(3, 3, debug=TRUE)
popViewport(2)
```

---

grid.display.list *Control the Grid Display List*

---

### Description

Turn the Grid display list on or off.

### Usage

```
grid.display.list(on=TRUE)
engine.display.list(on=TRUE)
```

### Arguments

`on` A logical value to indicate whether the display list should be on or off.

### Details

All drawing and viewport-setting operations are (by default) recorded in the Grid display list. This allows redrawing to occur following an editing operation.

This display list could get very large so it may be useful to turn it off in some cases; this will of course disable redrawing.

All graphics output is also recorded on the main display list of the R graphics engine (by default). This supports redrawing following a device resize and allows copying between devices.

Turning off this display list means that grid will redraw from its own display list for device resizes and copies. This will be slower than using the graphics engine display list.

### Value

None.

### WARNING

Turning the display list on causes the display list to be erased!

Turning off both the grid display list and the graphics engine display list will result in no redrawing whatsoever.

### Author(s)

Paul Murrell

---

grid.draw                      *Draw a grid grob*

---

### Description

Produces graphical output from a graphical object.

### Usage

```
grid.draw(x, recording=TRUE)
```

### Arguments

x	An object of class "grob" or NULL.
recording	A logical value to indicate whether the drawing operation should be recorded on the Grid display list.

### Details

This is a generic function with methods for grob and gTree objects.

The grob and gTree methods automatically push any viewports in a vp slot and automatically apply any gpar settings in a gp slot. In addition, the gTree method pushes and ups any viewports in a childrenvp slot and automatically calls grid.draw for any grobs in a children slot.

The methods for grob and gTree call the generic hook functions preDrawDetails, drawDetails, and postDrawDetails to allow classes derived from grob or gTree to perform additional viewport pushing/popping and produce additional output beyond the default behaviour for grobs and gTrees.

### Value

None.

### Author(s)

Paul Murrell

### See Also

[grob](#).

### Examples

```
grid.newpage()
## Create a graphical object, but don't draw it
l <- linesGrob()
## Draw it
grid.draw(l)
```

grid.edit

*Edit the Description of a Grid Graphical Object***Description**

Changes the value of one of the slots of a grob and redraws the grob.

**Usage**

```
grid.edit(gPath, ..., strict = FALSE, grep = FALSE,
          global = FALSE, allDevices = FALSE, redraw = TRUE)

grid.gedit(..., grep = TRUE, global = TRUE)

editGrob(grob, gPath = NULL, ..., strict = FALSE, grep = FALSE,
          global = FALSE, warn = TRUE)
```

**Arguments**

grob	A grob object.
...	Zero or more named arguments specifying new slot values.
gPath	A gPath object. For <code>grid.edit</code> this specifies a grob on the display list. For <code>editGrob</code> this specifies a descendant of the specified grob.
strict	A boolean indicating whether the gPath must be matched exactly.
grep	A boolean indicating whether the gPath should be treated as a regular expression. Values are recycled across elements of the gPath (e.g., <code>c(TRUE, FALSE)</code> means that every odd element of the gPath will be treated as a regular expression).
global	A boolean indicating whether the function should affect just the first match of the gPath, or whether all matches should be affected.
warn	A logical to indicate whether failing to find the specified gPath should trigger an error.
allDevices	A boolean indicating whether all open devices should be searched for matches, or just the current device. NOT YET IMPLEMENTED.
redraw	A logical value to indicate whether to redraw the grob.

**Details**

`editGrob` copies the specified grob and returns a modified grob.

`grid.edit` destructively modifies a grob on the display list. If `redraw` is `TRUE` it then redraws everything to reflect the change.

Both functions call `editDetails` to allow a grob to perform custom actions and `validDetails` to check that the modified grob is still coherent.

`grid.gedit` (g for global) is just a convenience wrapper for `grid.edit` with different defaults.

**Value**

`editGrob` returns a grob object; `grid.edit` returns `NULL`.

**Author(s)**

Paul Murrell

**See Also**[grob](#), [getGrob](#), [addGrob](#), [removeGrob](#).**Examples**

```

grid.newpage()
grid.xaxis(name = "xa", vp = viewport(width=.5, height=.5))
grid.edit("xa", gp = gpar(col="red"))
# won't work because no ticks (at is NULL)
try(grid.edit(gPath("xa", "ticks"), gp = gpar(col="green")))
grid.edit("xa", at = 1:4/5)
# Now it should work
try(grid.edit(gPath("xa", "ticks"), gp = gpar(col="green")))

```

grid.frame

*Create a Frame for Packing Objects***Description**

These functions, together with `grid.pack`, `grid.place`, `packGrob`, and `placeGrob` are part of a GUI-builder-like interface to constructing graphical images. The idea is that you create a frame with this function then use `grid.pack` or whatever to pack/place objects into the frame.

**Usage**

```

grid.frame(layout=NULL, name=NULL, gp=gpar(), vp=NULL, draw=TRUE)
frameGrob(layout=NULL, name=NULL, gp=gpar(), vp=NULL)

```

**Arguments**

<code>layout</code>	A Grid layout, or NULL. This can be used to initialise the frame with a number of rows and columns, with initial widths and heights, etc.
<code>name</code>	A character identifier.
<code>vp</code>	An object of class <code>viewport</code> , or NULL.
<code>gp</code>	An object of class <code>gpar</code> ; typically the output from a call to the function <code>gpar</code> .
<code>draw</code>	Should the frame be drawn.

**Details**

Both functions create a frame `grob` (a graphical object describing a frame), but only `grid.frame()` draws the frame (and then only if `draw` is `TRUE`). Nothing will actually be drawn, but it will put the frame on the display list, which means that the output will be dynamically updated as objects are packed into the frame. Possibly useful for debugging.

**Value**

A frame `grob`. `grid.frame()` returns the value invisibly.

**Author(s)**

Paul Murrell

**See Also**[grid.pack](#)**Examples**

```
grid.newpage()
grid.frame(name="gf", draw=TRUE)
grid.pack("gf", rectGrob(gp=gpar(fill="grey")), width=unit(1, "null"))
grid.pack("gf", textGrob("hi there"), side="right")
```

---

grid.get

*Get a Grid Graphical Object*


---

**Description**

Retrieve a grob or a descendant of a grob.

**Usage**

```
grid.get(gPath, strict = FALSE, grep = FALSE, global = FALSE,
         allDevices = FALSE)

grid.gget(..., grep = TRUE, global = TRUE)

getGrob(gTree, gPath, strict = FALSE, grep = FALSE, global = FALSE)
```

**Arguments**

<code>gTree</code>	A <code>gTree</code> object.
<code>gPath</code>	A <code>gPath</code> object. For <code>grid.get</code> this specifies a grob on the display list. For <code>getGrob</code> this specifies a descendant of the specified <code>gTree</code> .
<code>strict</code>	A boolean indicating whether the <code>gPath</code> must be matched exactly.
<code>grep</code>	A boolean indicating whether the <code>gPath</code> should be treated as a regular expression. Values are recycled across elements of the <code>gPath</code> (e.g., <code>c(TRUE, FALSE)</code> means that every odd element of the <code>gPath</code> will be treated as a regular expression).
<code>global</code>	A boolean indicating whether the function should affect just the first match of the <code>gPath</code> , or whether all matches should be affected.
<code>allDevices</code>	A boolean indicating whether all open devices should be searched for matches, or just the current device. NOT YET IMPLEMENTED.
<code>...</code>	Arguments that are passed to <code>grid.get</code> .

**Details**

`grid.gget` (`g` for global) is just a convenience wrapper for `grid.get` with different defaults.

**Value**

A grob object.

**Author(s)**

Paul Murrell

**See Also**

[grob](#), [getGrob](#), [addGrob](#), [removeGrob](#).

**Examples**

```
grid.xaxis(name="xa")
grid.get("xa")
grid.get(gPath("xa", "ticks"))

grid.draw(gTree(name="gt", children=gList(xaxisGrob(name="axis"))))
grid.get(gPath("gt", "axis", "ticks"))
```

---

grid.grab

*Grab the current grid output*


---

**Description**

Creates a gTree object from the current grid display list or from a scene generated by user-specified code.

**Usage**

```
grid.grab(warn = 2, wrap = FALSE, ...)
grid.grabExpr(expr, warn = 2, wrap = FALSE, ...)
```

**Arguments**

expr	An expression to be evaluated. Typically, some calls to grid drawing functions.
warn	An integer specifying the amount of warnings to emit. 0 means no warnings, 1 means warn when it is certain that the grab will not faithfully represent the original scene. 2 means warn if there's any possibility that the grab will not faithfully represent the original scene.
wrap	A logical indicating how the output should be captured. If TRUE, each non-grob element on the display list is captured by wrapping it in a grob.
...	arguments passed to gTree, for example, a name and/or class for the gTree that is created.



## Details

There are four ways to capture grid output as a gTree.

There are two functions for capturing output: use `grid.grab` to capture an existing drawing and `grid.grabExpr` to capture the output from an expression (without drawing anything).

For each of these functions, the output can be captured in two ways. One way tries to be clever and make a gTree with a `childrenvp` slot containing all viewports on the display list (including those that are popped) and every grob on the display list as a child of the new gTree; each child has a `vpPath` in the `vp` slot so that it is drawn in the appropriate viewport. In other words, the gTree contains all elements on the display list, but in a slightly altered form.

The other way, `wrap=TRUE`, is to create a grob for every element on the display list (and make all of those grobs children of the gTree).

The first approach creates a more compact and elegant gTree, which is more flexible to work with, but is not guaranteed to faithfully replicate all possible grid output. The second approach is more brute force, and harder to work with, but should always faithfully replicate the original output.

## Value

A gTree object.

## See Also

[gTree](#)

## Examples

```
pushViewport(viewport(w=.5, h=.5))
grid.rect()
grid.points(stats::runif(10), stats::runif(10))
popViewport()
grab <- grid.grab()
grid.newpage()
grid.draw(grab)
```

---

grid.grill

*Draw a Grill*

---

## Description

This function draws a grill within a Grid viewport.

## Usage

```
grid.grill(h = unit(seq(0.25, 0.75, 0.25), "npc"),
           v = unit(seq(0.25, 0.75, 0.25), "npc"),
           default.units = "npc", gp=gpar(col = "grey"), vp = NULL)
```

**Arguments**

<code>h</code>	A numeric vector or unit object indicating the horizontal location of the vertical grill lines.
<code>v</code>	A numeric vector or unit object indicating the vertical location of the horizontal grill lines.
<code>default.units</code>	A string indicating the default units to use if <code>h</code> or <code>v</code> are only given as numeric vectors.
<code>gp</code>	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
<code>vp</code>	A Grid viewport object.

**Value**

None.

**Author(s)**

Paul Murrell

**See Also**

[Grid](#), [viewport](#).

---

grid.grob

*Create a Grid Graphical Object*

---

**Description**

These functions create grid graphical objects.

**Usage**

```
grid.grob(list.struct, cl = NULL, draw = TRUE)
grob(..., name = NULL, gp = NULL, vp = NULL, cl = NULL)
gTree(..., name = NULL, gp = NULL, vp = NULL, children = NULL,
       childrenvp = NULL, cl = NULL)
grobTree(..., name = NULL, gp = NULL, vp = NULL,
         childrenvp = NULL, cl = NULL)
childNames(gTree)
gList(...)
is.grob(x)
```

**Arguments**

<code>...</code>	For <code>grob</code> and <code>gTree</code> , the named slots describing important features of the graphical object. For <code>gList</code> and <code>grobTree</code> , a series of grob objects.
<code>list.struct</code>	A list (preferably with each element named).
<code>name</code>	A character identifier for the grob. Used to find the grob on the display list and/or as a child of another grob.

<code>children</code>	A <code>gList</code> object.
<code>childrenvp</code>	A viewport object (or <code>NULL</code> ).
<code>gp</code>	A <code>gpar</code> object, typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
<code>vp</code>	A viewport object (or <code>NULL</code> ).
<code>cl</code>	A string giving the class attribute for the <code>list.struct</code>
<code>draw</code>	A logical value to indicate whether to produce graphical output.
<code>gTree</code>	A <code>gTree</code> object.
<code>x</code>	An R object.

### Details

These functions can be used to create a basic `grob`, `gTree`, or `gList` object, or a new class derived from one of these.

A `grid` graphical object (`grob`) is a description of a graphical item. These basic classes provide default behaviour for validating, drawing, and modifying graphical objects. Both call the function `validDetails` to check that the object returned is coherent.

A `gTree` can have other `grobs` as children; when a `gTree` is drawn, it draws all of its children. Before drawing its children, a `gTree` pushes its `childrenvp` slot and then navigates back up (calls `upViewport`) so that the children can specify their location within the `childrenvp` via a `vpPath`.

`Grob` names need not be unique in general, but all children of a `gTree` must have different names. A `grob` name can be any string, though it is not advisable to use the `gPath` separator (currently `:`) in `grob` names.

The function `childNames` returns the names of the `grobs` which are children of a `gTree`.

All `grid` primitives (`grid.lines`, `grid.rect`, ...) and some higher-level `grid` components (e.g., `grid.xaxis` and `grid.yaxis`) are derived from these classes.

`grobTree` is just a convenient wrapper for `gTree` when the only components of the `gTree` are `grobs` (so all unnamed arguments become children of the `gTree`).

`grid.grob` is deprecated.

### Value

A `grob` object.

### Author(s)

Paul Murrell

### See Also

[grid.draw](#), [grid.edit](#), [grid.get](#).

---

grid.layout	<i>Create a Grid Layout</i>
-------------	-----------------------------

---

### Description

This function returns a Grid layout, which describes a subdivision of a rectangular region.

### Usage

```
grid.layout(nrow = 1, ncol = 1,
            widths = unit(rep(1, ncol), "null"),
            heights = unit(rep(1, nrow), "null"),
            default.units = "null", respect = FALSE,
            just="centre")
```

### Arguments

nrow	An integer describing the number of rows in the layout.
ncol	An integer describing the number of columns in the layout.
widths	A numeric vector or unit object describing the widths of the columns in the layout.
heights	A numeric vector or unit object describing the heights of the rows in the layout.
default.units	A string indicating the default units to use if widths or heights are only given as numeric vectors.
respect	A logical value or a numeric matrix. If a logical, this indicates whether row heights and column widths should respect each other. If a matrix, non-zero values indicate that the corresponding row and column should be respected (see examples below).
just	A string vector indicating how the layout should be justified if it is not the same size as its parent viewport. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible values are: "left", "right", "centre", "center", "bottom", and "top". NOTE that in this context, "left", for example, means align the left edge of the left-most layout column with the left edge of the parent viewport.

### Details

The unit objects given for the widths and heights of a layout may use a special units that only has meaning for layouts. This is the "null" unit, which indicates what relative fraction of the available width/height the column/row occupies. See the reference for a better description of relative widths and heights in layouts.

### Value

A Grid layout object.

**WARNING**

This function must NOT be confused with the base R graphics function `layout`. In particular, do not use `layout` in combination with Grid graphics. The documentation for `layout` may provide some useful information and this function should behave identically in comparable situations. The `grid.layout` function has *added* the ability to specify a broader range of units for row heights and column widths, and allows for nested layouts (see `viewport`).

**Author(s)**

Paul Murrell

**References**

Murrell, P. R. (1999), Layouts: A Mechanism for Arranging Plots on a Page, *Journal of Computational and Graphical Statistics*, **8**, 121–134.

**See Also**

[Grid](#), [grid.show.layout](#), [viewport](#), [layout](#)

**Examples**

```
## A variety of layouts (some a bit mid-bending ...)
layout.torture()
## Demonstration of layout justification
grid.newpage()
testlay <- function(just="centre") {
  pushViewport(viewport(layout=grid.layout(1, 1, widths=unit(1, "inches"),
    heights=unit(0.25, "npc"),
    just=just))
  pushViewport(viewport(layout.pos.col=1, layout.pos.row=1))
  grid.rect()
  grid.text(paste(just, collapse="-"))
  popViewport(2)
}
testlay()
testlay(c("left", "top"))
testlay(c("right", "top"))
testlay(c("right", "bottom"))
testlay(c("left", "bottom"))
testlay(c("left"))
testlay(c("right"))
testlay(c("bottom"))
testlay(c("top"))
```

---

grid.lines

*Draw Lines in a Grid Viewport*

---

**Description**

These functions create and draw a series of lines.

**Usage**

```

grid.lines(x = unit(c(0, 1), "npc"),
           y = unit(c(0, 1), "npc"),
           default.units = "npc",
           arrow = NULL, name = NULL,
           gp=gpar(), draw = TRUE, vp = NULL)
linesGrob(x = unit(c(0, 1), "npc"),
           y = unit(c(0, 1), "npc"),
           default.units = "npc",
           arrow = NULL, name = NULL,
           gp=gpar(), vp = NULL)
grid.polyline(...)
polylineGrob(x = unit(c(0, 1), "npc"),
             y = unit(c(0, 1), "npc"),
             id=NULL, id.lengths=NULL,
             default.units = "npc",
             arrow = NULL, name = NULL,
             gp=gpar(), vp = NULL)

```

**Arguments**

<code>x</code>	A numeric vector or unit object specifying x-values.
<code>y</code>	A numeric vector or unit object specifying y-values.
<code>default.units</code>	A string indicating the default units to use if <code>x</code> or <code>y</code> are only given as numeric vectors.
<code>arrow</code>	A list describing arrow heads to place at either end of the line, as produced by the <code>arrow</code> function.
<code>name</code>	A character identifier.
<code>gp</code>	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
<code>draw</code>	A logical value indicating whether graphics output should be produced.
<code>vp</code>	A Grid viewport object (or <code>NULL</code> ).
<code>id</code>	A numeric vector used to separate locations in <code>x</code> and <code>y</code> into multiple lines. All locations with the same <code>id</code> belong to the same line.
<code>id.lengths</code>	A numeric vector used to separate locations in <code>x</code> and <code>y</code> into multiple lines. Specifies consecutive blocks of locations which make up separate lines.
<code>...</code>	Arguments passed to <code>polylineGrob</code> .

**Details**

The first two functions create a lines grob (a graphical object describing lines), and `grid.lines` draws the lines (if `draw` is `TRUE`).

The second two functions create or draw a polyline grob, which is just like a lines grob, except that there can be multiple distinct lines drawn.

**Value**

A lines grob or a polyline grob. `grid.lines` returns a lines grob invisibly.

**Author(s)**

Paul Murrell

**See Also**[Grid](#), [viewport](#), [arrow](#)**Examples**

```

grid.lines()
# Using id (NOTE: locations are not in consecutive blocks)
grid.newpage()
grid.polyline(x=c((0:4)/10, rep(.5, 5), (10:6)/10, rep(.5, 5)),
             y=c(rep(.5, 5), (10:6/10), rep(.5, 5), (0:4)/10),
             id=rep(1:5, 4),
             gp=gpar(col=1:5, lwd=3))
# Using id.lengths
grid.newpage()
grid.polyline(x=outer(c(0, .5, 1, .5), 5:1/5),
             y=outer(c(.5, 1, .5, 0), 5:1/5),
             id.lengths=rep(4, 5),
             gp=gpar(col=1:5, lwd=3))

```

---

grid.locator

*Capture a Mouse Click*


---

**Description**

Allows the user to click the mouse once within the current graphics device and returns the location of the mouse click within the current viewport, in the specified coordinate system.

**Usage**

```
grid.locator(unit = "native")
```

**Arguments**

`unit`            The coordinate system in which to return the location of the mouse click. See the [unit](#) function for valid coordinate systems.

**Details**

This function is modal (like the graphics package function `locator`) so the command line and graphics drawing is blocked until the use has clicked the mouse in the current device.

**Value**

A unit object representing the location of the mouse click within the current viewport, in the specified coordinate system.

If the user did not click mouse button 1, the function (invisibly) returns `NULL`.

**Author(s)**

Paul Murrell

**See Also**

[viewport](#), [unit](#), [locator](#) in package **graphics**, and for an application see [trellis.focus](#) and [panel.identify](#) in package **lattice**.

**Examples**

```
if (interactive()) {
  ## Need to write a more sophisticated unit as.character method
  unittrim <- function(unit) {
    sub("^([0-9]+|[0-9]+.[0-9])[0-9]*", "\\1", as.character(unit))
  }
  do.click <- function(unit) {
    click.locn <- grid.locator(unit)
    grid.segments(unit.c(click.locn$x, unit(0, "npc")),
                  unit.c(unit(0, "npc"), click.locn$y),
                  click.locn$x, click.locn$y,
                  gp=gpar(lty="dashed", col="grey"))
    grid.points(click.locn$x, click.locn$y, pch=16, size=unit(1, "mm"))
    clickx <- unittrim(click.locn$x)
    clicky <- unittrim(click.locn$y)
    grid.text(paste("(", clickx, ", ", clicky, ")", sep=""),
              click.locn$x + unit(2, "mm"), click.locn$y,
              just="left")
  }
  do.click("inches")
  pushViewport(viewport(width=0.5, height=0.5,
                        xscale=c(0, 100), yscale=c(0, 10)))

  grid.rect()
  grid.xaxis()
  grid.yaxis()
  do.click("native")
  popViewport()
}
```

grid.ls

*List the names of grobs or viewports***Description**

Returns a listing of the names of grobs or viewports.

This is a generic function with methods for grobs (including gTrees) and viewports (including vpTrees).

**Usage**

```
grid.ls(x=NULL, grobs=TRUE, viewports=FALSE, fullNames=FALSE,
        recursive=TRUE, print=TRUE, flatten=TRUE, ...)
```

```
nestedListing(x, gindent=" ", vpendent=gindent)
```



```
pathListing(x, gvpSep=" | ", gAlign=TRUE)
grobPathListing(x, ...)
```

### Arguments

<code>x</code>	A grob or viewport or NULL. If NULL, the current grid display list is listed. For print functions, this should be the result of a call to <code>grid.ls</code> .
<code>grobs</code>	A logical value indicating whether to list grobs.
<code>viewports</code>	A logical value indicating whether to list viewports.
<code>fullNames</code>	A logical value indicating whether to embellish object names with information about the object type.
<code>recursive</code>	A logical value indicating whether recursive structures should also list their children.
<code>print</code>	A logical indicating whether to print the listing or a function that will print the listing.
<code>flatten</code>	A logical value indicating whether to flatten the listing. Otherwise a more complex hierarchical object is produced.
<code>gindent</code>	The indent used to show nesting in the output for grobs.
<code>vpindent</code>	The indent used to show nesting in the output for viewports.
<code>gvpSep</code>	The string used to separate viewport paths from grob paths.
<code>gAlign</code>	Logical indicating whether to align the left hand edge of all grob paths.
<code>...</code>	Arguments passed to the <code>print</code> function.

### Details

If the argument `x` is NULL, the current contents of the grid display list are listed (both viewports and grobs). In other words, all objects representing the current scene are listed.

Otherwise, `x` should be a grob or a viewport.

The default behaviour of this function is to print information about the grobs in the current scene. It is also possible to add information about the viewports in the scene. By default, the listing is recursive, so all children of `gTrees` and all nested viewports are reported.

The format of the information can be controlled via the `print` argument, which can be given a function to perform the formatting. The `nestedListing` function produces a line per grob or viewport, with indenting used to show nesting. The `pathListing` function produces a line per grob or viewport, with viewport paths and grob paths used to show nesting. The `grobPathListing` is a simple derivation that only shows lines for grobs. The user can define new functions.

### Value

The result of this function is either a "gridFlatListing" object (if `flatten` is TRUE) or a "gridListing" object.

The former is a simple (flat) list of vectors. This is convenient, for example, for working programmatically with the list of grob and viewport names, or for writing a new display function for the listing.

The latter is a more complex hierarchical object (list of lists), but it does contain more detailed information so may be of use for more advanced customisations.

**Author(s)**

Paul Murrell

**See Also**[grob viewport](#)**Examples**

```
# A gTree, called "parent", with childrenvp vpTree (vp2 within vp1)
# and child grob, called "child", with vp vpPath (down to vp2)
sampleGTree <- gTree(name="parent",
                     children=gList(grob(name="child", vp="vp1::vp2")),
                     childrenvp=vpTree(parent=viewport(name="vp1"),
                                       children=vpList(viewport(name="vp2"))))

grid.ls(sampleGTree)
# Show viewports too
grid.ls(sampleGTree, view=TRUE)
# Only show viewports
grid.ls(sampleGTree, view=TRUE, grob=FALSE)
# Alternate displays
# nested listing, custom indent
grid.ls(sampleGTree, view=TRUE, print=nestedListing, gindent="--")
# path listing
grid.ls(sampleGTree, view=TRUE, print=pathListing)
# path listing, without grobs aligned
grid.ls(sampleGTree, view=TRUE, print=pathListing, gAlign=FALSE)
# grob path listing
grid.ls(sampleGTree, view=TRUE, print=grobPathListing)
# path listing, grobs only
grid.ls(sampleGTree, print=pathListing)
# path listing, viewports only
grid.ls(sampleGTree, view=TRUE, grob=FALSE, print=pathListing)
# raw flat listing
str(grid.ls(sampleGTree, view=TRUE, print=FALSE))
```

grid.move.to

*Move or Draw to a Specified Position***Description**

Grid has the notion of a current location. These functions sets that location.

**Usage**

```
grid.move.to(x = 0, y = 0, default.units = "npc", name = NULL,
            draw = TRUE, vp = NULL)

moveToGrob(x = 0, y = 0, default.units = "npc", name = NULL, vp = NULL)

grid.line.to(x = 1, y = 1, default.units = "npc",
            arrow = NULL, name = NULL,
            gp = gpar(), draw = TRUE, vp = NULL)
```

```
lineToGrob(x = 1, y = 1, default.units = "npc", arrow = NULL,
           name = NULL, gp = gpar(), vp = NULL)
```

### Arguments

<code>x</code>	A numeric value or a unit object specifying an x-value.
<code>y</code>	A numeric value or a unit object specifying a y-value.
<code>default.units</code>	A string indicating the default units to use if <code>x</code> or <code>y</code> are only given as numeric values.
<code>arrow</code>	A list describing arrow heads to place at either end of the line, as produced by the <code>arrow</code> function.
<code>name</code>	A character identifier.
<code>draw</code>	A logical value indicating whether graphics output should be produced.
<code>gp</code>	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
<code>vp</code>	A Grid viewport object (or <code>NULL</code> ).

### Details

Both functions create a `move.to/line.to` grob (a graphical object describing a `move.to/line.to`), but only `grid.move.to/line.to()` draws the `move.to/line.to` (and then only if `draw` is `TRUE`).

### Value

A `move.to/line.to` grob. `grid.move.to/line.to()` returns the value invisibly.

### Author(s)

Paul Murrell

### See Also

[Grid](#), [viewport](#), [arrow](#)

### Examples

```
grid.newpage()
grid.move.to(0.5, 0.5)
grid.line.to(1, 1)
grid.line.to(0.5, 0)
pushViewport(viewport(x=0, y=0, w=0.25, h=0.25, just=c("left", "bottom")))
grid.rect()
grid.grill()
grid.line.to(0.5, 0.5)
popViewport()
```

---

grid.newpage	<i>Move to a New Page on a Grid Device</i>
--------------	--

---

**Description**

This function erases the current device or moves to a new page.

**Usage**

```
grid.newpage(recording = TRUE)
```

**Arguments**

recording	A logical value to indicate whether the new-page operation should be saved onto the Grid display list.
-----------	--

**Details**

The new page is painted with the fill colour (`gpar("fill")`), which is often transparent. For devices with a *canvas* colour (the on-screen devices `X11`, `windows` and `quartz`), the page is first painted with the canvas colour and then the background colour.

There is a hook called "grid.newpage" (see `setHook`) which is used in the testing code to annotate the new page. The hook function(s) are called with no argument. (If the value is a character string, `get` is called on it from within the **grid** name space.)

**Value**

None.

**Author(s)**

Paul Murrell

**See Also**

[Grid](#)

---

grid.null	<i>Null Graphical Object</i>
-----------	------------------------------

---

**Description**

These functions create a NULL graphical object, which has zero width, zero height, and draw nothing. It can be used as a place-holder or as an invisible reference point for other drawing.

**Usage**

```
nullGrob(x = unit(0.5, "npc"), y = unit(0.5, "npc"),
         default.units = "npc",
         name = NULL, vp = NULL)
grid.null(...)
```

**Arguments**

<code>x</code>	A numeric vector or unit object specifying x-location.
<code>y</code>	A numeric vector or unit object specifying y-location.
<code>default.units</code>	A string indicating the default units to use if <code>x</code> , <code>y</code> , <code>width</code> , or <code>height</code> are only given as numeric vectors.
<code>name</code>	A character identifier.
<code>vp</code>	A Grid viewport object (or NULL).
<code>...</code>	Arguments passed to <code>nullGrob()</code> .

**Value**

A null grob.

**Author(s)**

Paul Murrell

**See Also**

[Grid](#), [viewport](#)

**Examples**

```
grid.newpage()
grid.null(name="ref")
grid.rect(height=grobHeight("ref"))
grid.segments(0, 0, grobX("ref", 0), grobY("ref", 0))
```

---

grid.pack

*Pack an Object within a Frame*

---

**Description**

This functions, together with `grid.frame` and `frameGrob` are part of a GUI-builder-like interface to constructing graphical images. The idea is that you create a frame with `grid.frame` or `frameGrob` then use this functions to pack objects into the frame.

**Usage**

```
grid.pack(gPath, grob, redraw = TRUE, side = NULL,
          row = NULL, row.before = NULL, row.after = NULL,
          col = NULL, col.before = NULL, col.after = NULL,
          width = NULL, height = NULL,
          force.width = FALSE, force.height = FALSE, border = NULL,
          dynamic = FALSE)

packGrob(frame, grob, side = NULL,
          row = NULL, row.before = NULL, row.after = NULL,
          col = NULL, col.before = NULL, col.after = NULL,
```

```
width = NULL, height = NULL,
force.width = FALSE, force.height = FALSE, border = NULL,
dynamic = FALSE)
```

### Arguments

<code>gPath</code>	A <code>gPath</code> object, which specifies a frame on the display list.
<code>frame</code>	An object of class <code>frame</code> , typically the output from a call to <code>grid.frame</code> .
<code>grob</code>	An object of class <code>grob</code> . The object to be packed.
<code>redraw</code>	A boolean indicating whether the output should be updated.
<code>side</code>	One of "left", "top", "right", "bottom" to indicate which side to pack the object on.
<code>row</code>	Which row to add the object to. Must be between 1 and the-number-of-rows-currently-in-the-frame + 1, or NULL in which case the object occupies all rows.
<code>row.before</code>	Add the object to a new row just before this row.
<code>row.after</code>	Add the object to a new row just after this row.
<code>col</code>	Which col to add the object to. Must be between 1 and the-number-of-cols-currently-in-the-frame + 1, or NULL in which case the object occupies all cols.
<code>col.before</code>	Add the object to a new col just before this col.
<code>col.after</code>	Add the object to a new col just after this col.
<code>width</code>	Specifies the width of the column that the object is added to (rather than allowing the width to be taken from the object).
<code>height</code>	Specifies the height of the row that the object is added to (rather than allowing the height to be taken from the object).
<code>force.width</code>	A logical value indicating whether the width of the column that the grob is being packed into should be EITHER the width specified in the call to <code>grid.pack</code> OR the maximum of that width and the pre-existing width.
<code>force.height</code>	A logical value indicating whether the height of the column that the grob is being packed into should be EITHER the height specified in the call to <code>grid.pack</code> OR the maximum of that height and the pre-existing height.
<code>border</code>	A <code>unit</code> object of length 4 indicating the borders around the object.
<code>dynamic</code>	If the width/height is taken from the grob being packed, this boolean flag indicates whether the <code>grobwidth/height</code> unit refers directly to the grob, or uses a <code>gPath</code> to the grob. In the latter case, changes to the grob will trigger a recalculation of the width/height.

### Details

`packGrob` modifies the given frame `grob` and returns the modified frame `grob`.

`grid.pack` destructively modifies a frame `grob` on the display list (and redraws the display list if `redraw` is TRUE).

These are (meant to be) very flexible functions. There are many different ways to specify where the new object is to be added relative to the objects already in the frame. The function checks that the specification is not self-contradictory.

NOTE that the width/height of the row/col that the object is added to is taken from the object itself unless the `width/height` is specified.

**Value**

packGrob returns a frame grob, but grid.pack returns NULL.

**Author(s)**

Paul Murrell

**See Also**

[grid.frame](#), [grid.place](#), [grid.edit](#), and [gPath](#).

---

grid.place

*Place an Object within a Frame*

---

**Description**

These functions provide a simpler (and faster) alternative to the `grid.pack()` and `packGrob` functions. They can be used to place objects within the existing rows and columns of a frame layout. They do not provide the ability to add new rows and columns nor do they affect the heights and widths of the rows and columns.

**Usage**

```
grid.place(gPath, grob, row = 1, col = 1, redraw = TRUE)
placeGrob(frame, grob, row = NULL, col = NULL)
```

**Arguments**

<code>gPath</code>	A <code>gPath</code> object, which specifies a frame on the display list.
<code>frame</code>	An object of class <code>frame</code> , typically the output from a call to <code>grid.frame</code> .
<code>grob</code>	An object of class <code>grob</code> . The object to be placed.
<code>row</code>	Which row to add the object to. Must be between 1 and the-number-of-rows-currently-in-the-frame.
<code>col</code>	Which col to add the object to. Must be between 1 and the-number-of-cols-currently-in-the-frame.
<code>redraw</code>	A boolean indicating whether the output should be updated.

**Details**

`placeGrob` modifies the given frame `grob` and returns the modified frame `grob`.

`grid.place` destructively modifies a frame `grob` on the display list (and redraws the display list if `redraw` is `TRUE`).

**Value**

`placeGrob` returns a frame `grob`, but `grid.place` returns NULL.

**Author(s)**

Paul Murrell

**See Also**

[grid.frame](#), [grid.pack](#), [grid.edit](#), and [gPath](#).

---

grid.plot.and.legend

*A Simple Plot and Legend Demo*

---

**Description**

This function is just a wrapper for a simple demonstration of how a basic plot and legend can be drawn from scratch using grid.

**Usage**

```
grid.plot.and.legend()
```

**Author(s)**

Paul Murrell

**Examples**

```
grid.plot.and.legend()
```

---

grid.points

*Draw Data Symbols*

---

**Description**

These functions create and draw data symbols.

**Usage**

```
grid.points(x = stats::runif(10),  
            y = stats::runif(10),  
            pch = 1, size = unit(1, "char"),  
            default.units = "native", name = NULL,  
            gp = gpar(), draw = TRUE, vp = NULL)  
pointsGrob(x = stats::runif(10),  
            y = stats::runif(10),  
            pch = 1, size = unit(1, "char"),  
            default.units = "native", name = NULL,  
            gp = gpar(), vp = NULL)
```



**Arguments**

<code>x</code>	A numeric vector or unit object specifying x-values.
<code>y</code>	A numeric vector or unit object specifying y-values.
<code>pch</code>	A numeric or character vector indicating what sort of plotting symbol to use. See <a href="#">points</a> for the interpretation of these values.
<code>size</code>	A unit object specifying the size of the plotting symbols.
<code>default.units</code>	A string indicating the default units to use if <code>x</code> or <code>y</code> are only given as numeric vectors.
<code>name</code>	A character identifier.
<code>gp</code>	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
<code>draw</code>	A logical value indicating whether graphics output should be produced.
<code>vp</code>	A Grid viewport object (or NULL).

**Details**

Both functions create a points grob (a graphical object describing points), but only `grid.points` draws the points (and then only if `draw` is TRUE).

**Value**

A points grob. `grid.points` returns the value invisibly.

**Author(s)**

Paul Murrell

**See Also**

[Grid](#), [viewport](#)

---

grid.polygon

*Draw a Polygon*

---

**Description**

These functions create and draw a polygon. The final point will automatically be connected to the initial point.

**Usage**

```
grid.polygon(x=c(0, 0.5, 1, 0.5), y=c(0.5, 1, 0.5, 0),
             id=NULL, id.lengths=NULL,
             default.units="npc", name=NULL,
             gp=gpar(), draw=TRUE, vp=NULL)
polygonGrob(x=c(0, 0.5, 1, 0.5), y=c(0.5, 1, 0.5, 0),
            id=NULL, id.lengths=NULL,
            default.units="npc", name=NULL,
            gp=gpar(), vp=NULL)
```

**Arguments**

<code>x</code>	A numeric vector or unit object specifying x-locations.
<code>y</code>	A numeric vector or unit object specifying y-locations.
<code>id</code>	A numeric vector used to separate locations in <code>x</code> and <code>y</code> into multiple polygons. All locations with the same <code>id</code> belong to the same polygon.
<code>id.lengths</code>	A numeric vector used to separate locations in <code>x</code> and <code>y</code> into multiple polygons. Specifies consecutive blocks of locations which make up separate polygons.
<code>default.units</code>	A string indicating the default units to use if <code>x</code> , <code>y</code> , <code>width</code> , or <code>height</code> are only given as numeric vectors.
<code>name</code>	A character identifier.
<code>gp</code>	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
<code>draw</code>	A logical value indicating whether graphics output should be produced.
<code>vp</code>	A Grid viewport object (or NULL).

**Details**

Both functions create a polygon `grob` (a graphical object describing a polygon), but only `grid.polygon` draws the polygon (and then only if `draw` is `TRUE`).

**Value**

A `grob` object.

**Author(s)**

Paul Murrell

**See Also**

[Grid, viewport](#)

**Examples**

```
grid.polygon()
# Using id (NOTE: locations are not in consecutive blocks)
grid.newpage()
grid.polygon(x=c((0:4)/10, rep(.5, 5), (10:6)/10, rep(.5, 5)),
             y=c(rep(.5, 5), (10:6)/10, rep(.5, 5), (0:4)/10),
             id=rep(1:5, 4),
             gp=gpar(fill=1:5))
# Using id.lengths
grid.newpage()
grid.polygon(x=outer(c(0, .5, 1, .5), 5:1/5),
             y=outer(c(.5, 1, .5, 0), 5:1/5),
             id.lengths=rep(4, 5),
             gp=gpar(fill=1:5))
```

grid.pretty                    *Generate a Sensible Set of Breakpoints*

---

**Description**

Produces a pretty set of breakpoints within the range given.

**Usage**

```
grid.pretty(range)
```

**Arguments**

range                    A numeric vector

**Value**

A numeric vector of breakpoints.

**Author(s)**

Paul Murrell

---

grid.prompt                    *Prompt before New Page*

---

**Description**

This function can be used to control whether the user is prompted before starting a new page of output.

**Usage**

```
grid.prompt(ask)
```

**Arguments**

ask                    a logical value. If TRUE, the user is prompted before a new page of output is started.

**Details**

This is deprecated in favour of `devAskNewPage` as a single setting inside the device affects both the base and grid graphics systems.

The default value when a device is opened is taken from the setting of `options("device.ask.default")`.

**Value**

The current prompt setting *before* any new setting is applied.

**Author(s)**

Paul Murrell

**See Also**[grid.newpage](#)


---

grid.raster	<i>Render a raster object</i>
-------------	-------------------------------

---

**Description**

Render a raster object (bitmap image) at the given location, size, and orientation.

**Usage**

```
grid.raster(image,
            x = unit(0.5, "npc"), y = unit(0.5, "npc"),
            width = unit(1, "npc"), height = NULL,
            just = "centre", hjust = NULL, vjust = NULL,
            interpolate = TRUE, default.units = "npc",
            name = NULL, gp = gpar(), vp = NULL)
```

```
rasterGrob(image,
            x = unit(0.5, "npc"), y = unit(0.5, "npc"),
            width = unit(1, "npc"), height = NULL,
            just = "centre", hjust = NULL, vjust = NULL,
            interpolate = TRUE, default.units = "npc",
            name = NULL, gp = gpar(), vp = NULL)
```

**Arguments**

image	Any R object that can be coerced to a raster object.
x	A numeric vector or unit object specifying x-location.
y	A numeric vector or unit object specifying y-location.
width	A numeric vector or unit object specifying width.
height	A numeric vector or unit object specifying height.
just	The justification of the rectangle relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". For numeric values, 0 means left alignment and 1 means right alignment.
hjust	A numeric vector specifying horizontal justification. If specified, overrides the just setting.
vjust	A numeric vector specifying vertical justification. If specified, overrides the just setting.
default.units	A string indicating the default units to use if x, y, width, or height are only given as numeric vectors.

name	A character identifier.
gp	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or <code>NULL</code> ).
interpolate	A logical value indicating whether to linearly interpolate the image (the alternative is to use nearest-neighbour interpolation, which gives a more blocky result).

### Details

Only one of `width` or `height` needs to be specified, in which case, the aspect ratio of the image is preserved. If both `width` and `height` are specified, it is likely that the image will be distorted.

Not all graphics devices are capable of rendering raster images and some may not be able to produce rotated images (i.e., if a raster object is rendered within a rotated viewport).

All graphical parameter settings in `gp` will be ignored, including `alpha`.

### Value

A raster object `grob`.

### Author(s)

Paul Murrell

### See Also

[as.raster](#).

### Examples

```
redGradient <- matrix(hcl(0, 80, seq(50, 80, 10)),
                     nrow=4, ncol=5)

# interpolated
grid.newpage()
grid.raster(redGradient)

# blocky
grid.newpage()
grid.raster(redGradient, interpolate=FALSE)

# blocky and stretched
grid.newpage()
grid.raster(redGradient, interpolate=FALSE, height=unit(1, "npc"))

# The same raster drawn several times
grid.newpage()
grid.raster(0, x=1:3/4, y=1:3/4, w=.1, interp=FALSE)
```

---

grid.record	<i>Encapsulate calculations and drawing</i>
-------------	---

---

### Description

Evaluates an expression that includes both calculations and drawing that depends on the calculations so that both the calculations and the drawing will be rerun when the scene is redrawn (e.g., device resize or editing).

Intended *only* for expert use.

### Usage

```
recordGrob(expr, list, name=NULL, gp=NULL, vp=NULL)
grid.record(expr, list, name=NULL, gp=NULL, vp=NULL)
```

### Arguments

expr	object of mode <a href="#">expression</a> or <code>call</code> or an unevaluated expression.
list	a list defining the environment in which <code>expr</code> is to be evaluated.
name	A character identifier.
gp	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or <code>NULL</code> ).

### Details

A grob is created of special class "recordedGrob" (and drawn, in the case of `grid.record`). The `drawDetails` method for this class evaluates the expression with the list as the evaluation environment (and the grid Namespace as the parent of that environment).

### Note

This function *must* be used instead of the function `recordGraphics`; all of the dire warnings about using `recordGraphics` responsibly also apply here.

### Author(s)

Paul Murrell

### See Also

[recordGraphics](#)

### Examples

```
grid.record({
  w <- convertWidth(unit(1, "inches"), "npc")
  grid.rect(width=w)
},
list())
```

grid.rect

*Draw rectangles***Description**

These functions create and draw rectangles.

**Usage**

```
grid.rect(x = unit(0.5, "npc"), y = unit(0.5, "npc"),
          width = unit(1, "npc"), height = unit(1, "npc"),
          just = "centre", hjust = NULL, vjust = NULL,
          default.units = "npc", name = NULL,
          gp=gpar(), draw = TRUE, vp = NULL)
rectGrob(x = unit(0.5, "npc"), y = unit(0.5, "npc"),
          width = unit(1, "npc"), height = unit(1, "npc"),
          just = "centre", hjust = NULL, vjust = NULL,
          default.units = "npc", name = NULL,
          gp=gpar(), vp = NULL)
```

**Arguments**

<code>x</code>	A numeric vector or unit object specifying x-location.
<code>y</code>	A numeric vector or unit object specifying y-location.
<code>width</code>	A numeric vector or unit object specifying width.
<code>height</code>	A numeric vector or unit object specifying height.
<code>just</code>	The justification of the rectangle relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". For numeric values, 0 means left alignment and 1 means right alignment.
<code>hjust</code>	A numeric vector specifying horizontal justification. If specified, overrides the <code>just</code> setting.
<code>vjust</code>	A numeric vector specifying vertical justification. If specified, overrides the <code>just</code> setting.
<code>default.units</code>	A string indicating the default units to use if <code>x</code> , <code>y</code> , <code>width</code> , or <code>height</code> are only given as numeric vectors.
<code>name</code>	A character identifier.
<code>gp</code>	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
<code>draw</code>	A logical value indicating whether graphics output should be produced.
<code>vp</code>	A Grid viewport object (or <code>NULL</code> ).

**Details**

Both functions create a `rect grob` (a graphical object describing rectangles), but only `grid.rect` draws the rectangles (and then only if `draw` is `TRUE`).

**Value**

A rect grob. `grid.rect` returns the value invisibly.

**Author(s)**

Paul Murrell

**See Also**

[Grid](#), [viewport](#)

---

<code>grid.refresh</code>	<i>Refresh the current grid scene</i>
---------------------------	---------------------------------------

---

**Description**

Replays the current grid display list.

**Usage**

```
grid.refresh()
```

**Author(s)**

Paul Murrell

---

<code>grid.remove</code>	<i>Remove a Grid Graphical Object</i>
--------------------------	---------------------------------------

---

**Description**

Remove a grob from a `gTree` or a descendant of a `gTree`.

**Usage**

```
grid.remove(gPath, warn = TRUE, strict = FALSE, grep = FALSE,  
            global = FALSE, allDevices = FALSE, redraw = TRUE)
```

```
grid.gremove(..., grep = TRUE, global = TRUE)
```

```
removeGrob(gTree, gPath, strict = FALSE, grep = FALSE,  
            global = FALSE, warn = TRUE)
```



**Arguments**

<code>gTree</code>	A <code>gTree</code> object.
<code>gPath</code>	A <code>gPath</code> object. For <code>grid.remove</code> this specifies a <code>gTree</code> on the display list. For <code>removeGrob</code> this specifies a descendant of the specified <code>gTree</code> .
<code>strict</code>	A boolean indicating whether the <code>gPath</code> must be matched exactly.
<code>grep</code>	A boolean indicating whether the <code>gPath</code> should be treated as a regular expression. Values are recycled across elements of the <code>gPath</code> (e.g., <code>c(TRUE, FALSE)</code> means that every odd element of the <code>gPath</code> will be treated as a regular expression).
<code>global</code>	A boolean indicating whether the function should affect just the first match of the <code>gPath</code> , or whether all matches should be affected.
<code>allDevices</code>	A boolean indicating whether all open devices should be searched for matches, or just the current device. NOT YET IMPLEMENTED.
<code>warn</code>	A logical to indicate whether failing to find the specified grob should trigger an error.
<code>redraw</code>	A logical value to indicate whether to redraw the grob.
<code>...</code>	Arguments that are passed to <code>grid.get</code> .

**Details**

`removeGrob` copies the specified grob and returns a modified grob.

`grid.remove` destructively modifies a grob on the display list. If `redraw` is `TRUE` it then redraws everything to reflect the change.

`grid.gremove` (`g` for global) is just a convenience wrapper for `grid.remove` with different defaults.

**Value**

`removeGrob` returns a grob object; `grid.remove` returns `NULL`.

**Author(s)**

Paul Murrell

**See Also**

[grob](#), [getGrob](#), [removeGrob](#), [removeGrob](#).

---

`grid.segments`

*Draw Line Segments*

---

**Description**

These functions create and draw line segments.

**Usage**

```

grid.segments(x0 = unit(0, "npc"), y0 = unit(0, "npc"),
             x1 = unit(1, "npc"), y1 = unit(1, "npc"),
             default.units = "npc",
             arrow = NULL,
             name = NULL, gp = gpar(), draw = TRUE, vp = NULL)
segmentsGrob(x0 = unit(0, "npc"), y0 = unit(0, "npc"),
            x1 = unit(1, "npc"), y1 = unit(1, "npc"),
            default.units = "npc",
            arrow = NULL, name = NULL, gp = gpar(), vp = NULL)

```

**Arguments**

<code>x0</code>	Numeric indicating the starting x-values of the line segments.
<code>y0</code>	Numeric indicating the starting y-values of the line segments.
<code>x1</code>	Numeric indicating the stopping x-values of the line segments.
<code>y1</code>	Numeric indicating the stopping y-values of the line segments.
<code>default.units</code>	A string.
<code>arrow</code>	A list describing arrow heads to place at either end of the line segments, as produced by the <code>arrow</code> function.
<code>name</code>	A character identifier.
<code>gp</code>	An object of class <code>gpar</code> .
<code>draw</code>	A logical value indicating whether graphics output should be produced.
<code>vp</code>	A Grid viewport object (or <code>NULL</code> ).

**Details**

Both functions create a segments grob (a graphical object describing segments), but only `grid.segments` draws the segments (and then only if `draw` is `TRUE`).

**Value**

A segments grob. `grid.segments` returns the value invisibly.

**Author(s)**

Paul Murrell

**See Also**

[Grid](#), [viewport](#), [arrow](#)

---

`grid.set`*Set a Grid Graphical Object*

---

**Description**

Replace a grob or a descendant of a grob.

**Usage**

```
grid.set(gPath, newGrob, strict = FALSE, grep = FALSE,  
         redraw = TRUE)
```

```
setGrob(gTree, gPath, newGrob, strict = FALSE, grep = FALSE)
```

**Arguments**

<code>gTree</code>	A <code>gTree</code> object.
<code>gPath</code>	A <code>gPath</code> object. For <code>grid.set</code> this specifies a grob on the display list. For <code>setGrob</code> this specifies a descendant of the specified <code>gTree</code> .
<code>newGrob</code>	A grob object.
<code>strict</code>	A boolean indicating whether the <code>gPath</code> must be matched exactly.
<code>grep</code>	A boolean indicating whether the <code>gPath</code> should be treated as a regular expression. Values are recycled across elements of the <code>gPath</code> (e.g., <code>c(TRUE, FALSE)</code> means that every odd element of the <code>gPath</code> will be treated as a regular expression).
<code>redraw</code>	A logical value to indicate whether to redraw the grob.

**Details**

`setGrob` copies the specified grob and returns a modified grob.

`grid.set` destructively replaces a grob on the display list. If `redraw` is `TRUE` it then redraws everything to reflect the change.

These functions should not normally be called by the user.

**Value**

`setGrob` returns a grob object; `grid.set` returns `NULL`.

**Author(s)**

Paul Murrell

**See Also**

[grid.grob](#).

---

grid.show.layout     *Draw a Diagram of a Grid Layout*

---

### Description

This function uses Grid graphics to draw a diagram of a Grid layout.

### Usage

```
grid.show.layout(l, newpage=TRUE, bg = "light grey",  
                cell.border = "blue", cell.fill = "light blue",  
                cell.label = TRUE, label.col = "blue",  
                unit.col = "red", vp = NULL)
```

### Arguments

<code>l</code>	A Grid layout object.
<code>newpage</code>	A logical value indicating whether to move on to a new page before drawing the diagram.
<code>bg</code>	The colour used for the background.
<code>cell.border</code>	The colour used to draw the borders of the cells in the layout.
<code>cell.fill</code>	The colour used to fill the cells in the layout.
<code>cell.label</code>	A logical indicating whether the layout cells should be labelled.
<code>label.col</code>	The colour used for layout cell labels.
<code>unit.col</code>	The colour used for labelling the widths/heights of columns/rows.
<code>vp</code>	A Grid viewport object (or NULL).

### Details

A viewport is created within `vp` to provide a margin for annotation, and the layout is drawn within that new viewport. The margin is filled with light grey, the new viewport is filled with white and framed with a black border, and the layout regions are filled with light blue and framed with a blue border. The diagram is annotated with the widths and heights (including units) of the columns and rows of the layout using red text. (All colours are defaults and may be customised via function arguments.)

### Value

None.

### Author(s)

Paul Murrell

### See Also

[Grid](#), [viewport](#), [grid.layout](#)

**Examples**

```
## Diagram of a simple layout
grid.show.layout (grid.layout (4, 2,
    heights=unit (rep(1, 4),
        c("lines", "lines", "lines", "null")),
    widths=unit (c(1, 1), "inches")))
```

---

grid.show.viewport *Draw a Diagram of a Grid Viewport*

---

**Description**

This function uses Grid graphics to draw a diagram of a Grid viewport.

**Usage**

```
grid.show.viewport (v, parent.layout = NULL, newpage = TRUE,
    border.fill="light grey",
    vp.col="blue", vp.fill="light blue",
    scale.col="red",
    vp = NULL)
```

**Arguments**

<code>v</code>	A Grid viewport object.
<code>parent.layout</code>	A grid layout object. If this is not NULL and the viewport given in <code>v</code> has its location specified relative to the layout, then the diagram shows the layout and which cells <code>v</code> occupies within the layout.
<code>newpage</code>	A logical value to indicate whether to move to a new page before drawing the diagram.
<code>border.fill</code>	Colour to fill the border margin.
<code>vp.col</code>	Colour for the border of the viewport region.
<code>vp.fill</code>	Colour to fill the viewport region.
<code>scale.col</code>	Colour to draw the viewport axes.
<code>vp</code>	A Grid viewport object (or NULL).

**Details**

A viewport is created within `vp` to provide a margin for annotation, and the diagram is drawn within that new viewport. By default, the margin is filled with light grey, the new viewport is filled with white and framed with a black border, and the viewport region is filled with light blue and framed with a blue border. The diagram is annotated with the width and height (including units) of the viewport, the (x, y) location of the viewport, and the x- and y-scales of the viewport, using red lines and text.

**Value**

None.

**Author(s)**

Paul Murrell

**See Also**[Grid](#), [viewport](#)**Examples**

```
## Diagram of a sample viewport
grid.show.viewport(viewport(x=0.6, y=0.6,
                            w=unit(1, "inches"), h=unit(1, "inches")))
grid.show.viewport(viewport(layout.pos.row=2, layout.pos.col=2:3),
                  grid.layout(3, 4))
```

grid.text

*Draw Text***Description**

These functions create and draw text and [plotmath](#) expressions.

**Usage**

```
grid.text(label, x = unit(0.5, "npc"), y = unit(0.5, "npc"),
          just = "centre", hjust = NULL, vjust = NULL, rot = 0,
          check.overlap = FALSE, default.units = "npc",
          name = NULL, gp = gpar(), draw = TRUE, vp = NULL)
```

```
textGrob(label, x = unit(0.5, "npc"), y = unit(0.5, "npc"),
          just = "centre", hjust = NULL, vjust = NULL, rot = 0,
          check.overlap = FALSE, default.units = "npc",
          name = NULL, gp = gpar(), vp = NULL)
```

**Arguments**

label	A character or <a href="#">expression</a> vector. Other objects are coerced by <a href="#">as.graphicsAnnot</a> .
x	A numeric vector or unit object specifying x-values.
y	A numeric vector or unit object specifying y-values.
just	The justification of the text relative to its (x, y) location. If there are two values, the first value specifies horizontal justification and the second value specifies vertical justification. Possible string values are: "left", "right", "centre", "center", "bottom", and "top". For numeric values, 0 means left alignment and 1 means right alignment.
hjust	A numeric vector specifying horizontal justification. If specified, overrides the just setting.
vjust	A numeric vector specifying vertical justification. If specified, overrides the just setting.
rot	The angle to rotate the text.

<code>check.overlap</code>	A logical value to indicate whether to check for and omit overlapping text.
<code>default.units</code>	A string indicating the default units to use if <code>x</code> or <code>y</code> are only given as numeric vectors.
<code>name</code>	A character identifier.
<code>gp</code>	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
<code>draw</code>	A logical value indicating whether graphics output should be produced.
<code>vp</code>	A Grid viewport object (or <code>NULL</code> ).

### Details

Both functions create a text grob (a graphical object describing text), but only `grid.text` draws the text (and then only if `draw` is `TRUE`).

If the `label` argument is an expression, the output is formatted as a mathematical annotation, as for base graphics text.

### Value

A text grob. `grid.text` returns the value invisibly.

### Author(s)

Paul Murrell

### See Also

[Grid, viewport](#)

### Examples

```
grid.newpage()
x <- stats::runif(20)
y <- stats::runif(20)
rot <- stats::runif(20, 0, 360)
grid.text("SOMETHING NICE AND BIG", x=x, y=y, rot=rot,
         gp=gpar(fontsize=20, col="grey"))
grid.text("SOMETHING NICE AND BIG", x=x, y=y, rot=rot,
         gp=gpar(fontsize=20), check=TRUE)
grid.newpage()
draw.text <- function(just, i, j) {
  grid.text("ABCD", x=x[j], y=y[i], just=just)
  grid.text(deparse(substitute(just)), x=x[j], y=y[i] + unit(2, "lines"),
           gp=gpar(col="grey", fontsize=8))
}
x <- unit(1:4/5, "npc")
y <- unit(1:4/5, "npc")
grid.grill(h=y, v=x, gp=gpar(col="grey"))
draw.text(c("bottom"), 1, 1)
draw.text(c("left", "bottom"), 2, 1)
draw.text(c("right", "bottom"), 3, 1)
draw.text(c("centre", "bottom"), 4, 1)
draw.text(c("centre"), 1, 2)
```

```

draw.text(c("left", "centre"), 2, 2)
draw.text(c("right", "centre"), 3, 2)
draw.text(c("centre", "centre"), 4, 2)
draw.text(c("top"), 1, 3)
draw.text(c("left", "top"), 2, 3)
draw.text(c("right", "top"), 3, 3)
draw.text(c("centre", "top"), 4, 3)
draw.text(c(), 1, 4)
draw.text(c("left"), 2, 4)
draw.text(c("right"), 3, 4)
draw.text(c("centre"), 4, 4)

```

---

grid.xaxis

*Draw an X-Axis*


---

### Description

These functions create and draw an x-axis.

### Usage

```

grid.xaxis(at = NULL, label = TRUE, main = TRUE,
           edits = NULL, name = NULL,
           gp = gpar(), draw = TRUE, vp = NULL)

```

```

xaxisGrob(at = NULL, label = TRUE, main = TRUE,
           edits = NULL, name = NULL,
           gp = gpar(), vp = NULL)

```

### Arguments

at	A numeric vector of x-value locations for the tick marks.
label	A logical value indicating whether to draw the labels on the tick marks, or an expression or character vector which specify the labels to use. If not logical, must be the same length as the at argument.
main	A logical value indicating whether to draw the axis at the bottom (TRUE) or at the top (FALSE) of the viewport.
edits	A gEdit or gEditList containing edit operations to apply (to the children of the axis) when the axis is first created and during redrawing whenever at is NULL.
name	A character identifier.
gp	An object of class gpar, typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
draw	A logical value indicating whether graphics output should be produced.
vp	A Grid viewport object (or NULL).

### Details

Both functions create an xaxis grob (a graphical object describing an axis), but only grid.xaxis draws the axis (and then only if draw is TRUE).



**Value**

An axis grob. `grid.xaxis` returns the value invisibly.

**Children**

If the `at` slot of an `xaxis` grob is not `NULL` then the `xaxis` will have the following children:

**major** representing the line at the base of the tick marks.

**ticks** representing the tick marks.

**labels** representing the tick labels.

If the `at` slot is `NULL` then there are no children and ticks are drawn based on the current viewport scale.

**Author(s)**

Paul Murrell

**See Also**

[Grid](#), [viewport](#), [grid.yaxis](#)

---

`grid.xspline`

*Draw an Xspline*

---

**Description**

These functions create and draw an `xspline`, a curve drawn relative to control points.

**Usage**

```
grid.xspline(...)
xsplineGrob(x = c(0, 0.5, 1, 0.5), y = c(0.5, 1, 0.5, 0),
            id = NULL, id.lengths = NULL,
            default.units = "npc",
            shape = 0, open = TRUE, arrow = NULL, repEnds = TRUE,
            name = NULL, gp = gpar(), vp = NULL)
```

**Arguments**

<code>x</code>	A numeric vector or unit object specifying x-locations of spline control points.
<code>y</code>	A numeric vector or unit object specifying y-locations of spline control points.
<code>id</code>	A numeric vector used to separate locations in <code>x</code> and <code>y</code> into multiple <code>xsplines</code> . All locations with the same <code>id</code> belong to the same <code>xspline</code> .
<code>id.lengths</code>	A numeric vector used to separate locations in <code>x</code> and <code>y</code> into multiple <code>xspline</code> . Specifies consecutive blocks of locations which make up separate <code>xsplines</code> .
<code>default.units</code>	A string indicating the default units to use if <code>x</code> or <code>y</code> are only given as numeric vectors.

shape	A numeric vector of values between -1 and 1, which control the shape of the spline relative to the control points.
open	A logical value indicating whether the spline is a line or a closed shape.
arrow	A list describing arrow heads to place at either end of the xspline, as produced by the <code>arrow</code> function.
repEnds	A logical value indicating whether the first and last control points should be replicated for drawing the curve (see Details below).
name	A character identifier.
gp	An object of class <code>gpar</code> , typically the output from a call to the function <code>gpar</code> . This is basically a list of graphical parameter settings.
vp	A Grid viewport object (or NULL).
...	Arguments to be passed to <code>xsplineGrob</code> .

## Details

Both functions create an `xspline grob` (a graphical object describing an `xspline`), but only `grid.xspline` draws the `xspline`.

An `xspline` is a line drawn relative to control points. For each control point, the line may pass through (interpolate) the control point or it may only approach (approximate) the control point; the behaviour is determined by a `shape` parameter for each control point.

If the `shape` parameter is greater than zero, the spline approximates the control points (and is very similar to a cubic B-spline when the `shape` is 1). If the `shape` parameter is less than zero, the spline interpolates the control points (and is very similar to a Catmull-Rom spline when the `shape` is -1). If the `shape` parameter is 0, the spline forms a sharp corner at that control point.

For open `xsplines`, the start and end control points must have a `shape` of 0 (and non-zero values are silently converted to zero without warning).

For open `xsplines`, by default the start and end control points are actually replicated before the curve is drawn. A curve is drawn between (interpolating or approximating) the second and third of each set of four control points, so this default behaviour ensures that the resulting curve starts at the first control point you have specified and ends at the last control point. The default behaviour can be turned off via the `repEnds` argument, in which case the curve that is drawn starts (approximately) at the second control point and ends (approximately) at the first and second-to-last control point.

The `repEnds` argument is ignored for closed `xsplines`.

Missing values are not allowed for `x` and `y` (i.e., it is not valid for a control point to be missing).

For closed `xsplines`, a curve is automatically drawn between the final control point and the initial control point.

## Value

A `grob` object.

## References

Blanc, C. and Schlick, C. (1995), "X-splines : A Spline Model Designed for the End User", in *Proceedings of SIGGRAPH 95*, pp. 377–386. <http://dept-info.labri.fr/~schlick/DOC/sig1.html>

**See Also**

[Grid](#), [viewport](#), [arrow](#).

[xspline](#).

**Examples**

```
x <- c(0.25, 0.25, 0.75, 0.75)
y <- c(0.25, 0.75, 0.75, 0.25)

xsplineTest <- function(s, i, j, open) {
  pushViewport(viewport(layout.pos.col=j, layout.pos.row=i))
  grid.points(x, y, default.units="npc", pch=16, size=unit(2, "mm"))
  grid.xspline(x, y, shape=s, open=open, gp=gpar(fill="grey"))
  grid.text(s, gp=gpar(col="grey"),
            x=unit(x, "npc") + unit(c(-1, -1, 1, 1), "mm"),
            y=unit(y, "npc") + unit(c(-1, 1, 1, -1), "mm"),
            hjust=c(1, 1, 0, 0),
            vjust=c(1, 0, 0, 1))
  popViewport()
}

pushViewport(viewport(width=.5, x=0, just="left",
                     layout=grid.layout(3, 3, respect=TRUE)))
pushViewport(viewport(layout.pos.row=1))
grid.text("Open Splines", y=1, just="bottom")
popViewport()
xsplineTest(c(0, -1, -1, 0), 1, 1, TRUE)
xsplineTest(c(0, -1, 0, 0), 1, 2, TRUE)
xsplineTest(c(0, -1, 1, 0), 1, 3, TRUE)
xsplineTest(c(0, 0, -1, 0), 2, 1, TRUE)
xsplineTest(c(0, 0, 0, 0), 2, 2, TRUE)
xsplineTest(c(0, 0, 1, 0), 2, 3, TRUE)
xsplineTest(c(0, 1, -1, 0), 3, 1, TRUE)
xsplineTest(c(0, 1, 0, 0), 3, 2, TRUE)
xsplineTest(c(0, 1, 1, 0), 3, 3, TRUE)
popViewport()
pushViewport(viewport(width=.5, x=1, just="right",
                     layout=grid.layout(3, 3, respect=TRUE)))
pushViewport(viewport(layout.pos.row=1))
grid.text("Closed Splines", y=1, just="bottom")
popViewport()
xsplineTest(c(-1, -1, -1, -1), 1, 1, FALSE)
xsplineTest(c(-1, -1, 0, -1), 1, 2, FALSE)
xsplineTest(c(-1, -1, 1, -1), 1, 3, FALSE)
xsplineTest(c(0, 0, -1, 0), 2, 1, FALSE)
xsplineTest(c(0, 0, 0, 0), 2, 2, FALSE)
xsplineTest(c(0, 0, 1, 0), 2, 3, FALSE)
xsplineTest(c(1, 1, -1, 1), 3, 1, FALSE)
xsplineTest(c(1, 1, 0, 1), 3, 2, FALSE)
xsplineTest(c(1, 1, 1, 1), 3, 3, FALSE)
popViewport()
```

---

grid.yaxis	<i>Draw a Y-Axis</i>
------------	----------------------

---

### Description

These functions create and draw a y-axis.

### Usage

```
grid.yaxis(at = NULL, label = TRUE, main = TRUE,
           edits = NULL, name = NULL,
           gp = gpar(), draw = TRUE, vp = NULL)
```

```
yaxisGrob(at = NULL, label = TRUE, main = TRUE,
           edits = NULL, name = NULL,
           gp = gpar(), vp = NULL)
```

### Arguments

at	A numeric vector of y-value locations for the tick marks.
label	A logical value indicating whether to draw the labels on the tick marks, or an expression or character vector which specify the labels to use. If not logical, must be the same length as the at argument.
main	A logical value indicating whether to draw the axis at the left (TRUE) or at the right (FALSE) of the viewport.
edits	A gEdit or gEditList containing edit operations to apply (to the children of the axis) when the axis is first created and during redrawing whenever at is NULL.
name	A character identifier.
gp	An object of class gpar, typically the output from a call to the function gpar. This is basically a list of graphical parameter settings.
draw	A logical value indicating whether graphics output should be produced.
vp	A Grid viewport object (or NULL).

### Details

Both functions create a yaxis grob (a graphical object describing a yaxis), but only grid.yaxis draws the yaxis (and then only if draw is TRUE).

### Value

A yaxis grob. grid.yaxis returns the value invisibly.

### Children

If the at slot of an xaxis grob is not NULL then the xaxis will have the following children:

**major** representing the line at the base of the tick marks.

**ticks** representing the tick marks.

**labels** representing the tick labels.

If the at slot is NULL then there are no children and ticks are drawn based on the current viewport scale.

**Author(s)**

Paul Murrell

**See Also**[Grid](#), [viewport](#), [grid.xaxis](#)


---

grobName	<i>Generate a Name for a Grob</i>
----------	-----------------------------------

---

**Description**

This function generates a unique (within-session) name for a grob, based on the grob's class.

**Usage**

```
grobName(grob = NULL, prefix = "GRID")
```

**Arguments**

grob	A grob object or NULL.
prefix	The prefix part of the name.

**Value**

A character string of the form `prefix.class(grob).index`

**Author(s)**

Paul Murrell

---

grobWidth	<i>Create a Unit Describing the Width of a Grob</i>
-----------	---

---

**Description**

These functions create a unit object describing the width or height of a grob. They are generic.

**Usage**

```
grobWidth(x)
grobHeight(x)
```

**Arguments**

x	A grob object.
---	----------------

**Value**

A unit object.

**Author(s)**

Paul Murrell

**See Also**[unit](#) and [stringWidth](#)

grobX

*Create a Unit Describing a Grob Boundary Location***Description**

These functions create a unit object describing a location somewhere on the boundary of a grob. They are generic.

**Usage**

```
grobX(x, theta)
grobY(x, theta)
```

**Arguments**

<code>x</code>	A grob, or gList, or gTree, or gPath.
<code>theta</code>	An angle indicating where the location is on the grob boundary. Can be one of "east", "north", "west", or "south", which correspond to angles 0, 90, 180, and 270, respectively.

**Details**

The angle is anti-clockwise with zero corresponding to a line with an origin centred between the extreme points of the shape, and pointing at 3 o'clock.

If the grob describes a single shape, the boundary value should correspond to the exact edge of the shape.

If the grob describes multiple shapes, the boundary value will either correspond to the edge of a bounding box around all of the shapes described by the grob (for multiple rectangles, circles, xsplines, or text), or to a convex hull around all vertices of all shapes described by the grob (for multiple polygons, points, lines, polylines, and segments).

Points grobs are currently a special case because the convex hull is based on the data symbol *locations* and does not take into account the extent of the data symbols themselves.

The extents of any arrow heads are currently *not* taken into account.

**Value**

A unit object.

**Author(s)**

Paul Murrell

**See Also**[unit](#) and [grobWidth](#)

---

plotViewport                    *Create a Viewport with a Standard Plot Layout*

---

### Description

This is a convenience function for producing a viewport with the common S-style plot layout – i.e., a central plot region surrounded by margins given in terms of a number of lines of text.

### Usage

```
plotViewport(margins=c(5.1, 4.1, 4.1, 2.1), ...)
```

### Arguments

`margins`                    A numeric vector interpreted in the same way as `par(mar)` in base graphics.  
`...`                        All other arguments will be passed to a call to the `viewport()` function.

### Value

A grid viewport object.

### Author(s)

Paul Murrell

### See Also

[viewport](#) and [dataViewport](#).

---

pop.viewport                    *Pop a Viewport off the Grid Viewport Stack*

---

### Description

Grid maintains a viewport stack — a list of nested drawing contexts.

This function makes the parent of the specified viewport the new default viewport.

### Usage

```
pop.viewport(n=1, recording=TRUE)
```

### Arguments

`n`                                An integer giving the number of viewports to pop. Defaults to 1.  
`recording`                    A logical value to indicate whether the set-viewport operation should be recorded on the Grid display list.

### Value

None.

**Warning**

This function has been deprecated. Please use `popViewport` instead.

**Author(s)**

Paul Murrell

**See Also**

[push.viewport.](#)

---

push.viewport

*Push a Viewport onto the Grid Viewport Stack*

---

**Description**

Grid maintains a viewport stack — a list of nested drawing contexts.

This function makes the specified viewport the default viewport and makes its parent the previous default viewport (i.e., nests the specified context within the previous default context).

**Usage**

```
push.viewport(..., recording=TRUE)
```

**Arguments**

<code>...</code>	One or more objects of class "viewport", or NULL.
<code>recording</code>	A logical value to indicate whether the set-viewport operation should be recorded on the Grid display list.

**Value**

None.

**Warning**

This function has been deprecated. Please use `pushViewport` instead.

**Author(s)**

Paul Murrell

**See Also**

[pop.viewport.](#)



---

Querying the Viewport Tree

*Get the Current Grid Viewport (Tree)*

---

### Description

`current.viewport()` returns the viewport that Grid is going to draw into.  
`current.vpTree` returns the entire Grid viewport tree.  
`current.vpPath` returns the viewport path to the current viewport.  
`current.transform` returns the transformation matrix for the current viewport.

### Usage

```
current.viewport(vp=NULL)
current.vpTree(all=TRUE)
current.vpPath()
current.transform()
```

### Arguments

<code>vp</code>	A Grid viewport object. Use of this argument has been deprecated.
<code>all</code>	A logical value indicating whether the entire viewport tree should be returned.

### Details

If `all` is `FALSE` then `current.vpTree` only returns the subtree below the current viewport.

### Value

A Grid viewport object from `current.viewport` or `current.vpTree`.  
`current.transform` returns a 4x4 transformation matrix.  
The viewport path returned by `current.vpPath` is `NULL` if the current viewport is the `ROOT` viewport

### Author(s)

Paul Murrell

### See Also

[viewport](#)

### Examples

```
grid.newpage()
pushViewport(viewport(width=0.8, height=0.8, name="A"))
pushViewport(viewport(x=0.1, width=0.3, height=0.6,
  just="left", name="B"))
upViewport(1)
pushViewport(viewport(x=0.5, width=0.4, height=0.8,
  just="left", name="C"))
```

```

pushViewport (viewport (width=0.8, height=0.8, name="D"))
current.vpPath ()
upViewport (1)
current.vpPath ()
current.vpTree ()
current.viewport ()
current.vpTree (all=FALSE)
popViewport (0)

```

---

roundrect

*Draw a rectangle with rounded corners*


---

### Description

Draw a *single* rectangle with rounded corners.

### Usage

```

roundrectGrob (x=0.5, y=0.5, width=1, height=1,
               default.units="npc",
               r=unit (0.1, "snpc"),
               just="centre",
               name=NULL, gp=NULL, vp=NULL)
grid.roundrect (...)

```

### Arguments

<code>x, y, width, height</code>	The location and size of the rectangle.
<code>default.units</code>	A string indicating the default units to use if <code>x, y, width, or height</code> are only given as numeric vectors.
<code>r</code>	The radius of the rounded corners.
<code>just</code>	The justification of the rectangle relative to its location.
<code>name</code>	A name to identify the grob.
<code>gp</code>	Graphical parameters to apply to the grob.
<code>vp</code>	A viewport object or <code>NULL</code> .
<code>...</code>	Arguments to be passed to <code>roundrectGrob()</code> .

### Details

At present, this function can only be used to draw *one* rounded rectangle.

### Examples

```

grid.roundrect (width=.5, height=.5, name="rr")
theta <- seq (0, 360, length=50)
for (i in 1:50)
  grid.circle (x=grobX ("rr", theta[i]),
              y=grobY ("rr", theta[i]),
              r=unit (1, "mm"),
              gp=gpar (fill="black"))

```

---

showViewport                    *Display grid viewports.*

---

### Description

Produces a graphical display of (by default) the current grid viewport tree. It is also possible to display only specific viewports. Each viewport is drawn as a rectangle and the leaf viewports are labelled with the viewport name.

### Usage

```
showViewport(vp = NULL, recurse = TRUE, depth = NULL,
             newpage = FALSE, leaves = FALSE,
             col = rgb(0, 0, 1, 0.2), fill = rgb(0, 0, 1, 0.1),
             label = TRUE, nrow = 3, ncol = nrow)
```

### Arguments

vp	If NULL, the current viewport tree is displayed. Otherwise, a viewport (or vpList, or vpStack, or vpTree) or a vpPath that specifies which viewport to display.
recurse	Should the children of the specified viewport also be displayed?
depth	Only display viewports at the specified depth (may be a vector of depths).
newpage	Start a new page for the display? Otherwise, the viewports are displayed on top of the current plot.
leaves	Produce a matrix of smaller displays, with each leaf viewport in its own display.
col	The colour used to draw the border of the rectangle for each viewport <i>and</i> to draw the label for each viewport. If a vector, then the first colour is used for the top-level viewport, the second colour is used for its children, the third colour for their children, and so on.
fill	The colour used to fill each viewport. May be a vector as per col.
label	Should the viewports be labelled (with the viewport name)?
nrow, ncol	The number of rows and columns when leaves is TRUE. Otherwise ignored.

### See Also

[viewport](#) and [grid.show.viewport](#)

### Examples

```
showViewport(viewport(width=.5, height=.5))

showViewport(vpStack(viewport(width=.5, height=.5),
                    viewport(width=.5, height=.5)),
             newpage=TRUE)

showViewport(vpStack(viewport(width=.5, height=.5),
                    viewport(width=.5, height=.5)),
             fill=rgb(1:0, 0:1, 0, .1),
             newpage=TRUE)
```

---

stringWidth	<i>Create a Unit Describing the Width of a String</i>
-------------	---

---

**Description**

These functions create a unit object describing the width or height of a string.

**Usage**

```
stringWidth(string)
stringHeight(string)
```

**Arguments**

string	A character vector.
--------	---------------------

**Value**

A unit object.

**Author(s)**

Paul Murrell

**See Also**

[unit](#) and [grobWidth](#)

---

unit	<i>Function to Create a Unit Object</i>
------	---

---

**Description**

This function creates a unit object — a vector of unit values. A unit value is typically just a single numeric value with an associated unit.

**Usage**

```
unit(x, units, data=NULL)
```

**Arguments**

x	A numeric vector.
units	A character vector specifying the units for the corresponding numeric values.
data	This argument is used to supply extra information for special <code>unit</code> types.

## Details

Unit objects allow the user to specify locations and dimensions in a large number of different coordinate systems. All drawing occurs relative to a viewport and the `units` specifies what coordinate system to use within that viewport.

Possible `units` (coordinate systems) are:

"npc" Normalised Parent Coordinates (the default). The origin of the viewport is (0, 0) and the viewport has a width and height of 1 unit. For example, (0.5, 0.5) is the centre of the viewport.

"cm" Centimetres.

"inches" Inches. 1 in = 2.54 cm.

"mm" Millimetres. 10 mm = 1 cm.

"points" Points. 72.27 pt = 1 in.

"picas" Picas. 1 pc = 12 pt.

"bigpts" Big Points. 72 bp = 1 in.

"dida" Dida. 1157 dd = 1238 pt.

"cicero" Cicero. 1 cc = 12 dd.

"scaledpts" Scaled Points. 65536 sp = 1 pt.

"lines" Lines of text. Locations and dimensions are in terms of multiples of the default text size of the viewport (as specified by the viewport's `fontsize` and `lineheight`).

"char" Multiples of nominal font height of the viewport (as specified by the viewport's `fontsize`).

"native" Locations and dimensions are relative to the viewport's `xscale` and `yscale`.

"snpc" Square Normalised Parent Coordinates. Same as Normalised Parent Coordinates, except gives the same answer for horizontal and vertical locations/dimensions. It uses the *lesser* of `npc-width` and `npc-height`. This is useful for making things which are a proportion of the viewport, but have to be square (or have a fixed aspect ratio).

"strwidth" Multiples of the width of the string specified in the `data` argument. The font size is determined by the `pointsize` of the viewport.

"strheight" Multiples of the height of the string specified in the `data` argument. The font size is determined by the `pointsize` of the viewport.

"grobwidth" Multiples of the width of the grob specified in the `data` argument.

"grobheight" Multiples of the height of the grob specified in the `data` argument.

A number of variations are also allowed for the most common units. For example, it is possible to use `"in"` or `"inch"` instead of `"inches"` and `"centimetre"` or `"centimeter"` instead of `"cm"`.

A special `units` value of `"null"` is also allowed, but only makes sense when used in specifying widths of columns or heights of rows in grid layouts (see [grid.layout](#)).

The `data` argument must be a list when the `unit.length()` is greater than 1. For example, `unit(rep(1, 3), c("npc", "strwidth", "inches"), data=list(NULL, "my string", NULL))`.

It is possible to subset unit objects in the normal way (e.g., `unit(1:5, "npc")[2:4]`), but a special function `unit.c` is provided for combining unit objects.

Certain arithmetic and summary operations are defined for unit objects. In particular, it is possible to add and subtract unit objects (e.g., `unit(1, "npc") - unit(1, "inches")`), and to specify the minimum or maximum of a list of unit objects (e.g., `min(unit(0.5, "npc"), unit(1, "inches"))`).

**Value**

An object of class "unit".

**WARNING**

There is a special function `unit.c` for concatenating several unit objects.

The `c` function will not give the right answer.

There used to be "mylines", "mychar", "mystrwidth", "mystrheight" units. These will still be accepted, but work exactly the same as "lines", "char", "strwidth", "strheight".

**Author(s)**

Paul Murrell

**See Also**

[unit.c](#)

**Examples**

```
unit(1, "npc")
unit(1:3/4, "npc")
unit(1:3/4, "npc") + unit(1, "inches")
min(unit(0.5, "npc"), unit(1, "inches"))
unit.c(unit(0.5, "npc"), unit(2, "inches") + unit(1:3/4, "npc"),
        unit(1, "strwidth", "hi there"))
```

---

unit.c

*Combine Unit Objects*

---

**Description**

This function produces a new unit object by combining the unit objects specified as arguments.

**Usage**

```
unit.c(...)
```

**Arguments**

...            An arbitrary number of unit objects.

**Value**

An object of class `unit`.

**Author(s)**

Paul Murrell

**See Also**

[unit.](#)

---

unit.length	<i>Length of a Unit Object</i>
-------------	--------------------------------

---

**Description**

The length of a unit object is defined as the number of unit values in the unit object.

This function has been deprecated in favour of a unit method for the generic length function.

**Usage**

```
unit.length(unit)
```

**Arguments**

unit	A unit object.
------	----------------

**Value**

An integer value.

**Author(s)**

Paul Murrell

**See Also**

[unit](#)

**Examples**

```
length(unit(1:3, "npc"))
length(unit(1:3, "npc") + unit(1, "inches"))
length(max(unit(1:3, "npc") + unit(1, "inches")))
length(max(unit(1:3, "npc") + unit(1, "strwidth", "a"))*4)
length(unit(1:3, "npc") + unit(1, "strwidth", "a")*4)
```

---

unit.pmin	<i>Parallel Unit Minima and Maxima</i>
-----------	--

---

**Description**

Returns a unit object whose i'th value is the minimum (or maximum) of the i'th values of the arguments.

**Usage**

```
unit.pmin(...)
unit.pmax(...)
```

**Arguments**

... One or more unit objects.

**Details**

The length of the result is the maximum of the lengths of the arguments; shorter arguments are recycled in the usual manner.

**Value**

A unit object.

**Author(s)**

Paul Murrell

**Examples**

```
max(unit(1:3, "cm"), unit(0.5, "npc"))
unit.pmax(unit(1:3, "cm"), unit(0.5, "npc"))
```

---

unit.rep

*Replicate Elements of Unit Objects*

---

**Description**

Replicates the units according to the values given in `times` and `length.out`.

This function has been deprecated in favour of a unit method for the generic `rep` function.

**Usage**

```
unit.rep(x, ...)
```

**Arguments**

`x` An object of class "unit".

... arguments to be passed to `rep` such as `times` and `length.out`.

**Value**

An object of class "unit".

**Author(s)**

Paul Murrell

**See Also**

[rep](#)



**Examples**

```
rep(unit(1:3, "npc"), 3)
rep(unit(1:3, "npc"), 1:3)
rep(unit(1:3, "npc") + unit(1, "inches"), 3)
rep(max(unit(1:3, "npc") + unit(1, "inches")), 3)
rep(max(unit(1:3, "npc") + unit(1, "strwidth", "a"))*4, 3)
rep(unit(1:3, "npc") + unit(1, "strwidth", "a")*4, 3)
```

---

 valid.just

*Validate a Justification*


---

**Description**

This utility function is useful for determining whether a justification specification is valid. An error is given if the justification is not valid.

**Usage**

```
valid.just(just)
```

**Arguments**

just	A justification either as a character value, e.g., "left", or as a numeric value, e.g., 0.
------	--

**Details**

This function is useful within a `validDetails` method when writing a new grob class.

**Value**

A numeric representation of the justification (e.g., "left" becomes 0, "right" becomes 1, etc, ...).

**Author(s)**

Paul Murrell

---

 validDetails

*Customising grid grob Validation*


---

**Description**

This generic hook function is called whenever a grid grob is created or edited via `grob`, `gTree`, `grid.edit` or `editGrob`. This provides an opportunity for customising the validation of a new class derived from `grob` (or `gTree`).

**Usage**

```
validDetails(x)
```

**Arguments**

x                    A grid grob.

**Details**

This function is called by `grob`, `gTree`, `grid.edit` and `editGrob`. A method should be written for classes derived from `grob` or `gTree` to validate the values of slots specific to the new class. (e.g., see `grid::validDetails.axis`).

Note that the standard slots for grobs and gTrees are automatically validated (e.g., `vp`, `gp` slots for grobs and, in addition, `children`, and `childrenvp` slots for gTrees) so only slots specific to a new class need to be addressed.

**Value**

The function MUST return the validated grob.

**Author(s)**

Paul Murrell

**See Also**

[grid.edit](#)

---

vpPath                    *Concatenate Viewport Names*

---

**Description**

This function can be used to generate a viewport path for use in `downViewport` or `seekViewport`.

A viewport path is a list of nested viewport names.

**Usage**

```
vpPath(...)
```

**Arguments**

...                    Character values which are viewport names.

**Details**

Viewport names must only be unique amongst viewports which share the same parent in the viewport tree.

This function can be used to generate a specification for a viewport that includes the viewport's parent's name (and the name of its parent and so on).

For interactive use, it is possible to directly specify a path, but it is strongly recommended that this function is used otherwise in case the path separator is changed in future versions of grid.

**Value**

A `vpPath` object.

**See Also**

[viewport](#), [pushViewport](#), [popViewport](#), [downViewport](#), [seekViewport](#), [upViewport](#)

**Examples**

```
vpPath("vp1", "vp2")
```

---

widthDetails

*Width and Height of a grid grob*

---

**Description**

These generic functions are used to determine the size of grid grobs.

**Usage**

```
widthDetails(x)  
heightDetails(x)
```

**Arguments**

`x`                    A grid grob.

**Details**

These functions are called in the calculation of "grobwidth" and "grobheight" units. Methods should be written for classes derived from `grob` or `gTree` where the size of the grob can be determined (see, for example `grid::widthDetails.frame`).

**Value**

A unit object.

**Author(s)**

Paul Murrell

**See Also**

[absolute.size](#).

---

 Working with Viewports

*Maintaining and Navigating the Grid Viewport Tree*


---

## Description

Grid maintains a tree of viewports — nested drawing contexts.

These functions provide ways to add or remove viewports and to navigate amongst viewports in the tree.

## Usage

```
pushViewport(..., recording=TRUE)
popViewport(n, recording=TRUE)
downViewport(name, strict=FALSE, recording=TRUE)
seekViewport(name, recording=TRUE)
upViewport(n, recording=TRUE)
```

## Arguments

<code>...</code>	One or more objects of class "viewport".
<code>n</code>	An integer value indicating how many viewports to pop or navigate up. The special value 0 indicates to pop or navigate viewports right up to the root viewport.
<code>name</code>	A character value to identify a viewport in the tree.
<code>strict</code>	A boolean indicating whether the vpPath must be matched exactly.
<code>recording</code>	A logical value to indicate whether the viewport operation should be recorded on the Grid display list.

## Details

Objects created by the `viewport()` function are only descriptions of a drawing context. A viewport object must be pushed onto the viewport tree before it has any effect on drawing.

The viewport tree always has a single root viewport (created by the system) which corresponds to the entire device (and default graphical parameter settings). Viewports may be added to the tree using `pushViewport()` and removed from the tree using `popViewport()`.

There is only ever one current viewport, which is the current position within the viewport tree. All drawing and viewport operations are relative to the current viewport. When a viewport is pushed it becomes the current viewport. When a viewport is popped, the parent viewport becomes the current viewport. Use `upViewport` to navigate to the parent of the current viewport, without removing the current viewport from the viewport tree. Use `downViewport` to navigate to a viewport further down the viewport tree and `seekViewport` to navigate to a viewport anywhere else in the tree.

If a viewport is pushed and it has the same name as a viewport at the same level in the tree, then it replaces the existing viewport in the tree.

## Value

`downViewport` returns the number of viewports it went down.

This can be useful for returning to your starting point by doing something like `depth <- downViewport() then upViewport(depth)`.

**Author(s)**

Paul Murrell

**See Also**[viewport](#) and [vpPath](#).**Examples**

```

# push the same viewport several times
grid.newpage()
vp <- viewport(width=0.5, height=0.5)
pushViewport(vp)
grid.rect(gp=gpar(col="blue"))
grid.text("Quarter of the device",
  y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="blue"))
pushViewport(vp)
grid.rect(gp=gpar(col="red"))
grid.text("Quarter of the parent viewport",
  y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="red"))
popViewport(2)
# push several viewports then navigate amongst them
grid.newpage()
grid.rect(gp=gpar(col="grey"))
grid.text("Top-level viewport",
  y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="grey"))
if (interactive()) Sys.sleep(1.0)
pushViewport(viewport(width=0.8, height=0.7, name="A"))
grid.rect(gp=gpar(col="blue"))
grid.text("1. Push Viewport A",
  y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="blue"))
if (interactive()) Sys.sleep(1.0)
pushViewport(viewport(x=0.1, width=0.3, height=0.6,
  just="left", name="B"))
grid.rect(gp=gpar(col="red"))
grid.text("2. Push Viewport B (in A)",
  y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="red"))
if (interactive()) Sys.sleep(1.0)
upViewport(1)
grid.text("3. Up from B to A",
  y=unit(1, "npc") - unit(2, "lines"), gp=gpar(col="blue"))
if (interactive()) Sys.sleep(1.0)
pushViewport(viewport(x=0.5, width=0.4, height=0.8,
  just="left", name="C"))
grid.rect(gp=gpar(col="green"))
grid.text("4. Push Viewport C (in A)",
  y=unit(1, "npc") - unit(1, "lines"), gp=gpar(col="green"))
if (interactive()) Sys.sleep(1.0)
pushViewport(viewport(width=0.8, height=0.6, name="D"))
grid.rect()
grid.text("5. Push Viewport D (in C)",
  y=unit(1, "npc") - unit(1, "lines"))
if (interactive()) Sys.sleep(1.0)
upViewport(0)
grid.text("6. Up from D to top-level",
  y=unit(1, "npc") - unit(2, "lines"), gp=gpar(col="grey"))

```

```

if (interactive()) Sys.sleep(1.0)
downViewport("D")
grid.text("7. Down from top-level to D",
  y=unit(1, "npc") - unit(2, "lines"))
if (interactive()) Sys.sleep(1.0)
seekViewport("B")
grid.text("8. Seek from D to B",
  y=unit(1, "npc") - unit(2, "lines"), gp=gpar(col="red"))
pushViewport(viewport(width=0.9, height=0.5, name="A"))
grid.rect()
grid.text("9. Push Viewport A (in B)",
  y=unit(1, "npc") - unit(1, "lines"))
if (interactive()) Sys.sleep(1.0)
seekViewport("A")
grid.text("10. Seek from B to A (in ROOT)",
  y=unit(1, "npc") - unit(3, "lines"), gp=gpar(col="blue"))
if (interactive()) Sys.sleep(1.0)
seekViewport(vpPath("B", "A"))
grid.text("11. Seek from\nA (in ROOT)\nto A (in B)")
popViewport(0)

```

xDetails

*Boundary of a grid grob***Description**

These generic functions are used to determine a location on the boundary of a grid grob.

**Usage**

```

xDetails(x, theta)
yDetails(x, theta)

```

**Arguments**

x	A grid grob.
theta	A numeric angle, in degrees, measured anti-clockwise from the 3 o'clock <i>or</i> one of the following character strings: "north", "east", "west", "south".

**Details**

The location on the grob boundary is determined by taking a line from the centre of the grob at the angle `theta` and intersecting it with the convex hull of the grob (for the basic grob primitives, the centre is determined as half way between the minimum and maximum values in x and y directions).

These functions are called in the calculation of "grobX" and "grobY" units as produced by the `grobX` and `grobY` functions. Methods should be written for classes derived from `grob` or `gTree` where the boundary of the grob can be determined.

**Value**

A unit object.

**Author(s)**

Paul Murrell

**See Also**[grobX](#), [grobY](#).

---

`xsplinePoints`*Return the points that would be used to draw an Xspline.*

---

**Description**

Rather than drawing an Xspline, this function returns the points that would be used to draw the series of line segments for the Xspline. This may be useful to post-process the Xspline curve, for example, to clip the curve.

**Usage**

```
xsplinePoints(x)
```

**Arguments**

`x` An Xspline grob, as produced by the `xsplineGrob()` function.

**Details**

The points returned by this function will only be relevant for the drawing context in force when this function was called.

**Value**

Depends on how many Xsplines would be drawn. If only one, then a list with two components, named `x` and `y`, both of which are unit objects (in inches). If several Xsplines would be drawn then the result of this function is a list of lists.

**Author(s)**

Paul Murrell

**See Also**[xsplineGrob](#)**Examples**

```
grid.newpage()
xsg <- xsplineGrob(c(.1, .1, .9, .9), c(.1, .9, .9, .1), shape=1)
grid.draw(xsg)
trace <- xsplinePoints(xsg)
grid.circle(trace$x, trace$y, default.units="inches", r=unit(.5, "mm"))
```

# Chapter 6

## The methods package

---

methods-package      *Formal Methods and Classes*

---

### Description

Formally defined methods and classes for R objects, plus other programming tools, as described in the references.

### Details

This package provides the ‘S4’ or ‘S version 4’ approach to methods and classes in a functional language.

See the documentation entries [Classes](#), [Methods](#), and [GenericFunctions](#) for general discussion of these topics, at a fairly technical level. Links from those pages, and the documentation of [setClass](#) and [setMethod](#) cover the main programming tools needed.

For a complete list of functions and classes, use `library(help="methods")`.

### Author(s)

R Development Core Team

Maintainer: R Core Team <R-core@r-project.org>

### References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)



---

`.BasicFunsList`*List of Builtin and Special Functions*

---

**Description**

A named list providing instructions for turning builtin and special functions into generic functions.

Functions in R that are defined as `.Primitive(<name>)` are not suitable for formal methods, because they lack the basic reflectance property. You can't find the argument list for these functions by examining the function object itself.

Future versions of R may fix this by attaching a formal argument list to the corresponding function. While generally the names of arguments are not checked by the internal code implementing the function, the number of arguments frequently is.

In any case, some definition of a formal argument list is needed if users are to define methods for these functions. In particular, if methods are to be merged from multiple packages, the different sets of methods need to agree on the formal arguments.

In the absence of reflectance, this list provides the relevant information via a dummy function associated with each of the known specials for which methods are allowed.

At the same, the list flags those specials for which methods are meaningless (e.g., `for`) or just a very bad idea (e.g., `.Primitive`).

A generic function created via `setMethod`, for example, for one of these special functions will have the argument list from `.BasicFunsList`. If no entry exists, the argument list `(x, ...)` is assumed.

---

`as`*Force an Object to Belong to a Class*

---

**Description**

These functions manage the relations that allow coercing an object to a given class.

**Usage**

```
as(object, Class, strict=TRUE, ext)
```

```
as(object, Class) <- value
```

```
setAs(from, to, def, replace, where = topenv(parent.frame()))
```

**Arguments**

`object` any R object.

`Class` the name of the class to which `object` should be coerced.

<code>strict</code>	logical flag. If <code>TRUE</code> , the returned object must be strictly from the target class (unless that class is a virtual class, in which case the object will be from the closest actual class, in particular the original object, if that class extends the virtual class directly).  If <code>strict = FALSE</code> , any simple extension of the target class will be returned, without further change. A simple extension is, roughly, one that just adds slots to an existing class.
<code>value</code>	The value to use to modify <code>object</code> (see the discussion below). You should supply an object with class <code>Class</code> ; some coercion is done, but you're unwise to rely on it.
<code>from, to</code>	The classes between which the coerce methods <code>def</code> and <code>replace</code> perform coercion.
<code>def</code>	function of one argument. It will get an object from class <code>from</code> and had better return an object of class <code>to</code> . The convention is that the name of the argument is <code>from</code> ; if another argument name is used, <code>setAs</code> will attempt to substitute <code>from</code> .
<code>replace</code>	if supplied, the function to use as a replacement method, when <code>as</code> is used on the left of an assignment. Should be a function of two arguments, <code>from, value</code> , although <code>setAs</code> will attempt to substitute if the arguments differ.
<code>where</code>	the position or environment in which to store the resulting methods. For most applications, it is recommended to omit this argument and to include the call to <code>setAs</code> in source code that is evaluated at the top level; that is, either in an R session by something equivalent to a call to <code>source</code> , or as part of the R source code for a package.
<code>ext</code>	the optional object defining how <code>Class</code> is extended by the class of the object (as returned by <code>possibleExtends</code> ). This argument is used internally (to provide essential information for non-public classes), but you are unlikely to want to use it directly.

### Summary of Functions

`as`: Returns the version of this object coerced to be the given `Class`. When used in the replacement form on the left of an assignment, the portion of the object corresponding to `Class` is replaced by `value`.

The operation of `as()` in either form depends on the definition of coerce methods. Methods are defined automatically when the two classes are related by inheritance; that is, when one of the classes is a subclass of the other. See the section on inheritance below for details.

Coerce methods are also predefined for basic classes (including all the types of vectors, functions and a few others). See `showMethods(coerce)` for a list of these.

Beyond these two sources of methods, further methods are defined by calls to the `setAs` function.

`setAs`: Define methods for coercing an object of class `from` to be of class `to`; the `def` argument provides for direct coercing and the `replace` argument, if included, provides for replacement. See the "How" section below for details.

`coerce, coerce<-`: Coerce `from` to be of the same class as `to`.

These functions should not be called explicitly. The function `setAs` creates methods for them for the `as` function to use.

## Inheritance and Coercion

Objects from one class can turn into objects from another class either automatically or by an explicit call to the `as` function. Automatic conversion is special, and comes from the designer of one class of objects asserting that this class extends another class. The most common case is that one or more class names are supplied in the `contains=` argument to `setClass`, in which case the new class extends each of the earlier classes (in the usual terminology, the earlier classes are *superclasses* of the new class and it is a *subclass* of each of them).

This form of inheritance is called *simple* inheritance in R. See `setClass` for details. Inheritance can also be defined explicitly by a call to `setIs`. The two versions have slightly different implications for coerce methods. Simple inheritance implies that inherited slots behave identically in the subclass and the superclass. Whenever two classes are related by simple inheritance, corresponding coerce methods are defined for both direct and replacement use of `as`. In the case of simple inheritance, these methods do the obvious computation: they extract or replace the slots in the object that correspond to those in the superclass definition.

The implicitly defined coerce methods may be overridden by a call to `setAs`; note, however, that the implicit methods are defined for each subclass-superclass pair, so that you must override each of these explicitly, not rely on inheritance.

When inheritance is defined by a call to `setIs`, the coerce methods are provided explicitly, not generated automatically. Inheritance will apply (to the `from` argument, as described in the section below). You could also supply methods via `setAs` for non-inherited relationships, and now these also can be inherited.

For further on the distinction between simple and explicit inheritance, see `setIs`.

## How Functions 'as' and 'setAs' Work

The function `as` turns `object` into an object of class `Class`. In doing so, it applies a “coerce method”, using S4 classes and methods, but in a somewhat special way. Coerce methods are methods for the function `coerce` or, in the replacement case the function ``coerce<-``. These functions have two arguments in method signatures, `from` and `to`, corresponding to the class of the object and the desired coerce class. These functions must not be called directly, but are used to store tables of methods for the use of `as`, directly and for replacements. In this section we will describe the direct case, but except where noted the replacement case works the same way, using ``coerce<-`` and the `replace` argument to `setAs`, rather than `coerce` and the `def` argument.

Assuming the `object` is not already of the desired class, `as` first looks for a method in the table of methods for the function `coerce` for the signature `c(from = class(object), to = Class)`, in the same way method selection would do its initial lookup. To be precise, this means the table of both direct and inherited methods, but inheritance is used specially in this case (see below).

If no method is found, `as` looks for one. First, if either `Class` or `class(object)` is a superclass of the other, the class definition will contain the information needed to construct a coerce method. In the usual case that the subclass contains the superclass (i.e., has all its slots), the method is constructed either by extracting or replacing the inherited slots. Non-simple extensions (the result of a call to `setIs`) will usually contain explicit methods, though possibly not for replacement.

If no subclass/superclass relationship provides a method, `as` looks for an inherited method, but applying inheritance for the argument `from` only, not for the argument `to` (if you think about it, you'll probably agree that you wouldn't want the result to be from some class other than the `Class` specified). Thus, `selectMethod("coerce", sig, useInherited= c(from=TRUE, to= FALSE))` replicates the method selection used by `as()`.

In nearly all cases the method found in this way will be cached in the table of coerce methods (the exception being subclass relationships with a test, which are legal but discouraged). So the detailed

calculations should be done only on the first occurrence of a coerce from `class(object)` to `Class`.

Note that `coerce` is not a standard generic function. It is not intended to be called directly. To prevent accidentally caching an invalid inherited method, calls are routed to an equivalent call to `as`, and a warning is issued. Also, calls to `selectMethod` for this function may not represent the method that `as` will choose. You can only trust the result if the corresponding call to `as` has occurred previously in this session.

With this explanation as background, the function `setAs` does a fairly obvious computation: It constructs and sets a method for the function `coerce` with signature `c(from, to)`, using the `def` argument to define the body of the method. The function supplied as `def` can have one argument (interpreted as an object to be coerced) or two arguments (the `from` object and the `to` class). Either way, `setAs` constructs a function of two arguments, with the second defaulting to the name of the `to` class. The method will be called from `as` with the object as the `from` argument and no `to` argument, with the default for this argument being the name of the intended `to` class, so the method can use this information in messages.

The direct version of the `as` function also has a `strict=` argument that defaults to `TRUE`. Calls during the evaluation of methods for other functions will set this argument to `FALSE`. The distinction is relevant when the object being coerced is from a simple subclass of the `to` class; if `strict=FALSE` in this case, nothing need be done. For most user-written `coerce` methods, when the two classes have no subclass/superclass, the `strict=` argument is irrelevant.

The `replace` argument to `setAs` provides a method for ``coerce<-``. As with all replacement methods, the last argument of the method must have the name `value` for the object on the right of the assignment. As with the `coerce` method, the first two arguments are `from, to`; there is no `strict=` option for the `replace` case.

The function `coerce` exists as a repository for such methods, to be selected as described above by the `as` function. Actually dispatching the methods using `standardGeneric` could produce incorrect inherited methods, by using inheritance on the `to` argument; as mentioned, this is not the logic used for `as`. To prevent selecting and caching invalid methods, calls to `coerce` are currently mapped into calls to `as`, with a warning message.

### Basic Coercion Methods

Methods are pre-defined for coercing any object to one of the basic datatypes. For example, `as(x, "numeric")` uses the existing `as.numeric` function. These built-in methods can be listed by `showMethods("coerce")`.

### References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

### See Also

If you think of using `try(as(x, cl))`, consider `canCoerce(x, cl)` instead.

### Examples

```
## using the definition of class "track" from \link{Classes}
```

```

setAs("track", "numeric", function(from) from@y)

t1 <- new("track", x=1:20, y=(1:20)^2)

as(t1, "numeric")

## The next example shows:
## 1. A virtual class to define setAs for several classes at once.
## 2. as() using inherited information

setClass("ca", representation(a = "character", id = "numeric"))

setClass("cb", representation(b = "character", id = "numeric"))

setClass("id")
setIs("ca", "id")
setIs("cb", "id")

setAs("id", "numeric", function(from) from@id)

CA <- new("ca", a = "A", id = 1)
CB <- new("cb", b = "B", id = 2)

setAs("cb", "ca", function(from, to )new(to, a=from@b, id = from@id))

as(CB, "numeric")

```

---

BasicClasses

---

*Classes Corresponding to Basic Data Types*


---

## Description

Formal classes exist corresponding to the basic R object types, allowing these types to be used in method signatures, as slots in class definitions, and to be extended by new classes.

## Usage

```

### The following are all basic vector classes.
### They can appear as class names in method signatures,
### in calls to as(), is(), and new().
"character"
"complex"
"double"
"expression"
"integer"
"list"
"logical"
"numeric"
"single"
"raw"

```

```

### the class
"vector"
### is a virtual class, extended by all the above

### the class
"S4"
### is an object type for S4 objects that do not extend
### any of the basic vector classes. It is a virtual class.

### The following are additional basic classes
"NULL"      # NULL objects
"function"  # function objects, including primitives
"externalptr" # raw external pointers for use in C code

"ANY"      # virtual classes used by the methods package itself
"VIRTUAL"
"missing"

"namedList" # the alternative to "list" that preserves the names attribute

```

### Objects from the Classes

Objects can be created by calls of the form `new(Class, ...)`, where `Class` is the quoted class name, and the remaining arguments if any are objects to be interpreted as vectors of this class. Multiple arguments will be concatenated.

The class `"expression"` is slightly odd, in that the `...` arguments will *not* be evaluated; therefore, don't enclose them in a call to `quote()`.

Note that class `"list"` is a pure vector. Although lists with names go back to the earliest versions of S, they are an extension of the vector concept in that they have an attribute (which can now be a slot) and which is either `NULL` or a character vector of the same length as the vector. If you want to guarantee that list names are preserved, use class `"namedList"`, rather than `"list"`. Objects from this class must have a `names` attribute, corresponding to slot `"names"`, of type `"character"`. Internally, R treats names for lists specially, which makes it impractical to have the corresponding slot in class `"namedList"` be a union of character names and `NULL`.

### Classes and Types

The basic classes include classes for the basic R types. Note that objects of these types will not usually be S4 objects (`isS4` will return `FALSE`), although objects from classes that contain the basic class will be S4 objects, still with the same type. The type as returned by `typeof` will sometimes differ from the class, either just from a choice of terminology (type `"symbol"` and class `"name"`, for example) or because there is not a one-to-one correspondence between class and type (most of the classes that inherit from class `"language"` have type `"language"`, for example).

### Extends

The vector classes extend `"vector"`, directly.

## Methods

**coerce** Methods are defined to coerce arbitrary objects to the vector classes, by calling the corresponding basic function, for example, `as(x, "numeric")` calls `as.numeric(x)`.

---

callGeneric

*Call the Current Generic Function from a Method*

---

## Description

A call to `callGeneric` can only appear inside a method definition. It then results in a call to the current generic function. The value of that call is the value of `callGeneric`. While it can be called from any method, it is useful and typically used in methods for group generic functions.

## Usage

```
callGeneric(...)
```

## Arguments

...            Optionally, the arguments to the function in its next call.  
 If no arguments are included in the call to `callGeneric`, the effect is to call the function with the current arguments. See the detailed description for what this really means.

## Details

The name and package of the current generic function is stored in the environment of the method definition object. This name is looked up and the corresponding function called.

The statement that passing no arguments to `callGeneric` causes the generic function to be called with the current arguments is more precisely as follows. Arguments that were missing in the current call are still missing (remember that "missing" is a valid class in a method signature). For a formal argument, say `x`, that appears in the original call, there is a corresponding argument in the generated call equivalent to `x = x`. In effect, this means that the generic function sees the same actual arguments, but arguments are evaluated only once.

Using `callGeneric` with no arguments is prone to creating infinite recursion, unless one of the arguments in the signature has been modified in the current method so that a different method is selected.

## Value

The value returned by the new call.

## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

**See Also**

[GroupGenericFunctions](#) for other information about group generic functions; [Methods](#) for the general behavior of method dispatch

**Examples**

```
## the method for group generic function Ops
## for signature( e1="structure", e2="vector")
function (e1, e2)
{
  value <- callGeneric(e1@.Data, e2)
  if (length(value) == length(e1)) {
    e1@.Data <- value
    e1
  }
  else value
}

## For more examples
## Not run:
showMethods("Ops", includeDefs = TRUE)

## End(Not run)
```

---

callNextMethod	<i>Call an Inherited Method</i>
----------------	---------------------------------

---

**Description**

A call to `callNextMethod` can only appear inside a method definition. It then results in a call to the first inherited method after the current method, with the arguments to the current method passed down to the next method. The value of that method call is the value of `callNextMethod`.

**Usage**

```
callNextMethod(...)
```

**Arguments**

...      Optionally, the arguments to the function in its next call (but note that the dispatch is as in the detailed description below; the arguments have no effect on selecting the next method.)

If no arguments are included in the call to `callNextMethod`, the effect is to call the method with the current arguments. See the detailed description for what this really means.

Calling with no arguments is often the natural way to use `callNextMethod`; see the examples.



## Details

The ‘next’ method (i.e., the first inherited method) is defined to be that method which *would* have been called if the current method did not exist. This is more-or-less literally what happens: The current method (to be precise, the method with signature given by the `defined` slot of the method from which `callNextMethod` is called) is deleted from a copy of the methods for the current generic, and `selectMethod` is called to find the next method (the result is cached in a special object, so the search only typically happens once per session per combination of argument classes).

Note that the preceding definition means that the next method is defined uniquely when `setMethod` inserts the method containing the `callNextMethod` call, given the definitions of the classes in the signature. The choice does not depend on the path that gets us to that method (for example, through inheritance or from another `callNextMethod` call). This definition was not enforced in versions of R prior to 2.3.0, where the method was selected based on the target signature, and so could vary depending on the actual arguments.

It is also legal, and often useful, for the method called by `callNextMethod` to itself have a call to `callNextMethod`. This generally works as you would expect, but for completeness be aware that it is possible to have ambiguous inheritance in the S structure, in the sense that the same two classes can appear as superclasses *in the opposite order* in two other class definitions. In this case the effect of a nested instance of `callNextMethod` is not well defined. Such inconsistent class hierarchies are both rare and nearly always the result of bad design, but they are possible, and currently undetected.

The statement that the method is called with the current arguments is more precisely as follows. Arguments that were missing in the current call are still missing (remember that `"missing"` is a valid class in a method signature). For a formal argument, say `x`, that appears in the original call, there is a corresponding argument in the next method call equivalent to `x = x`. In effect, this means that the next method sees the same actual arguments, but arguments are evaluated only once.

## Value

The value returned by the selected method.

## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

## See Also

`callGeneric` to call the generic function with the current dispatch rules (typically for a group generic function); `Methods` for the general behavior of method dispatch

## Examples

```
## some class definitions with simple inheritance
setClass("B0" , representation(b0 = "numeric"))

setClass("B1", representation(b1 = "character"), contains = "B0")

setClass("B2", representation(b2 = "logical"), contains = "B1")

## and a rather silly function to illustrate callNextMethod
```

```
f <- function(x) class(x)

setMethod("f", "B0", function(x) c(x@b0^2, callNextMethod()))
setMethod("f", "B1", function(x) c(paste(x@b1, ":"), callNextMethod()))
setMethod("f", "B2", function(x) c(x@b2, callNextMethod()))

b1 <- new("B1", b0 = 2, b1 = "Testing")

b2 <- new("B2", b2 = FALSE, b1 = "More testing", b0 = 10)

f(b2)
stopifnot(identical(f(b2), c(b2@b2, paste(b2@b1, ":"), b2@b0^2, "B2")))

f(b1)

## a sneakier method: the *changed* x is used:
setMethod("f", "B2", function(x) {x@b0 <- 111; c(x@b2, callNextMethod())})
f(b2)
stopifnot(identical(f(b2), c(b2@b2, paste(b2@b1, ":"), 111^2, "B2")))
```

---

canCoerce

*Can an Object be Coerced to a Certain S4 Class?*


---

## Description

Test if an object can be coerced to a given S4 class. Maybe useful inside `if()` to ensure that calling `as(object, Class)` will find a method.

## Usage

```
canCoerce(object, Class)
```

## Arguments

object	any R object, typically of a formal S4 class.
Class	an S4 class (see <a href="#">isClass</a> ).

## Value

a scalar logical, TRUE if there is a `coerce` method (as defined by [setAs](#), e.g.) for the signature (from = `class(object)`, to = `Class`).

## See Also

[as](#), [setAs](#), [selectMethod](#), [setClass](#),

## Examples

```
m <- matrix(pi, 2, 3)
canCoerce(m, "numeric") # TRUE
canCoerce(m, "array")   # TRUE
```

cbind2

*Combine two Objects by Columns or Rows***Description**

Combine two matrix-like R objects by columns (`cbind2`) or rows (`rbind2`). These are (S4) generic functions with default methods.

**Usage**

```
cbind2(x, y)
rbind2(x, y)
```

**Arguments**

`x` any R object, typically matrix-like.  
`y` any R object, typically similar to `x`, or missing completely.

**Details**

The main use of `cbind2` (`rbind2`) is to be called by `cbind()` (`rbind()`) if these are activated. This allows `cbind` (`rbind`) to work for formally classed (aka ‘S4’) objects by providing S4 methods for these objects. Currently, a call `methods:::bind_activation(TRUE)` is needed to install a `cbind2`-calling version of `cbind` (into the **base** name space) and the same for `rbind`. `methods:::bind_activation(FALSE)` reverts to the previous internal version of `cbind` which does not build on `cbind2`, see the examples.

**Value**

A matrix (or matrix like object) combining the columns (or rows) of `x` and `y`.

**Methods**

`signature(x = "ANY", y = "ANY")` the default method using R’s internal code.  
`signature(x = "ANY", y = "missing")` the default method for one argument using R’s internal code.

**See Also**

[cbind](#), [rbind](#).

**Examples**

```
cbind2(1:3, 4)
m <- matrix(3:8, 2,3, dimnames=list(c("a","b"), LETTERS[1:3]))
cbind2(1:2, m) # keeps dimnames from m

### Note: Use the following activation if you want cbind() to work
### ---- on S4 objects -- be careful otherwise!
```

```

methods:::bind_activation(on = TRUE)
trace("cbind2")
cbind(a=1:3)# no call to cbind2()
cbind(a=1:3, four=4, 7:9)# calling cbind2() twice
untrace("cbind2")

## The following fails currently,
## since cbind() works recursively from the tail:
try( cbind(m, a=1, b=3) )

## turn off the `special cbind()` :
methods:::bind_activation(FALSE)

```

---

Classes

---

Class Definitions

---

## Description

Class definitions are objects that contain the formal definition of a class of R objects, usually referred to as an S4 class, to distinguish them from the informal S3 classes. This document gives an overview of S4 classes; for details of the class representation objects, see help for the class [classRepresentation](#).

## Metadata Information

When a class is defined, an object is stored that contains the information about that class. The object, known as the *metadata* defining the class, is not stored under the name of the class (to allow programmers to write generating functions of that name), but under a specially constructed name. To examine the class definition, call [getClass](#). The information in the metadata object includes:

**Slots:** The data contained in an object from an S4 class is defined by the *slots* in the class definition.

Each slot in an object is a component of the object; like components (that is, elements) of a list, these may be extracted and set, using the function [slot\(\)](#) or more often the operator "@". However, they differ from list components in important ways. First, slots can only be referred to by name, not by position, and there is no partial matching of names as with list elements.

All the objects from a particular class have the same set of slot names; specifically, the slot names that are contained in the class definition. Each slot in each object always is an object of the class specified for this slot in the definition of the current class. The word “is” corresponds to the R function of the same name ([is](#)), meaning that the class of the object in the slot must be the same as the class specified in the definition, or some class that extends the one in the definition (a *subclass*).

One slot name is special, `.Data`. This stands for the ‘data part’ of the object. An object from a class with a data part is defined by specifying that the class contains one of the R object types or one of the special pseudo-classes, `matrix` or `array`, usually because the definition of the class, or of one of its superclasses, has included the type or pseudo-class in its `contains` argument. See the section on inheriting from non-S4 classes for more details.

**Superclasses:** The definition of a class includes the *superclasses*—the classes that this class extends. A class `Fancy`, say, extends a class `Simple` if an object from the `Fancy` class has all the capabilities of the `Simple` class (and probably some more as well). In particular, and very usefully, any method defined to work for a `Simple` object can be applied to a `Fancy` object as well.

This relationship is expressed equivalently by saying that `Simple` is a superclass of `Fancy`, or that `Fancy` is a subclass of `Simple`.

The direct superclasses of a class are those superclasses explicitly defined. Direct superclasses can be defined in three ways. Most commonly, the superclasses are listed in the `contains=` argument in the call to `setClass` that creates the subclass. In this case the subclass will contain all the slots of the superclass, and the relation between the class is called *simple*, as it in fact is. Superclasses can also be defined explicitly by a call to `setIs`; in this case, the relation requires methods to be specified to go from subclass to superclass. Thirdly, a class union is a superclass of all the members of the union. In this case too the relation is *simple*, but notice that the relation is defined when the superclass is created, not when the subclass is created as with the `contains=` mechanism.

The definition of a superclass will also potentially contain its own direct superclasses. These are considered (and shown) as superclasses at distance 2 from the original class; their direct superclasses are at distance 3, and so on. All these are legitimate superclasses for purposes such as method selection.

When superclasses are defined by including the names of superclasses in the `contains=` argument to `setClass`, an object from the class will have all the slots defined for its own class *and* all the slots defined for all its superclasses as well.

The information about the relation between a class and a particular superclass is encoded as an object of class `SClassExtension`. A list of such objects for the superclasses (and sometimes for the subclasses) is included in the metadata object defining the class. If you need to compute with these objects (for example, to compare the distances), call the function `extends` with argument `fullInfo=TRUE`.

**Prototype:** The objects from a class created by a call to `new` are defined by the *prototype* object for the class and by additional arguments in the call to `new`, which are passed to a method for that class for the function `initialize`.

Each class representation object contains a prototype object for the class (although for a virtual class the prototype may be `NULL`). The prototype object must have values for all the slots of the class. By default, these are the prototypes of the corresponding slot classes. However, the definition of the class can specify any valid object for any of the slots.

### Virtual classes; Basic classes

Classes exist for which no actual objects can be created by a call to `new`, the *virtual* classes, in fact a very important programming tool. They are used to group together ordinary classes that want to share some programming behavior, without necessarily restricting how the behavior is implemented. Virtual class definitions may if you want include slots (to provide some common behavior without fully defining the object—see the class `traceable` for an example).

A simple and useful form of virtual class is the *class union*, a virtual class that is defined in a call to `setClassUnion` by listing one or more of subclasses (classes that extend the class union). Class unions can include as subclasses basic object types (whose definition is otherwise sealed).

There are a number of ‘basic’ classes, corresponding to the ordinary kinds of data occurring in R. For example, `"numeric"` is a class corresponding to numeric vectors. The other vector basic classes are `"logical"`, `"integer"`, `"complex"`, `"character"`, `"raw"`, `"list"` and `"expression"`. The prototypes for the vector classes are vectors of length 0 of the corresponding type. Notice that basic classes are unusual in that the prototype object is from the class itself.

In addition to the vector classes there are also basic classes corresponding to objects in the language, such as "function" and "call". These classes are subclasses of the virtual class "language". Finally, there are object types and corresponding basic classes for "abnormal" objects, such as "environment" and "externalptr". These objects do not follow the functional behavior of the language; in particular, they are not copied and so cannot have attributes or slots defined locally.

All these classes can be used as slots or as superclasses for any other class definitions, although they do not themselves come with an explicit class. For the abnormal object types, a special mechanism is used to enable inheritance as described below.

### Inheriting from non-S4 Classes

A class definition can extend classes other than regular S4 classes, usually by specifying them in the `contains=` argument to `setClass`. Three groups of such classes behave distinctly:

1. S3 classes, which must have been registered by a previous call to `setOldClass` (you can check that this has been done by calling `getClass`, which should return a class that extends `oldClass`);
2. One of the R object types, typically a vector type, which then defines the type of the S4 objects, but also a type such as `environment` that can not be used directly as a type for an S4 object. See below.
3. One of the pseudo-classes `matrix` and `array`, implying objects with arbitrary vector types plus the `dim` and `dimnames` attributes.

This section describes the approach to combining S4 computations with older S3 computations by using such classes as superclasses. The design goal is to allow the S4 class to inherit S3 methods and default computations in as consistent a form as possible.

As part of a general effort to make the S4 and S3 code in R more consistent, when objects from an S4 class are used as the first argument to a non-default S3 method, either for an S3 generic function (one that calls `UseMethod`) or for one of the primitive functions that dispatches S3 methods, an effort is made to provide a valid object for that method. In particular, if the S4 class extends an S3 class or `matrix` or `array`, and there is an S3 method matching one of these classes, the S4 object will be coerced to a valid S3 object, to the extent that is possible given that there is no formal definition of an S3 class.

For example, suppose "myFrame" is an S4 class that includes the S3 class "data.frame" in the `contains=` argument to `setClass`. If an object from this S4 class is passed to a function, say `as.matrix`, that has an S3 method for "data.frame", the internal code for `UseMethod` will convert the object to a data frame; in particular, to an S3 object whose class attribute will be the vector corresponding to the S3 class (possibly containing multiple class names). Similarly for an S4 object inheriting from "matrix" or "array", the S4 object will be converted to a valid S3 matrix or array.

Note that the conversion is *not* applied when an S4 object is passed to the default S3 method. Some S3 generics attempt to deal with general objects, including S4 objects. Also, no transformation is applied to S4 objects that do not correspond to a selected S3 method; in particular, to objects from a class that does not contain either an S3 class or one of the basic types. See `asS4` for the transformation details.

In addition to explicit S3 generic functions, S3 methods are defined for a variety of operators and functions implemented as primitives. These methods are dispatched by some internal C code that operates partly through the same code as real S3 generic functions and partly via special considerations (for example, both arguments to a binary operator are examined when looking for methods). The same mechanism for adapting S4 objects to S3 methods has been applied to these computations

as well, with a few exceptions such as generating an error if an S4 object that does not extend an appropriate S3 class or type is passed to a binary operator.

The remainder of this section discusses the mechanisms for accessing the inherited objects of the second and third items above: basic object types and the matrix and array pseudo-classes. For the corresponding details for inheritance from S3 classes, see [setOldClass](#).

An object from a class that directly and simply contains one of the basic object types in R, has implicitly a corresponding `.Data` slot of that type, allowing computations to extract or replace the data part while leaving other slots unchanged. If the type is one that can accept attributes and is duplicated normally, the inheritance also determines the type of the object; if the class definition has a `.Data` slot corresponding to a normal type, the class of the slot determines the type of the object (that is, the value of `typeof(x)`). For such classes, `.Data` is a pseudo-slot; that is, extracting or setting it modifies the non-slot data in the object. The functions [getDataPart](#) and [setDataPart](#) are a cleaner, but essentially equivalent way to deal with the data part.

Extending a basic type this way allows objects to use old-style code for the corresponding type as well as S4 methods. Any basic type can be used for `.Data`, but a few types are treated differently because they do not behave like ordinary objects; for example, "NULL", environments, and external pointers. Classes extend these types by using a specially named slot, itself inherited from an internally defined S4 class. Inheritance from the nonstandard object type then requires an actual computation, rather than the "simple" inclusion for other types and classes. The intent is that programmers will not need to take account of the mechanism, but one implication is that you should *not* explicitly use the type of an S4 object that extends an arbitrary object type. Use [is](#) and similar functions instead.

There is one additional use of the data part, which is also an exception to the correspondence with the object's type. The exception arises from the special treatment of [matrix](#) and [array](#) "classes" in R. Matrix and array objects are managed internally and recognized without regard to any class attribute; therefore, they can be used as the data part of a new class. In this case, the object type for the new class depends on the type of the data in the matrix or array, but the `.Data` slot in the definition will be "matrix" or "array".

## References

- Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)
- Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)
- Chambers, John M. and Hastie, Trevor J. eds (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole (Appendix A for S3 classes.)
- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (Out of print.) (The description of vectors, matrix, array and time-series objects.)

## See Also

[Methods](#) for analogous discussion of methods, [setClass](#) for details of specifying class definitions, [is](#), [as](#), [new](#), [slot](#)

---

classesToAM	<i>Compute an Adjacency Matrix for Superclasses of one or more Class Definitions</i>
-------------	--

---

### Description

Given a vector of class names or a list of class definitions, the function returns an adjacency matrix of the superclasses of these classes; that is, a matrix with class names as the row and column names and with element  $[i, j]$  being 1 if the class in column  $j$  is a direct superclass of the class in row  $i$ , and 0 otherwise.

The matrix has the information implied by the `contains` slot of the class definitions, but in a form that is often more convenient for further analysis; for example, an adjacency matrix is used in packages and other software to construct graph representations of relationships.

### Usage

```
classesToAM(classes, includeSubclasses = FALSE,  
            abbreviate = 2)
```

### Arguments

<code>classes</code>	Either a character vector of class names or a list, whose elements can be either class names or class definitions. The list is convenient, for example, to include the package slot for the class name. See the examples.
<code>includeSubclasses</code>	A logical flag; if <code>TRUE</code> , then the matrix will include all the known subclasses of the specified classes as well as the superclasses. The argument can also be a logical vector of the same length as <code>classes</code> , to include subclasses for some but not all the classes.
<code>abbreviate</code>	Control of the abbreviation of the row and/or column labels of the matrix returned: values 0, 1, 2, or 3 abbreviate neither, rows, columns or both. The default, 2, is useful for printing the matrix, since class names tend to be more than one character long, making for spread-out printing. Values of 0 or 3 would be appropriate for making a graph (3 avoids the tendency of some graph plotting software to produce labels in minuscule font size).

### Details

For each of the classes, the calculation gets all the superclass names from the class definition, and finds the edges in those classes' definitions; that is, all the superclasses at distance 1. The corresponding elements of the adjacency matrix are set to 1.

The adjacency matrices for the individual class definitions are merged. Note two possible kinds of inconsistency, neither of which should cause problems except possibly with identically named classes from different packages. Edges are computed from each superclass definition, so that information overrides a possible inference from extension elements with distance  $> 1$  (and it should). When matrices from successive classes in the argument are merged, the computations do not currently check for inconsistencies—this is the area where possible multiple classes with the same name could cause confusion. A later revision may include consistency checks.



**Value**

As described, a matrix with entries 0 or 1, non-zero values indicating that the class corresponding to the column is a direct superclass of the class corresponding to the row. The row and column names are the class names (without package slot).

**See Also**

[extends](#) and [classRepresentation](#) for the underlying information from the class definition.

**Examples**

```
## the super- and subclasses of "standardGeneric" and "derivedDefaultMethod"
am <- classesToAM(list(class(show), class(getMethod(show))), TRUE)
am

## Not run:
## the following function depends on the Bioconductor package Rgraphviz
plotInheritance <- function(classes, subclasses = FALSE, ...) {
  if(!require("Rgraphviz", quietly=TRUE))
    stop("Only implemented if Rgraphviz is available")
  mm <- classesToAM(classes, subclasses)
  classes <- rownames(mm); rownames(mm) <- colnames(mm)
  graph <- new("graphAM", mm, "directed", ...)
  plot(graph)
  cat("Key:\n", paste(abbreviate(classes), " = ", classes, ", ",
    sep = ""), sep = "", fill = TRUE)
  invisible(graph)
}

## The plot of the class inheritance of the package "graph"
require(graph)
plotInheritance(getClasses("package:graph"))

## End(Not run)
```

---

classRepresentation-class  
*Class Objects*

---

**Description**

These are the objects that hold the definition of classes of objects. They are constructed and stored as meta-data by calls to the function [setClass](#). Don't manipulate them directly, except perhaps to look at individual slots.

**Details**

Class definitions are stored as metadata in various packages. Additional metadata supplies information on inheritance (the result of calls to [setIs](#)). Inheritance information implied by the class definition itself (because the class contains one or more other classes) is also constructed automatically.

When a class is to be used in an R session, this information is assembled to complete the class definition. The completion is a second object of class "classRepresentation", cached for the session or until something happens to change the information. A call to `getClass` returns the completed definition of a class; a call to `getClassDef` returns the stored definition (uncompleted).

In particular, completion fills in the upward- and downward-pointing inheritance information for the class, in slots `contains` and `subclasses` respectively. It's in principle important to note that this information can depend on which packages are installed, since these may define additional subclasses or superclasses.

### Slots

`slots`: A named list of the slots in this class; the elements of the list are the classes to which the slots must belong (or extend), and the names of the list gives the corresponding slot names.

`contains`: A named list of the classes this class 'contains'; the elements of the list are objects of `SClassExtension`. The list may be only the direct extensions or all the currently known extensions (see the details).

`virtual`: Logical flag, set to TRUE if this is a virtual class.

`prototype`: The object that represents the standard prototype for this class; i.e., the data and slots returned by a call to `new` for this class with no special arguments. Don't mess with the prototype object directly.

`validity`: Optionally, a function to be used to test the validity of objects from this class. See `validObject`.

`access`: Access control information. Not currently used.

`className`: The character string name of the class.

`package`: The character string name of the package to which the class belongs. Nearly always the package on which the metadata for the class is stored, but in operations such as constructing inheritance information, the internal package name rules.

`subclasses`: A named list of the classes known to extend this class'; the elements of the list are objects of class `SClassExtension`. The list is currently only filled in when completing the class definition (see the details).

`versionKey`: Object of class "externalptr"; eventually will perhaps hold some versioning information, but not currently used.

`sealed`: Object of class "logical"; is this class sealed? If so, no modifications are allowed.

### See Also

See function `setClass` to supply the information in the class definition. See [Classes](#) for a more basic discussion of class information.

### Description

Special documentation can be supplied to describe the classes and methods that are created by the software in the methods package. Techniques to access this documentation and to create it in R help files are described here.

## Getting documentation on classes and methods

You can ask for on-line help for class definitions, for specific methods for a generic function, and for general discussion of methods for a generic function. These requests use the `?` operator (see [help](#) for a general description of the operator). Of course, you are at the mercy of the implementer as to whether there *is* any documentation on the corresponding topics.

Documentation on a class uses the argument `class` on the left of the `?`, and the name of the class on the right; for example,

```
class ? genericFunction
```

to ask for documentation on the class `"genericFunction"`.

When you want documentation for the methods defined for a particular function, you can ask either for a general discussion of the methods or for documentation of a particular method (that is, the method that would be selected for a particular set of actual arguments).

Overall methods documentation is requested by calling the `?` operator with `methods` as the left-side argument and the name of the function as the right-side argument. For example,

```
methods ? initialize
```

asks for documentation on the methods for the `initialize` function.

Asking for documentation on a particular method is done by giving a function call expression as the right-hand argument to the `"?"` operator. There are two forms, depending on whether you prefer to give the class names for the arguments or expressions that you intend to use in the actual call.

If you planned to evaluate a function call, say `myFun(x, sqrt(wt))` and wanted to find out something about the method that would be used for this call, put the call on the right of the `"?"` operator:

```
?myFun(x, sqrt(wt))
```

A method will be selected, as it would be for the call itself, and documentation for that method will be requested. If `myFun` is not a generic function, ordinary documentation for the function will be requested.

If you know the actual classes for which you would like method documentation, you can supply these explicitly in place of the argument expressions. In the example above, if you want method documentation for the first argument having class `"maybeNumber"` and the second `"logical"`, call the `"?"` operator, this time with a left-side argument `method`, and with a function call on the right using the class names as arguments:

```
method ? myFun("maybeNumber", "logical")
```

Once again, a method will be selected, this time corresponding to the specified classes, and method documentation will be requested. This version only works with generic functions.

The two forms each have advantages. The version with actual arguments doesn't require you to figure out (or guess at) the classes of the arguments. On the other hand, evaluating the arguments may take some time, depending on the example. The version with class names does require you to pick classes, but it's otherwise unambiguous. It has a subtler advantage, in that the classes supplied may be virtual classes, in which case no actual argument will have specifically this class. The class `"maybeNumber"`, for example, might be a class union (see the example for [setClassUnion](#)).

In either form, methods will be selected as they would be in actual computation, including use of inheritance and group generic functions. See [selectMethod](#) for the details, since it is the function used to find the appropriate method.

## Writing Documentation for Methods

The on-line documentation for methods and classes uses some extensions to the R documentation format to implement the requests for class and method documentation described above. See the document *Writing R Extensions* for the available markup commands (you should have consulted this document already if you are at the stage of documenting your software).

In addition to the specific markup commands to be described, you can create an initial, overall file with a skeleton of documentation for the methods defined for a particular generic function:

```
promptMethods("myFun")
```

will create a file, 'myFun-methods.Rd' with a skeleton of documentation for the methods defined for function `myFun`. The output from `promptMethods` is suitable if you want to describe all or most of the methods for the function in one file, separate from the documentation of the generic function itself. Once the file has been filled in and moved to the 'man' subdirectory of your source package, requests for methods documentation will use that file, both for specific methods documentation as described above, and for overall documentation requested by

```
methods ? myFun
```

You are not required to use `promptMethods`, and if you do, you may not want to use the entire file created:

- If you want to document the methods in the file containing the documentation for the generic function itself, you can cut-and-paste to move the `\alias` lines and the `Methods` section from the file created by `promptMethods` to the existing file.
- On the other hand, if these are auxiliary methods, and you only want to document the added or modified software, you should strip out all but the relevant `\alias` lines for the methods of interest, and remove all but the corresponding `\item` entries in the `Methods` section. Note that in this case you will usually remove the first `\alias` line as well, since that is the marker for general methods documentation on this function (in the example, `\alias{myfun-methods}`).

If you simply want to direct documentation for one or more methods to a particular R documentation file, insert the appropriate alias.

## Description

The "..." argument in R functions is treated specially, in that it matches zero, one or more actual arguments (and so, objects). A mechanism has been added to R to allow "..." as the signature of a generic function. Methods defined for such functions will be selected and called when *all* the arguments matching "..." are from the specified class or from some subclass of that class.

## Using "..." in a Signature

Beginning with version 2.8.0 of R, S4 methods can be dispatched (selected and called) corresponding to the special argument "...". Currently, "..." cannot be mixed with other formal arguments: either the signature of the generic function is "..." only, or it does not contain "...". (This restriction may be lifted in a future version.)

Given a suitable generic function, methods are specified in the usual way by a call to `setMethod`. The method definition must be written expecting all the arguments corresponding to "..." to be

from the class specified in the method's signature, or from a class that extends that class (i.e., a subclass of that class).

Typically the methods will pass "... " down to another function or will create a list of the arguments and iterate over that. See the examples below.

When you have a computation that is suitable for more than one existing class, a convenient approach may be to define a union of these classes by a call to `setClassUnion`. See the example below.

### Method Selection and Dispatch for "... "

See [Methods](#) for a general discussion. The following assumes you have read the "Method Selection and Dispatch" section of that documentation.

A method selecting on "... " is specified by a single class in the call to `setMethod`. If all the actual arguments corresponding to "... " have this class, the corresponding method is selected directly.

Otherwise, the class of each argument and that class' superclasses are computed, beginning with the first "... " argument. For the first argument, eligible methods are those for any of the classes. For each succeeding argument that introduces a class not considered previously, the eligible methods are further restricted to those matching the argument's class or superclasses. If no further eligible classes exist, the iteration breaks out and the default method, if any, is selected.

At the end of the iteration, one or more methods may be eligible. If more than one, the selection looks for the method with the least distance to the actual arguments. For each argument, any inherited method corresponds to a distance, available from the `contains` slot of the class definition. Since the same class can arise for more than one argument, there may be several distances associated with it. Combining them is inevitably arbitrary: the current computation uses the minimum distance. Thus, for example, if a method matched one argument directly, one as first generation superclass and another as a second generation superclass, the distances are 0, 1 and 2. The current selection computation would use distance 0 for this method. In particular, this selection criterion tends to use a method that matches exactly one or more of the arguments' class.

As with ordinary method selection, there may be multiple methods with the same distance. A warning message is issued and one of the methods is chosen (the first encountered, which in this case is rather arbitrary).

Notice that, while the computation examines all arguments, the essential cost of dispatch goes up with the number of *distinct* classes among the arguments, likely to be much smaller than the number of arguments when the latter is large.

### Implementation Details

Methods dispatching on "... " were introduced in version 2.8.0 of R. The initial implementation of the corresponding selection and dispatch is in an R function, for flexibility while the new mechanism is being studied. In this implementation, a local version of `setGeneric` is inserted in the generic function's environment. The local version selects a method according to the criteria above and calls that method, from the environment of the generic function. This is slightly different from the action taken by the C implementation when "... " is not involved. Aside from the extra computing time required, the method is evaluated in a true function call, as opposed to the special context constructed by the C version (which cannot be exactly replicated in R code.) However, situations in which different computational results would be obtained have not been encountered so far, and seem very unlikely.

Methods dispatching on arguments other than "... " are *cached* by storing the inherited method in the table of all methods, where it will be found on the next selection with the same combination of classes in the actual arguments (but not used for inheritance searches). Methods based on "... " are

also cached, but not found quite as immediately. As noted, the selected method depends only on the set of classes that occur in the “...” arguments. Each of these classes can appear one or more times, so many combinations of actual argument classes will give rise to the same effective signature. The selection computation first computes and sorts the distinct classes encountered. This gives a label that will be cached in the table of all methods, avoiding any further search for inherited classes after the first occurrence. A call to `showMethods` will expose such inherited methods.

The intention is that the “...” features will be added to the standard C code when enough experience with them has been obtained. It is possible that at the same time, combinations of “...” with other arguments in signatures may be supported.

## References

- Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)
- Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

## See Also

For the general discussion of methods, see [Methods](#) and links from there.

## Examples

```
cc <- function(...)c(...)

setGeneric("cc")

setMethod("cc", "character", function(...)paste(...))

setClassUnion("Number", c("numeric", "complex"))

setMethod("cc", "Number", function(...) sum(...))

setClass("cdate", contains = "character", representation(date = "Date"))

setClass("vdate", contains = "vector", representation(date = "Date"))

cd1 <- new("cdate", "abcdef", date = Sys.Date())

cd2 <- new("vdate", "abcdef", date = Sys.Date())

stopifnot(identical(cc(letters, character(), cd1), paste(letters, character(), cd1))) # t

stopifnot(identical(cc(letters, character(), cd2), c(letters, character(), cd2))) # the c

stopifnot(identical(cc(1:10, 1+1i), sum(1:10, 1+1i))) # the "Number" method

stopifnot(identical(cc(1:10, 1+1i, TRUE), c(1:10, 1+1i, TRUE))) # the default

stopifnot(identical(cc(), c())) # no arguments implies the default method

setGeneric("numMax", function(...)standardGeneric("numMax"))

setMethod("numMax", "numeric", function(...)max(...)) # won't work for complex data
setMethod("numMax", "Number", function(...) paste(...)) # should not be selected w/o comp
```

```

stopifnot(identical(numMax(1:10, pi, 1+1i), paste(1:10, pi, 1+1i)))
stopifnot(identical(numMax(1:10, pi, 1), max(1:10, pi, 1)))

try(numMax(1:10, pi, TRUE)) # should be an error: no default method

## A generic version of paste(), dispatching on the "..." argument:
setGeneric("paste", signature = "...")

setMethod("paste", "Number", function(..., sep, collapse) c(...))

stopifnot(identical(paste(1:10, pi, 1), c(1:10, pi, 1)))

```

---

```
environment-class Class "environment"
```

---

### Description

A formal class for R environments.

### Objects from the Class

Objects can be created by calls of the form `new("environment", ...)`. The arguments in ..., if any, should be named and will be assigned to the newly created environment.

### Methods

**coerce** signature(from = "ANY", to = "environment"): calls `as.environment`.

**initialize** signature(object = "environment"): Implements the assignments in the new environment. Note that the `object` argument is ignored; a new environment is *always* created, since environments are not protected by copying.

### See Also

`new.env`

---

```
findClass Computations with Classes
```

---

### Description

Functions to find and manipulate class definitions.

**Usage**

```

removeClass(Class, where)

isClass(Class, formal=TRUE, where)

getClasses(where, inherits = missing(where))

findClass(Class, where, unique = "")

resetClass(Class, classDef, where)

sealClass(Class, where)

```

**Arguments**

Class	character string name for the class. The functions will usually take a class definition instead of the string. To restrict the class to those defined in a particular package, set the <code>packageSlot</code> of the character string.
where	The environment in which to modify or remove the definition. Defaults to the top-level environment of the calling function (the global environment for ordinary computations, but the environment or name space of a package in the source for a package). When searching for class definitions, <code>where</code> defines where to do the search, and the default is to search from the top-level environment or name space of the caller to this function.
unique	if <code>findClass</code> expects a unique location for the class, <code>unique</code> is a character string explaining the purpose of the search (and is used in warning and error messages). By default, multiple locations are possible and the function always returns a list.
inherits	in a call to <code>getClasses</code> , should the value returned include all parent environments of <code>where</code> , or that environment only? Defaults to <code>TRUE</code> if <code>where</code> is omitted, and to <code>FALSE</code> otherwise.
formal	Should a formal definition be required?
classDef	For <code>removeClass</code> , the optional class definition (but usually it's better for <code>Class</code> to be the class definition, and to omit <code>classDef</code> ).

**Details**

These are the functions that test and manipulate formal class definitions. Brief documentation is provided below. See the references for an introduction and for more details.

**removeClass:** Remove the definition of this class, from the environment `where` if this argument is supplied; if not, `removeClass` will search for a definition, starting in the top-level environment of the call to `removeClass`, and remove the (first) definition found.

**isClass:** Is this the name of a formally defined class? (Argument `formal` is for compatibility and is ignored.)

**getClasses:** The names of all the classes formally defined on `where`. If called with no argument, all the classes visible from the calling function (if called from the top-level, all the classes in any of the environments on the search list). The `inherits` argument can be used



to search a particular environment and all its parents, but usually the default setting is what you want.

**findClass:** The list of environments or positions on the search list in which a class definition of `Class` is found. If `where` is supplied, this is an environment (or name space) from which the search takes place; otherwise the top-level environment of the caller is used. If `unique` is supplied as a character string, `findClass` returns a single environment or position. By default, it always returns a list. The calling function should select, say, the first element as a position or environment for functions such as `get`.

If `unique` is supplied as a character string, `findClass` will warn if there is more than one definition visible (using the string to identify the purpose of the call), and will generate an error if no definition can be found.

**resetClass:** Reset the internal definition of a class. Causes the complete definition of the class to be re-computed, from the representation and superclasses specified in the original call to `setClass`.

This function is called when aspects of the class definition are changed. You would need to call it explicitly if you changed the definition of a class that this class extends (but doing that in the middle of a session is living dangerously, since it may invalidate existing objects).

**sealClass:** Seal the current definition of the specified class, to prevent further changes. It is possible to seal a class in the call to `setClass`, but sometimes further changes have to be made (e.g., by calls to `setIs`). If so, call `sealClass` after all the relevant changes have been made.

## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

## See Also

[setClassUnion](#), [Methods](#), [makeClassRepresentation](#)

---

findMethods

*Description of the Methods Defined for a Generic Function*

---

## Description

The function `findMethods` converts the methods defined in a table for a generic function (as used for selection of methods) into a list, for study or display. The list is actually from the class `listOfMethods` (see the section describing the class, below).

The list will be limited to the methods defined in environment `where` if that argument is supplied and limited to those including one or more of the specified `classes` in the method signature if that argument is supplied.

To see the actual table (an environment) used for methods dispatch, call `getMethodsForDispatch`. The names of the list returned by `findMethods` are the names of the objects in the table.

The function `findMethodSignatures` returns a character matrix whose rows are the class names from the signature of the corresponding methods; it operates either from a list returned by `findMethods`, or by computing such a list itself, given the same arguments as `findMethods`.

The function `hasMethods` returns `TRUE` or `FALSE` according to whether there is a non-empty table of methods for function `f` in the environment or search position `where` (or for the generic function generally if `where` is missing).

The deprecated function `getMethods` is an older alternative to `findMethods`, returning information in the form of an object of class `MethodsList`, previously used for method dispatch. It is not recommended, since this class of objects is deprecated generally and will disappear in a future version of R.

## Usage

```
findMethods(f, where, classes = character(), inherited = FALSE)

findMethodSignatures(..., target = TRUE, methods = )

hasMethods(f, where, package)

### DEPRECATED
getMethods(f, where, table = FALSE)
```

## Arguments

<code>f</code>	A generic function or the character-string name of one.
<code>where</code>	Optionally, an environment or position on the search list to look for methods metadata. If <code>where</code> is missing, <code>findMethods</code> uses the current table of methods in the generic function itself, and <code>hasMethods</code> looks for metadata anywhere in the search list.
<code>table</code>	If <code>TRUE</code> in a call to <code>getMethods</code> the returned value is the table used for dispatch, including inherited methods discovered to date. Used internally, but since the default result is the now unused <code>mlist</code> object, the default will likely be changed at some point.
<code>classes</code>	If supplied, only methods whose signatures contain at least one of the supplied classes will be included in the value returned.
<code>inherited</code>	Logical flag; if <code>TRUE</code> , the table of all methods, inherited or defined directly, will be used; otherwise, only the methods explicitly defined. Option <code>TRUE</code> is meaningful only if <code>where</code> is missing.
<code>...</code>	In the call to <code>findMethodSignatures</code> , any arguments that might be given to <code>findMethods</code> .
<code>target</code>	Optional flag to <code>findMethodSignatures</code> ; if <code>TRUE</code> , the signatures used are the target signatures (the classes for which the method will be selected); if <code>FALSE</code> , they will be the signatures are defined. The difference is only meaningful if <code>inherited</code> is <code>TRUE</code> .
<code>methods</code>	In the call to <code>findMethodSignatures</code> , an optional list of methods, presumably returned by a previous call to <code>findMethods</code> . If missing, that function will be call with the <code>...</code> arguments.
<code>package</code>	In a call to <code>hasMethods</code> , the package name for the generic function (e.g., "base" for primitives). If missing this will be inferred either from the "package" attribute of the function name, if any, or from the package slot of the generic function. See 'Details'.

## Details

The functions obtain a table of the defined methods, either from the generic function or from the stored metadata object in the environment specified by `where`. In a call to `getMethods`, the information in the table is converted as described above to produce the returned value, except with the `table` argument.

Note that `hasMethods`, but not the other functions, can be used even if no generic function of this name is currently found. In this case `package` must either be supplied as an argument or included as an attribute of `f`, since the package name is part of the identification of the methods tables.

## The Class for lists of methods

The class `"listOfMethods"` returns the methods as a named list of method definitions (or a primitive function, see the slot documentation below). The names are the strings used to store the corresponding objects in the environment from which method dispatch is computed. The current implementation uses the names of the corresponding classes in the method signature, separated by `"#"` if more than one argument is involved in the signature.

## Slots

`.Data`: Object of class `"list"` The method definitions.

Note that these may include the primitive function itself as default method, when the generic corresponds to a primitive. (Basically, because primitive functions are abnormal R objects, which cannot currently be extended as method definitions.) Computations that use the returned list to derive other information need to take account of this possibility. See the implementation of `findMethodSignatures` for an example.

`arguments`: Object of class `"character"`. The names of the formal arguments in the signature of the generic function.

`signatures`: Object of class `"list"`. A list of the signatures of the individual methods. This is currently the result of splitting the `names` according to the `"#"` separator.

If the object has been constructed from a table, as when returned by `findMethods`, the signatures will all have the same length. However, a list rather than a character matrix is used for generality. Calling `findMethodSignatures` as in the example below will always convert to the matrix form.

`generic`: Object of class `"genericFunction"`. The generic function corresponding to these methods. There are plans to generalize this slot to allow reference to the function.

`names`: Object of class `"character"`. The names as noted are the class names separated by `"#"`.

## Extends

Class `"namedList"`, directly.

Class `"list"`, by class `"namedList"`, distance 2.

Class `"vector"`, by class `"namedList"`, distance 3.

## See Also

[showMethods](#), [selectMethod](#), [Methods](#)

## Examples

```
mm <- findMethods("Ops")
findMethodSignatures(methods = mm)
```

---

`fixPre1.8`*Fix Objects Saved from R Versions Previous to 1.8*

---

## Description

Beginning with R version 1.8.0, the class of an object contains the identification of the package in which the class is defined. The function `fixPre1.8` fixes and re-assigns objects missing that information (typically because they were loaded from a file saved with a previous version of R.)

## Usage

```
fixPre1.8(names, where)
```

## Arguments

<code>names</code>	Character vector of the names of all the objects to be fixed and re-assigned.
<code>where</code>	The environment from which to look for the objects, and for class definitions. Defaults to the top environment of the call to <code>fixPre1.8</code> , the global environment if the function is used interactively.

## Details

The named object will be saved where it was found. Its class attribute will be changed to the full form required by R 1.8; otherwise, the contents of the object should be unchanged.

Objects will be fixed and re-assigned only if all the following conditions hold:

1. The named object exists.
2. It is from a defined class (not a basic datatype which has no actual class attribute).
3. The object appears to be from an earlier version of R.
4. The class is currently defined.
5. The object is consistent with the current class definition.

If any condition except the second fails, a warning message is generated.

Note that `fixPre1.8` currently fixes *only* the change in class attributes. In particular, it will not fix binary versions of packages installed with earlier versions of R if these use incompatible features. Such packages must be re-installed from source, which is the wise approach always when major version changes occur in R.

## Value

The names of all the objects that were in fact re-assigned.

---

```
genericFunction-class
```

*Generic Function Objects*

---

### Description

Generic functions (objects from or extending class `genericFunction`) are extended function objects, containing information used in creating and dispatching methods for this function. They also identify the package associated with the function and its methods.

### Objects from the Class

Generic functions are created and assigned by `setGeneric` or `setGroupGeneric` and, indirectly, by `setMethod`.

As you might expect `setGeneric` and `setGroupGeneric` create objects of class `"genericFunction"` and `"groupGenericFunction"` respectively.

### Slots

**.Data:** Object of class `"function"`, the function definition of the generic, usually created automatically as a call to `standardGeneric`.

**generic:** Object of class `"character"`, the name of the generic function.

**package:** Object of class `"character"`, the name of the package to which the function definition belongs (and *not* necessarily where the generic function is stored). If the package is not specified explicitly in the call to `setGeneric`, it is usually the package on which the corresponding non-generic function exists.

**group:** Object of class `"list"`, the group or groups to which this generic function belongs. Empty by default.

**valueClass:** Object of class `"character"`; if not an empty character vector, identifies one or more classes. It is asserted that all methods for this function return objects from these class (or from classes that extend them).

**signature:** Object of class `"character"`, the vector of formal argument names that can appear in the signature of methods for this generic function. By default, it is all the formal arguments, except for `...`. Order matters for efficiency: the most commonly used arguments in specifying methods should come first.

**default:** Object of class `"optionalMethod"` (a union of classes `"function"` and `"NULL"`), containing the default method for this function if any. Generated automatically and used to initialize method dispatch.

**skeleton:** Object of class `"call"`, a slot used internally in method dispatch. Don't expect to use it directly.

### Extends

Class `"function"`, from data part.

Class `"OptionalMethods"`, by class `"function"`.

Class `"PossibleMethod"`, by class `"function"`.

## Methods

Generic function objects are used in the creation and dispatch of formal methods; information from the object is used to create methods list objects and to merge or update the existing methods for this generic.

---

GenericFunctions    *Tools for Managing Generic Functions*

---

## Description

The functions documented here manage collections of methods associated with a generic function, as well as providing information about the generic functions themselves.

## Usage

```
isGeneric(f, where, fdef, getName = FALSE)
isGroup(f, where, fdef)
removeGeneric(f, where)

dumpMethod(f, signature, file, where, def)
findFunction(f, generic = TRUE, where = topenv(parent.frame()))
dumpMethods(f, file, signature, methods, where)
signature(...)

removeMethods(f, where = topenv(parent.frame()), all = missing(where))
setReplaceMethod(f, ..., where = topenv(parent.frame()))

getGenerics(where, searchForm = FALSE)
```

## Arguments

f	The character string naming the function.
where	The environment, name space, or search-list position from which to search for objects. By default, start at the top-level environment of the calling function, typically the global environment (i.e., use the search list), or the name space of a package from which the call came. It is important to supply this argument when calling any of these functions indirectly. With package name spaces, the default is likely to be wrong in such calls.
signature	The class signature of the relevant method. A signature is a named or unnamed vector of character strings. If named, the names must be formal argument names for the generic function. Signatures are matched to the arguments specified in the signature slot of the generic function (see the Details section of the <a href="#">setMethod</a> documentation). The signature argument to <code>dumpMethods</code> is ignored (it was used internally in previous implementations).
file	The file or connection on which to dump method definitions.
def	The function object defining the method; if omitted, the current method definition corresponding to the signature.
...	Named or unnamed arguments to form a signature.

<code>generic</code>	In testing or finding functions, should generic functions be included. Supply as <code>FALSE</code> to get only non-generic functions.
<code>fdef</code>	Optional, the generic function definition. Usually omitted in calls to <code>isGeneric</code>
<code>getName</code>	If <code>TRUE</code> , <code>isGeneric</code> returns the name of the generic. By default, it returns <code>TRUE</code> .
<code>methods</code>	The methods object containing the methods to be dumped. By default, the methods defined for this generic (optionally on the specified <code>where</code> location).
<code>all</code>	in <code>removeMethods</code> , logical indicating if all (default) or only the first method found should be removed.
<code>searchForm</code>	In <code>getGenerics</code> , if <code>TRUE</code> , the package slot of the returned result is in the form used by <code>search()</code> , otherwise as the simple package name (e.g, <code>"package:base"</code> vs <code>"base"</code> ).

### Summary of Functions

`isGeneric`: Is there a function named `f`, and if so, is it a generic?

The `getName` argument allows a function to find the name from a function definition. If it is `TRUE` then the name of the generic is returned, or `FALSE` if this is not a generic function definition.

The behavior of `isGeneric` and `getGeneric` for primitive functions is slightly different. These functions don't exist as formal function objects (for efficiency and historical reasons), regardless of whether methods have been defined for them. A call to `isGeneric` tells you whether methods have been defined for this primitive function, anywhere in the current search list, or in the specified position `where`. In contrast, a call to `getGeneric` will return what the generic for that function would be, even if no methods have been currently defined for it.

`removeGeneric`, `removeMethods`: Remove all the methods for the generic function of this name. In addition, `removeGeneric` removes the function itself; `removeMethods` restores the non-generic function which was the default method. If there was no default method, `removeMethods` leaves a generic function with no methods.

`standardGeneric`: Dispatches a method from the current function call for the generic function `f`. It is an error to call `standardGeneric` anywhere except in the body of the corresponding generic function.

Note that `standardGeneric` is a primitive function in the **base** package for efficiency reasons, but rather documented here where it belongs naturally.

`dumpMethod`: Dump the method for this generic function and signature.

`findFunction`: return a list of either the positions on the search list, or the current top-level environment, on which a function object for `name` exists. The returned value is *always* a list, use the first element to access the first visible version of the function. See the example.

*NOTE:* Use this rather than `find` with `mode="function"`, which is not as meaningful, and has a few subtle bugs from its use of regular expressions. Also, `findFunction` works correctly in the code for a package when attaching the package via a call to `library`.

`dumpMethods`: Dump all the methods for this generic.

`signature`: Returns a named list of classes to be matched to arguments of a generic function.

`getGenerics`: returns the names of the generic functions that have methods defined on `where`; this argument can be an environment or an index into the search list. By default, the whole search list is used.

The methods definitions are stored with package qualifiers; for example, methods for function `"initialize"` might refer to two different functions of that name, on different packages.

The package names corresponding to the method list object are contained in the slot `package` of the returned object. The form of the returned name can be plain (e.g., "base"), or in the form used in the search list ("`package:base`") according to the value of `searchForm`.

## Details

`setGeneric`: If there is already a non-generic function of this name, it will be used to define the generic unless `def` is supplied, and the current function will become the default method for the generic.

If `def` is supplied, this defines the generic function, and no default method will exist (often a good feature, if the function should only be available for a meaningful subset of all objects).

Arguments `group` and `valueClass` are retained for consistency with S-Plus, but are currently not used.

`isGeneric`: If the `fdef` argument is supplied, take this as the definition of the generic, and test whether it is really a generic, with `f` as the name of the generic. (This argument is not available in S-Plus.)

`removeGeneric`: If `where` supplied, just remove the version on this element of the search list; otherwise, removes the first version encountered.

`standardGeneric`: Generic functions should usually have a call to `standardGeneric` as their entire body. They can, however, do any other computations as well.

The usual `setGeneric` (directly or through calling `setMethod`) creates a function with a call to `standardGeneric`.

`dumpMethod`: The resulting source file will recreate the method.

`findFunction`: If `generic` is `FALSE`, ignore generic functions.

`dumpMethods`: If `signature` is supplied only the methods matching this initial signature are dumped. (This feature is not found in S-Plus: don't use it if you want compatibility.)

`signature`: The advantage of using `signature` is to provide a check on which arguments you meant, as well as clearer documentation in your method specification. In addition, `signature` checks that each of the elements is a single character string.

`removeMethods`: Returns `TRUE` if `f` was a generic function, `FALSE` (silently) otherwise.

If there is a default method, the function will be re-assigned as a simple function with this definition. Otherwise, the generic function remains but with no methods (so any call to it will generate an error). In either case, a following call to `setMethod` will consistently re-establish the same generic function as before.

## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

## See Also

[getMethod](#) (also for [selectMethod](#)), [setGeneric](#), [setClass](#), [showMethods](#)

## Examples

```
require(stats) # for lm

## get the function "myFun" -- throw an error if 0 or > 1 versions visible:
```



```

findFuncStrict <- function(fName) {
  allF <- findFunction(fName)
  if(length(allF) == 0)
    stop("No versions of ", fName, " visible")
  else if(length(allF) > 1)
    stop(fName, " is ambiguous: ", length(allF), " versions")
  else
    get(fName, allF[[1]])
}

try(findFuncStrict("myFun"))# Error: no version
lm <- function(x) x+1
try(findFuncStrict("lm"))# Error: 2 versions
findFuncStrict("findFuncStrict")# just 1 version
rm(lm)

## method dumping -----

setClass("A", representation(a="numeric"))
setMethod("plot", "A", function(x,y,...){ cat("A meth\n") })
dumpMethod("plot", "A", file="")
## Not run:
setMethod("plot", "A",
function (x, y, ...)
{
  cat("AAAAA\n")
}
)

## End(Not run)
tmp <- tempfile()
dumpMethod("plot", "A", file=tmp)
## now remove, and see if we can parse the dump
stopifnot(removeMethod("plot", "A"))
source(tmp)
stopifnot(is(getMethod("plot", "A"), "MethodDefinition"))

## same with dumpMethods() :
setClass("B", contains="A")
setMethod("plot", "B", function(x,y,...){ cat("B ... \n") })
dumpMethods("plot", file=tmp)
stopifnot(removeMethod("plot", "A"),
          removeMethod("plot", "B"))
source(tmp)
stopifnot(is(getMethod("plot", "A"), "MethodDefinition"),
          is(getMethod("plot", "B"), "MethodDefinition"))

```

---

 getClass

*Get Class Definition*


---

### Description

Get the definition of a class.

**Usage**

```
getClass(Class, .Force = FALSE, where)
getClassDef(Class, where, package, inherits = TRUE)
```

**Arguments**

<code>Class</code>	the character-string name of the class, often with a "package" attribute as noted below under <code>package</code> .
<code>.Force</code>	if <code>TRUE</code> , return <code>NULL</code> if the class is undefined; otherwise, an undefined class results in an error.
<code>where</code>	environment from which to begin the search for the definition; by default, start at the top-level (global) environment and proceed through the search list.
<code>package</code>	the name of the package asserted to hold the definition. If it is a non-empty string it is used instead of <code>where</code> , as the first place to look for the class. Note that the package must be loaded but need not be attached. By default, the package attribute of the <code>Class</code> argument is used, if any. There will usually be a package attribute if <code>Class</code> comes from <code>class(x)</code> for some object.
<code>inherits</code>	Should the class definition be retrieved from any enclosing environment and also from the cache? If <code>FALSE</code> only a definition in the environment <code>where</code> will be returned.

**Details**

Class definitions are stored in metadata objects in a package namespace or other environment where they are defined. When packages are loaded, the class definitions in the package are cached in an internal table. Therefore, most calls to `getClassDef` will find the class in the cache or fail to find it at all, unless `inherits` is `FALSE`, in which case only the environment(s) defined by `package` or `where` are searched.

The class cache allows for multiple definitions of the same class name in separate environments, with of course the limitation that the package attribute or package name must be provided in the call to

**Value**

The object defining the class. If the class definition is not found, `getClassDef` returns `NULL`, while `getClass`, which calls `getClassDef`, either generates an error or, if `.Force` is `TRUE`, returns a simple definition for the class. The latter case is used internally, but is not typically sensible in user code.

The non-null returned value is an object of class `classRepresentation`. For all reasonable purposes, use this object only to extract information, rather than trying to modify it: Use functions such as `setClass` and `setIs` to create or modify class definitions.

**References**

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

**See Also**

[Classes](#), [setClass](#), [isClass](#).

**Examples**

```

getClass("numeric") ## a built in class

cld <- getClass("thisIsAnUndefinedClass", .Force = TRUE)
cld ## a NULL prototype
## If you are really curious:
utils::str(cld)
## Whereas these generate errors:
try(getClass("thisIsAnUndefinedClass"))
try(getClassDef("thisIsAnUndefinedClass"))

```

---

 getMethod

*Get or Test for the Definition of a Method*


---

**Description**

Functions to look for a method corresponding to a given generic function and signature. The functions `getMethod` and `selectMethod` return the method; the functions `existsMethod` and `hasMethod` test for its existence. In both cases the first function only gets direct definitions and the second uses inheritance. In all cases, the search is in the generic function itself or in the package/environment specified by argument `where`.

The function `findMethod` returns the package(s) in the search list (or in the packages specified by the `where` argument) that contain a method for this function and signature.

**Usage**

```

getMethod(f, signature=character(), where, optional = FALSE,
          mlist, fdef)

existsMethod(f, signature = character(), where)

findMethod(f, signature, where)

selectMethod(f, signature, optional = FALSE, useInherited =,
            mlist = , fdef = , verbose = )

hasMethod(f, signature=character(), where)

```

**Arguments**

<code>f</code>	A generic function or the character-string name of one.
<code>signature</code>	the signature of classes to match to the arguments of <code>f</code> . See the details below.
<code>where</code>	The position or environment in which to look for the method(s): by default, the table of methods defined in the generic function itself is used.
<code>optional</code>	If the selection in <code>selectMethod</code> does find a valid method an error is generated, unless this argument is <code>TRUE</code> . In that case, the value returned is <code>NULL</code> if no method matches.
<code>mlist, fdef, useInherited, verbose</code>	Optional arguments to <code>getMethod</code> and <code>selectMethod</code> . Avoid these: some will work and others will not, and none of them is required for normal use of the functions.

## Details

The `signature` argument specifies classes, corresponding to formal arguments of the generic function; to be precise, to the `signature` slot of the generic function object. The argument may be a vector of strings identifying classes, and may be named or not. Names, if supplied, match the names of those formal arguments included in the signature of the generic. That signature is normally all the arguments except `...`. However, generic functions can be specified with only a subset of the arguments permitted, or with the signature taking the arguments in a different order.

It's a good idea to name the arguments in the signature to avoid confusion, if you're dealing with a generic that does something special with its signature. In any case, the elements of the signature are matched to the formal signature by the same rules used in matching arguments in function calls (see [match.call](#)).

The strings in the signature may be class names, "missing" or "ANY". See [Methods](#) for the meaning of these in method selection. Arguments not supplied in the signature implicitly correspond to class "ANY"; in particular, giving an empty signature means to look for the default method.

A call to `getMethod` returns the method for a particular function and signature. As with other `get` functions, argument `where` controls where the function looks (by default anywhere in the search list) and argument `optional` controls whether the function returns `NULL` or generates an error if the method is not found. The search for the method makes no use of inheritance.

The function `selectMethod` also looks for a method given the function and signature, but makes full use of the method dispatch mechanism; i.e., inherited methods and group generics are taken into account just as they would be in dispatching a method for the corresponding signature, with the one exception that conditional inheritance is not used. Like `getMethod`, `selectMethod` returns `NULL` or generates an error if the method is not found, depending on the argument `optional`.

The functions `existsMethod` and `hasMethod` return `TRUE` or `FALSE` according to whether a method is found, the first corresponding to `getMethod` (no inheritance) and the second to `selectMethod`.

## Value

The call to `selectMethod` or `getMethod` returns the selected method, if one is found. (This class extends `function`, so you can use the result directly as a function if that is what you want.) Otherwise an error is thrown if `optional` is `FALSE` and `NULL` is returned if `optional` is `TRUE`.

The returned method object is a [MethodDefinition](#) object, *except* that the default method for a primitive function is required to be the primitive itself. Note therefore that the only reliable test that the search failed is `is.null()`.

## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

## See Also

[Methods](#) for the details of method selection; [GenericFunctions](#) for other functions manipulating methods and generic function objects; [MethodDefinition](#) for the class that represents method definitions.

**Examples**

```

setGeneric("testFun", function(x) standardGeneric("testFun"))
setMethod("testFun", "numeric", function(x) x+1)
hasMethod("testFun", "numeric")
## Not run: [1] TRUE
hasMethod("testFun", "integer") #inherited
## Not run: [1] TRUE
existsMethod("testFun", "integer")
## Not run: [1] FALSE
hasMethod("testFun") # default method
## Not run: [1] FALSE
hasMethod("testFun", "ANY")
## Not run: [1] FALSE

```

---

getPackageName	<i>The Name associated with a Given Package</i>
----------------	---

---

**Description**

The functions below produce the package associated with a particular environment or position on the search list, or of the package containing a particular function. They are primarily used to support computations that need to differentiate objects on multiple packages.

**Usage**

```

getPackageName(where, create = TRUE)
setPackageName(pkg, env)

packageSlot(object)
packageSlot(object) <- value

```

**Arguments**

where	the environment or position on the search list associated with the desired package.
object	object providing a character string name, plus the package in which this object is to be found.
value	the name of the package.
create	flag, should a package name be created if none can be inferred? If TRUE and no non-empty package name is found, the current date and time are used as a package name, and a warning is issued. The created name is stored in the environment if that environment is not locked.
pkg, env	make the string in <code>pkg</code> the internal package name for all computations that set class and method definitions in environment <code>env</code> .

**Details**

Package names are normally installed during loading of the package, by the `INSTALL` script or by the `library` function. (Currently, the name is stored as the object `.packageName` but don't trust this for the future.)

**Value**

`packageName` returns the character-string name of the package (without the extraneous "package:" found in the search list).

`packageSlot` returns or sets the package name slot (currently an attribute, not a formal slot, but this may change someday).

`setPackageName` can be used to establish a package name in an environment that would otherwise not have one. This allows you to create classes and/or methods in an arbitrary environment, but it is usually preferable to create packages by the standard R programming tools (`package.skeleton`, etc.)

**See Also**

[search](#)

**Examples**

```
## all the following usually return "base"
getPackageName(length(search()))
getPackageName(baseenv())
getPackageName(asNamespace("base"))
getPackageName("package:base")
```

---

hasArg

*Look for an Argument in the Call*

---

**Description**

Returns TRUE if name corresponds to an argument in the call, either a formal argument to the function, or a component of . . . , and FALSE otherwise.

**Usage**

```
hasArg(name)
```

**Arguments**

name                    The unquoted name of a potential argument.

**Details**

The expression `hasArg(x)`, for example, is similar to `!missing(x)`, with two exceptions. First, `hasArg` will look for an argument named `x` in the call if `x` is not a formal argument to the calling function, but `. . .` is. Second, `hasArg` never generates an error if given a name as an argument, whereas `missing(x)` generates an error if `x` is not a formal argument.

**Value**

Always TRUE or FALSE as described above.

**See Also**[missing](#)**Examples**

```
ftest <- function(x1, ...) c(hasArg(x1), hasArg(y2))

ftest(1) ## c(TRUE, FALSE)
ftest(1, 2) ## c(TRUE, FALSE)
ftest(y2=2) ## c(FALSE, TRUE)
ftest(y=2) ## c(FALSE, FALSE) (no partial matching)
ftest(y2 = 2, x=1) ## c(TRUE, TRUE) partial match x1
```

---

implicitGeneric      *Manage Implicit Versions of Generic Functions*

---

**Description**

Create or access implicit generic functions, used to enforce consistent generic versions of functions that are not currently generic. Function `implicitGeneric()` returns the implicit generic version, `setGenericImplicit()` turns a generic implicit, `prohibitGeneric()` prevents your function from being made generic, and `registerImplicitGenerics()` saves a set of implicit generic definitions in the cached table of the current session.

**Usage**

```
implicitGeneric(name, where, generic)
setGenericImplicit(name, where, restore = TRUE)
prohibitGeneric(name, where)
registerImplicitGenerics(what, where)
```

**Arguments**

<code>name</code>	Character string name of the function.
<code>where</code>	Package or environment in which to register the implicit generics. When using the functions from the top level of your own package source, this argument can usually be omitted (and should be).
<code>generic</code>	Optionally, the generic function definition to be cached, but usually omitted. See Details section.
<code>restore</code>	Should the non-generic version of the function be restored after the current.
<code>what</code>	For <code>registerImplicitGenerics()</code> , Optional table of the implicit generics to register, but nearly always omitted. See Details section.

## Details

Multiple packages may define methods for the same function, using the version of a function stored in one package. All these methods should be marshaled and dispatched consistently when a user calls the function. For consistency, the generic version of the function must have a unique definition (the same arguments allowed in methods signatures, the same values for optional slots such as the value class, and the same standard or non-standard definition of the function itself).

If the original function is already an S4 generic, there is no problem. The implicit generic mechanism enforces consistency when the version in the package owning the function is *not* generic. If a call to `setGeneric()` attempts to turn a function in another package into a generic, the mechanism compares the proposed new generic function to the implicit generic version of that function. If the two agree, all is well. If not, and if the function belongs to another package, then the new generic will not be associated with that package. Instead, a warning is issued and a separate generic function is created, with its package slot set to the current package, not the one that owns the non-generic version of the function. The effect is that the new package can still define methods for this function, but it will not share the methods in other packages, since it is forcing a different definition of the generic function.

The right way to proceed in nearly all cases is to call `setGeneric("foo")`, giving *only* the name of the function; this will automatically use the implicit generic version. If you don't like that version, the best solution is to convince the owner of the other package to agree with you and to insert code to define the non-default properties of the function (even if the owner does not want `foo()` to be a generic by default).

For any function, the implicit generic form is a standard generic in which all formal arguments, except for `...`, are allowed in the signature of methods. If that is the suitable generic for a function, no action is needed. If not, the best mechanism is to set up the generic in the code of the package owning the function, and to then call `setGenericImplicit()` to record the implicit generic and restore the non-generic version. See the example.

Note that the package can define methods for the implicit generic as well; when the implicit generic is made a real generic, those methods will be included.

Other than predefining methods, the usual reason for having a non-default implicit generic is to provide a non-default signature, and the usual reason for *that* is to allow lazy evaluation of some arguments. See the example. All arguments in the signature of a generic function must be evaluated at the time the function needs to select a method. (But those arguments can be missing, with or without a default expression being defined; you can always examine `missing(x)` even for arguments in the signature.)

If you want to completely prohibit anyone from turning your function into a generic, call `prohibitGeneric()`.

## Value

Function `implicitGeneric()` returns the implicit generic definition (and caches that definition the first time if it has to construct it).

The other functions exist for their side effect and return nothing useful.

## See Also

`setGeneric`

## Examples

```
### How we would make the function \link{with}() into a generic:
```



```
## Since the second argument, 'expr' is used literally, we want
## with() to only have "data" in the signature.

## Note that 'methods'-internal code now has already extended with()
## to do the equivalent of the following
## Not run:
setGeneric("with", signature = "data")
## Now we could predefine methods for "with" if we wanted to.

## When ready, we store the generic as implicit, and restore the original
setGenericImplicit("with")

## (This example would only work if we "owned" function with(),
## but it is in base.)
## End(Not run)

implicitGeneric("with")
```

---

inheritedSlotNames *Names of Slots Inherited From a Super Class*

---

### Description

For a class (or class definition, see [getClass](#) and the description of class [classRepresentation](#)), give the names which are inherited from “above”, i.e., super classes, rather than by this class’ definition itself.

### Usage

```
inheritedSlotNames(Class, where = topenv(parent.frame()))
```

### Arguments

Class	character string or <a href="#">classRepresentation</a> , i.e., resulting from <a href="#">getClass</a> .
where	environment, to be passed further to <a href="#">isClass</a> and <a href="#">getClass</a> .

### Value

character vector of slot names, or [NULL](#).

### See Also

[slotNames](#), [slot](#), [setClass](#), etc.

### Examples

```
.srch <- search()
library(stats4)
inheritedSlotNames("mle")

## Not run:
```

```

if(require("Matrix")) {
  print( inheritedSlotNames("Matrix") ) # NULL
  ## whereas
  print( inheritedSlotNames("sparseMatrix") ) # --> Dim & Dimnames
  ## i.e. inherited from "Matrix" class

  print( cl <- getClass("dgCMatrix") ) # six slots, etc

  print( inheritedSlotNames(cl) ) # *all* six slots are inherited
}

## detach package we've attached above:
for(n in rev(which(is.na(match(search(), .srch))))
     detach(pos = n)

## End(Not run)

```

---

initialize-methods *Methods to Initialize New Objects from a Class*

---

## Description

The arguments to function `new` to create an object from a particular class can be interpreted specially for that class, by the definition of a method for function `initialize` for the class. This documentation describes some existing methods, and also outlines how to write new ones.

## Methods

`signature(.Object = "ANY")` The default method for `initialize` takes either named or unnamed arguments. Argument names must be the names of slots in this class definition, and the corresponding arguments must be valid objects for the slot (that is, have the same class as specified for the slot, or some superclass of that class). If the object comes from a superclass, it is not coerced strictly, so normally it will retain its current class (specifically, `as(object, Class, strict = FALSE)`).

Unnamed arguments must be objects of this class, of one of its superclasses, or one of its subclasses (from the class, from a class this class extends, or from a class that extends this class). If the object is from a superclass, this normally defines some of the slots in the object. If the object is from a subclass, the new object is that argument, coerced to the current class.

Unnamed arguments are processed first, in the order they appear. Then named arguments are processed. Therefore, explicit values for slots always override any values inferred from superclass or subclass arguments.

`signature(.Object = "traceable")` Objects of a class that extends `traceable` are used to implement debug tracing (see class `traceable` and `trace`).

The `initialize` method for these classes takes special arguments `def`, `tracer`, `exit`, `at`, `print`. The first of these is the object to use as the original definition (e.g., a function). The others correspond to the arguments to `trace`.

`signature(.Object = "environment")` The `initialize` method for environments takes a named list of objects to be used to initialize the environment.

`signature(.Object = "signature")` This is a method for internal use only. It takes an optional `functionDef` argument to provide a generic function with a `signature` slot to define the argument names. See [Methods](#) for details.

## Writing Initialization Methods

Initialization methods provide a general mechanism corresponding to generator functions in other languages.

The arguments to `initialize` are `.Object` and `...`. Nearly always, `initialize` is called from `new`, not directly. The `.Object` argument is then the prototype object from the class.

Two techniques are often appropriate for `initialize` methods: special argument names and `callNextMethod`.

You may want argument names that are more natural to your users than the (default) slot names. These will be the formal arguments to your method definition, in addition to `.Object` (always) and `...` (optionally). For example, the method for class "traceable" documented above would be created by a call to `setMethod` of the form:

```
setMethod("initialize", "traceable",
  function(.Object, def, tracer, exit, at, print) ...
)
```

In this example, no other arguments are meaningful, and the resulting method will throw an error if other names are supplied.

When your new class extends another class, you may want to call the `initialize` method for this superclass (either a special method or the default). For example, suppose you want to define a method for your class, with special argument `x`, but you also want users to be able to set slots specifically. If you want `x` to override the slot information, the beginning of your method definition might look something like this:

```
function(.Object, x, ...) {
  Object <- callNextMethod(.Object, ...)
  if(!missing(x)) { # do something with x
```

You could also choose to have the inherited method override, by first interpreting `x`, and then calling the next method.

---

is

*Is an Object from a Class?*

---

## Description

Functions to test inheritance relationships between an object and a class (`is`) or between two classes (`extends`), and to establish such relationships (`setIs`, an explicit alternative to the `contains=` argument to `setClass`).

## Usage

```
is(object, class2)
```

```
extends(class1, class2, maybe = TRUE, fullInfo = FALSE)
```

```
setIs(class1, class2, test=NULL, coerce=NULL, replace=NULL,
  by = character(), where = topenv(parent.frame()), classDef =,
  extensionObject = NULL, doComplete = TRUE)
```

## Arguments

<code>object</code>	any R object.
<code>class1, class2</code>	the names of the classes between which <code>is</code> relations are to be examined defined, or (more efficiently) the class definition objects for the classes.
<code>maybe, fullInfo</code>	In a call to <code>extends</code> , <code>maybe</code> is the value returned if a relation is conditional. In a call with <code>class2</code> missing, <code>fullInfo</code> is a flag, which if TRUE causes a list of objects of class <code>classExtension</code> to be returned, rather than just the names of the classes.
<code>test, coerce, replace</code>	In a call to <code>setIs</code> , functions optionally supplied to test whether the relation is defined, to coerce the object to <code>class2</code> , and to alter the object so that <code>is(object, class2)</code> is identical to <code>value</code> . See the details section below. The remaining arguments are for internal use and/or usually omitted.
<code>extensionObject</code>	alternative to the <code>test, coerce, replace, by</code> arguments; an object from class <code>SClassExtension</code> describing the relation. (Used in internal calls.)
<code>doComplete</code>	when TRUE, the class definitions will be augmented with indirect relations as well. (Used in internal calls.)
<code>by</code>	In a call to <code>setIs</code> , the name of an intermediary class. Coercion will proceed by first coercing to this class and from there to the target class. (The intermediate coercions have to be valid.)
<code>where</code>	In a call to <code>setIs</code> , where to store the metadata defining the relationship. Default is the global environment for calls from the top level of the session or a source file evaluated there. When the call occurs in the top level of a file in the source of a package, the default will be the name space or environment of the package. Other uses are tricky and not usually a good idea, unless you really know what you are doing.
<code>classDef</code>	Optional class definition for <code>class</code> , required internally when <code>setIs</code> is called during the initial definition of the class by a call to <code>setClass</code> . <i>Don't</i> use this argument, unless you really know why you're doing so.

## Summary of Functions

- `is`: With two arguments, tests whether `object` can be treated as from `class2`.  
With one argument, returns all the super-classes of this object's class.
- `extends`: Does the first class extend the second class? The call returns `maybe` if the extension includes a test.  
When called with one argument, the value is a vector of the superclasses of `class1`.  
If argument `fullInfo` is TRUE, the call returns a named list of objects of class `SClassExtension`; otherwise, just the names of the superclasses.
- `setIs`: Defines `class1` to be an extension (subclass) of `class2`. If `class2` is an existing virtual class, such as a class union, then only the two classes need to be supplied in the call, if the implied inherited methods work for `class1`. See the details section below.  
Alternatively, arguments `coerce` and `replace` should be supplied, defining methods to coerce to the superclass and to replace the part corresponding to the superclass. As discussed in the details and other sections below, this form is often less recommended than the corresponding call to `setAs`, to which it is an alternative.

## Details

Arranging for a class to inherit from another class is a key tool in programming. In R, there are three basic techniques, the first two providing what is called “simple” inheritance, the preferred form:

1. By the `contains=` argument in a call to `setClass`. This is and should be the most common mechanism. It arranges that the new class contains all the structure of the existing class, and in particular all the slots with the same class specified. The resulting class extension is defined to be `simple`, with important implications for method definition (see the section on this topic below).
2. Making `class1` a subclass of a virtual class either by a call to `setClassUnion` to make the subclass a member of a new class union, or by a call to `setIs` to add a class to an existing class union or as a new subclass of an existing virtual class. In either case, the implication should be that methods defined for the class union or other superclass all work correctly for the subclass. This may depend on some similarity in the structure of the subclasses or simply indicate that the superclass methods are defined in terms of generic functions that apply to all the subclasses. These relationships are also generally simple.
3. Supplying `coerce` and `replace` arguments to `setAs`. R allows arbitrary inheritance relationships, using the same mechanism for defining coerce methods by a call to `setAs`. The difference between the two is simply that `setAs` will require a call to `as` for a conversion to take place, whereas after the call to `setIs`, objects will be automatically converted to the superclass.

The automatic feature is the dangerous part, mainly because it results in the subclass potentially inheriting methods that do not work. See the section on inheritance below. If the two classes involved do not actually inherit a large collection of methods, as in the first example below, the danger may be relatively slight.

If the superclass inherits methods where the subclass has only a default or remotely inherited method, problems are more likely. In this case, a general recommendation is to use the `setAs` mechanism instead, unless there is a strong counter reason. Otherwise, be prepared to override some of the methods inherited.

With this caution given, the rest of this section describes what happens when `coerce=` and `replace=` arguments are supplied to `setIs`.

The `coerce` and `replace` arguments are functions that define how to coerce a `class1` object to `class2`, and how to replace the part of the subclass object that corresponds to `class2`. The first of these is a function of one argument (conventionally `from`) and the second of two arguments (`from, value`). For details, see the section on coerce functions below.

When `by` is specified, the coerce process first coerces to this class and then to `class2`. It’s unlikely you would use the `by` argument directly, but it is used in defining cached information about classes.

The value returned (invisibly) by `setIs` is the revised class definition of `class1`.

## Coerce, replace, and test functions

The `coerce` argument is a function that turns a `class1` object into a `class2` object. The `replace` argument is a function of two arguments that modifies a `class1` object (the first argument) to replace the part of it that corresponds to `class2` (supplied as `value`, the second argument). It then returns the modified object as the value of the call. In other words, it acts as a replacement method to implement the expression `as(object, class2) <- value`.

The easiest way to think of the `coerce` and `replace` functions is by thinking of the case that `class1` contains `class2` in the usual sense, by including the slots of the second class. (To repeat, in this situation you would not call `setIs`, but the analogy shows what happens when you do.)

The `coerce` function in this case would just make a `class2` object by extracting the corresponding slots from the `class1` object. The `replace` function would replace in the `class1` object the slots corresponding to `class2`, and return the modified object as its value.

For additional discussion of these functions, see the documentation of the `setAs` function. (Unfortunately, argument `def` to that function corresponds to argument `coerce` here.)

The inheritance relationship can also be conditional, if a function is supplied as the `test` argument. This should be a function of one argument that returns `TRUE` or `FALSE` according to whether the object supplied satisfies the relation `is(object, class2)`. Conditional relations between classes are slightly deprecated because they cannot be implemented as efficiently as ordinary relations and because they sometimes can lead to confusion (in thinking about what methods are dispatched for a particular function, for example). But they can correspond to distinctions such as two classes that have the same representation, but with only one of them obeying certain additional constraints.

### Inherited methods

A method written for a particular signature (classes matched to one or more formal arguments to the function) naturally assumes that the objects corresponding to the arguments can be treated as coming from the corresponding classes. The objects will have all the slots and available methods for the classes.

The code that selects and dispatches the methods ensures that this assumption is correct. If the inheritance was “simple”, that is, defined by one or more uses of the `contains=` argument in a call to `setClass`, no extra work is generally needed. Classes are inherited from the superclass, with the same definition.

When inheritance is defined by a general call to `setIs`, extra computations are required. This form of inheritance implies that the subclass does *not* just contain the slots of the superclass, but instead requires the explicit call to the `coerce` and/or `replace` method. To ensure correct computation, the inherited method is supplemented by calls to `as` before the body of the method is evaluated.

The calls to `as` generated in this case have the argument `strict = FALSE`, meaning that extra information can be left in the converted object, so long as it has all the appropriate slots. (It's this option that allows simple subclass objects to be used without any change.) When you are writing your `coerce` method, you may want to take advantage of that option.

Methods inherited through non-simple extensions can result in ambiguities or unexpected selections. If `class2` is a specialized class with just a few applicable methods, creating the inheritance relation may have little effect on the behavior of `class1`. But if `class2` is a class with many methods, you may find that you now inherit some undesirable methods for `class1`, in some cases, fail to inherit expected methods. In the second example below, the non-simple inheritance from class "factor" might be assumed to inherit S3 methods via that class. But the S3 class is ambiguous, and in fact is "character" rather than "factor".

For some generic functions, methods inherited by non-simple extensions are either known to be invalid or sufficiently likely to be so that the generic function has been defined to exclude such inheritance. For example `initialize` methods must return an object of the target class; this is straightforward if the extension is simple, because no change is made to the argument object, but is essentially impossible. For this reason, the generic function insists on only simple extensions for inheritance. See the `simpleInheritanceOnly` argument to `setGeneric` for the mechanism. You can use this mechanism when defining new generic functions.

If you get into problems with functions that do allow non-simple inheritance, there are two basic choices. Either back off from the `setIs` call and settle for explicit coercing defined by a call to `setAs`; or, define explicit methods involving `class1` to override the bad inherited methods. The first choice is the safer, when there are serious problems.

## References

- Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)
- Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

## See Also

`selectSuperClasses` (cl) has similar semantics as `extends` (cl), typically returning subsets of the latter.

## Examples

```
## Two examples of setIs() with coerce= and replace= arguments
## The first one works fairly well, because neither class has many
## inherited methods do be disturbed by the new inheritance

## The second example does NOT work well, because the new superclass,
## "factor", causes methods to be inherited that should not be.

## First example:
## a class definition (see \link{setClass} for class "track")
setClass("trackCurve", contains = "track",
        representation( smooth = "numeric"))
## A class similar to "trackCurve", but with different structure
## allowing matrices for the "y" and "smooth" slots
setClass("trackMultiCurve",
        representation(x="numeric", y="matrix", smooth="matrix"),
        prototype = structure(list(), x=numeric(), y=matrix(0,0,0),
                                smooth= matrix(0,0,0)))
## Automatically convert an object from class "trackCurve" into
## "trackMultiCurve", by making the y, smooth slots into 1-column matrices
setIs("trackCurve",
      "trackMultiCurve",
      coerce = function(obj) {
        new("trackMultiCurve",
            x = obj@x,
            y = as.matrix(obj@y),
            smooth = as.matrix(obj@smooth))
      },
      replace = function(obj, value) {
        obj@y <- as.matrix(value@y)
        obj@x <- value@x
        obj@smooth <- as.matrix(value@smooth)
        obj})

## Second Example:
## A class that adds a slot to "character"
setClass("stringsDated", contains = "character", representation(stamp="POSIXt"))

## Convert automatically to a factor by explicit coerce
setIs("stringsDated", "factor",
      coerce = function(from) factor(from@.Data),
```

```

replace= function(from, value) {
  from@.Data <- as.character(value); from })

ll <- sample(letters, 10, replace = TRUE)
ld <- new("stringsDated", ll, stamp = Sys.time())

levels(as(ld, "factor"))
levels(ld) # will be NULL--see comment in section on inheritance above.

## In contrast, a class that simply extends "factor" has no such ambiguities
setClass("factorDated", contains = "factor", representation(stamp="POSIXt"))
fd <- new("factorDated", factor(ll), stamp = Sys.time())
identical(levels(fd), levels(as(fd, "factor")))

```

---

isSealedMethod	<i>Check for a Sealed Method or Class</i>
----------------	---

---

## Description

These functions check for either a method or a class that has been *sealed* when it was defined, and which therefore cannot be re-defined.

## Usage

```

isSealedMethod(f, signature, fdef, where)
isSealedClass(Class, where)

```

## Arguments

<code>f</code>	The quoted name of the generic function.
<code>signature</code>	The class names in the method's signature, as they would be supplied to <a href="#">setMethod</a> .
<code>fdef</code>	Optional, and usually omitted: the generic function definition for <code>f</code> .
<code>Class</code>	The quoted name of the class.
<code>where</code>	where to search for the method or class definition. By default, searches from the top environment of the call to <code>isSealedMethod</code> or <code>isSealedClass</code> , typically the global environment or the name space of a package containing a call to one of the functions.

## Details

In the R implementation of classes and methods, it is possible to seal the definition of either a class or a method. The basic classes (numeric and other types of vectors, matrix and array data) are sealed. So also are the methods for the primitive functions on those data types. The effect is that programmers cannot re-define the meaning of these basic data types and computations. More precisely, for primitive functions that depend on only one data argument, methods cannot be specified for basic classes. For functions (such as the arithmetic operators) that depend on two arguments, methods can be specified if *one* of those arguments is a basic class, but not if both are.

Programmers can seal other class and method definitions by using the `sealed` argument to [setClass](#) or [setMethod](#).



**Value**

The functions return `FALSE` if the method or class is not sealed (including the case that it is not defined); `TRUE` if it is.

**References**

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

**Examples**

```
## these are both TRUE
isSealedMethod("+", c("numeric", "character"))
isSealedClass("matrix")

setClass("track",
         representation(x="numeric", y="numeric"))
## but this is FALSE
isSealedClass("track")
## and so is this
isSealedClass("A Name for an undefined Class")
## and so are these, because only one of the two arguments is basic
isSealedMethod("+", c("track", "numeric"))
isSealedMethod("+", c("numeric", "track"))
```

---

language-class

*Classes to Represent Unevaluated Language Objects*

---

**Description**

The virtual class "language" and the specific classes that extend it represent unevaluated objects, as produced for example by the parser or by functions such as `quote`.

**Usage**

```
### each of these classes corresponds to an unevaluated object
### in the S language.
### The class name can appear in method signatures,
### and in a few other contexts (such as some calls to as()).

" ("
"<-"
"call"
"for"
"if"
"repeat"
"while"
"name"
"{"
```

```
### Each of the classes above extends the virtual class
"language"
```

### Objects from the Class

"language" is a virtual class; no objects may be created from it.

Objects from the other classes can be generated by a call to `new(Class, ...)`, where `Class` is the quoted class name, and the `...` arguments are either empty or a *single* object that is from this class (or an extension).

### Methods

**coerce** signature(`from = "ANY", to = "call"`). A method exists for `as(object, "call"), calling as.call()`.

---

```
LinearMethodsList-class
      Class "LinearMethodsList"
```

---

### Description

A version of methods lists that has been 'linearized' for producing summary information. The actual objects from class "MethodsList" used for method dispatch are defined recursively over the arguments involved.

### Objects from the Class

The function `linearizeMlist` converts an ordinary methods list object into the linearized form.

### Slots

**methods:** Object of class "list", the method definitions.

**arguments:** Object of class "list", the corresponding formal arguments, namely as many of the arguments in the signature of the generic function as are active in the relevant method table.

**classes:** Object of class "list", the corresponding classes in the signatures.

**generic:** Object of class "genericFunction"; the generic function to which the methods correspond.

### Future Note

The current version of `linearizeMlist` does not take advantage of the `MethodDefinition` class, and therefore does more work for less effect than it could. In particular, we may move to redefine both the function and the class to take advantage of the stored signatures. Don't write code depending precisely on the present form, although all the current information will be obtainable in the future.

### See Also

Function `linearizeMlist` for the computation, and class `MethodsList` for the original, recursive form.

---

```
makeClassRepresentation
```

*Create a Class Definition*

---

### Description

Constructs an object of class `classRepresentation` to describe a particular class. Mostly a utility function, but you can call it to create a class definition without assigning it, as `setClass` would do.

### Usage

```
makeClassRepresentation(name, slots=list(), superClasses=character(),
                        prototype=NULL, package, validity, access,
                        version, sealed, virtual=NA, where)
```

### Arguments

<code>name</code>	character string name for the class
<code>slots</code>	named list of slot classes as would be supplied to <code>setClass</code> , but <i>without</i> the unnamed arguments for <code>superClasses</code> if any.
<code>superClasses</code>	what classes does this class extend
<code>prototype</code>	an object providing the default data for the class, e.g, the result of a call to <code>prototype</code> .
<code>package</code>	The character string name for the package in which the class will be stored; see <code>getPackageName</code> .
<code>validity</code>	Optional validity method. See <code>validObject</code> , and the discussion of validity methods in the reference.
<code>access</code>	Access information. Not currently used.
<code>version</code>	Optional version key for version control. Currently generated, but not used.
<code>sealed</code>	Is the class sealed? See <code>setClass</code> .
<code>virtual</code>	Is this known to be a virtual class?
<code>where</code>	The environment from which to look for class definitions needed (e.g., for slots or superclasses). See the discussion of this argument under <code>GenericFunctions</code> .

### References

- Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)
- Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

### See Also

`setClass`

---

method.skeleton      *Create a Skeleton File for a New Method*

---

## Description

This function writes a source file containing a call to [setMethod](#) to define a method for the generic function and signature supplied. By default the method definition is in line in the call, but can be made an external (previously assigned) function.

## Usage

```
method.skeleton(generic, signature, file, external = FALSE, where)
```

## Arguments

generic	the character string name of the generic function, or the generic function itself. In the first case, the function need not currently be a generic, as it would not for the resulting call to <a href="#">setMethod</a> .
signature	the method signature, as it would be given to <a href="#">setMethod</a>
file	a character string name for the output file, or a writable connection. By default the generic function name and the classes in the signature are concatenated, with separating underscore characters. The file name should normally end in ".R". To write multiple method skeletons to one file, open the file connection first and then pass it to <code>method.skeleton()</code> in multiple calls.
external	flag to control whether the function definition for the method should be a separate external object assigned in the source file, or included in line in the call to <a href="#">setMethod</a> . If supplied as a character string, this will be used as the name for the external function; by default the name concatenates the generic and signature names, with separating underscores.
where	The environment in which to look for the function; by default, the top-level environment of the call to <code>method.skeleton</code> .

## Value

The `file` argument, invisibly, but the function is used for its side effect.

## See Also

[setMethod](#), [package.skeleton](#)

## Examples

```
setClass("track", representation(x="numeric", y="numeric"))
method.skeleton("show", "track")                   ## writes show_track.R
method.skeleton("Ops", c("track", "track"))       ## writes "Ops_track_track.R"

## write multiple method skeletons to one file
con <- file("./Math_track.R", "w")
method.skeleton("Math", "track", con)
method.skeleton("exp", "track", con)
method.skeleton("log", "track", con)
```

```
close(con)
```

---

MethodDefinition-class

*Classes to Represent Method Definitions*

---

### Description

These classes extend the basic class "function" when functions are to be stored and used as method definitions.

### Details

Method definition objects are functions with additional information defining how the function is being used as a method. The `target` slot is the class signature for which the method will be dispatched, and the `defined` slot the signature for which the method was originally specified (that is, the one that appeared in some call to `setMethod`).

### Objects from the Class

The action of setting a method by a call to `setMethod` creates an object of this class. It's unwise to create them directly.

The class "SealedMethodDefinition" is created by a call to `setMethod` with argument `sealed = TRUE`. It has the same representation as "MethodDefinition".

### Slots

`.Data`: Object of class "function"; the data part of the definition.

`target`: Object of class "signature"; the signature for which the method was wanted.

`defined`: Object of class "signature"; the signature for which a method was found. If the method was inherited, this will not be identical to `target`.

`generic`: Object of class "character"; the function for which the method was created.

### Extends

Class "function", from data part.

Class "PossibleMethod", directly.

Class "OptionalMethods", by class "function".

### See Also

class `MethodsList` for the objects defining sets of methods associated with a particular generic function. The individual method definitions stored in these objects are from class `MethodDefinition`, or an extension. Class `MethodWithNext` for an extension used by `callNextMethod`.

## Description

This documentation section covers some general topics on how methods work and how the **methods** package interacts with the rest of R. The information is usually not needed to get started with methods and classes, but may be helpful for moderately ambitious projects, or when something doesn't work as expected.

The section "How Methods Work" describes the underlying mechanism; "S3 Methods" gives the rules applied when S4 classes and methods interact with older S3 methods; "Method Selection and Dispatch" provides more details on how class definitions determine which methods are used; "Generic Functions" discusses generic functions as objects. For additional information specifically about class definitions, see [Classes](#).

## How Methods Work

A generic function has associated with it a collection of other functions (the methods), all of which have the same formal arguments as the generic. See the "Generic Functions" section below for more on generic functions themselves.

Each R package will include methods metadata objects corresponding to each generic function for which methods have been defined in that package. When the package is loaded into an R session, the methods for each generic function are *cached*, that is, stored in the environment of the generic function along with the methods from previously loaded packages. This merged table of methods is used to dispatch or select methods from the generic, using class inheritance and possibly group generic functions (see [GroupGenericFunctions](#)) to find an applicable method. See the "Method Selection and Dispatch" section below. The caching computations ensure that only one version of each generic function is visible globally; although different attached packages may contain a copy of the generic function, these behave identically with respect to method selection. In contrast, it is possible for the same function name to refer to more than one generic function, when these have different `package` slots. In the latter case, R considers the functions unrelated: A generic function is defined by the combination of name and package. See the "Generic Functions" section below.

The methods for a generic are stored according to the corresponding *signature* in the call to [setMethod](#) that defined the method. The signature associates one class name with each of a subset of the formal arguments to the generic function. Which formal arguments are available, and the order in which they appear, are determined by the "signature" slot of the generic function itself. By default, the signature of the generic consists of all the formal arguments except `...`, in the order they appear in the function definition.

Trailing arguments in the signature of the generic will be *inactive* if no method has yet been specified that included those arguments in its signature. Inactive arguments are not needed or used in labeling the cached methods. (The distinction does not change which methods are dispatched, but ignoring inactive arguments improves the efficiency of dispatch.)

All arguments in the signature of the generic function will be evaluated when the function is called, rather than using the traditional lazy evaluation rules of S. Therefore, it's important to *exclude* from the signature any arguments that need to be dealt with symbolically (such as the first argument to function [substitute](#)). Note that only actual arguments are evaluated, not default expressions. A missing argument enters into the method selection as class "missing".

The cached methods are stored in an environment object. The names used for assignment are a concatenation of the class names for the active arguments in the method signature.

### S3 Methods

The functions for which S4 methods will be written often include some for which S3 methods exist, corresponding to S3 classes for the first formal argument of an S3 generic function or of a primitive function, or for either of the arguments in a call to one of the primitive binary operators. In the case of true functions, S3 methods will be dispatched by the original version of the function. The usual way this happens is by the function becoming the default method for the S4 generic, implicitly by a call to `setMethod` or explicitly by the call

```
setGeneric("f")
```

where the original `f()` contained the call `UseMethod("f")`. The S4 method selection code matches the classes of the arguments as described in the previous section. Matching will be applied for the class of S3 objects as well as S4 objects, but only the first string in an S3 class attribute is used. If no non-default S4 method matches the call, the default S4 method can then operate as an S3 generic to select S3 methods for `f()`.

Primitive functions and operators dispatch both S4 and S3 methods from the internal C code. The method selection mechanism works essentially the same way, with two exceptions. There is no explicit generic function, either S3 or S4, meaning that the selection of an S3 method if no S4 method is found is built in and not a result of an explicit default method. Also, the internal code does not look for S4 methods unless the first argument or one of the arguments to an operator is an S4 object. S4 methods can be defined for an S3 generic function and an S3 class. But if the function is a primitive, such methods will not be selected if the object in question is not an S4 object. In the examples below, for instance, an S4 method for signature `"data.frame"` for function `f3()` would be called for the S3 object `df1`. A similar S4 method for primitive function ``[ `` would be ignored for that object, but would be called for the S4 object `mydf1` that inherits from `"data.frame"`. It's an unfortunate inconsistency, but enforced by the passion for efficiency in dispatching methods for primitives.

The common case is that objects from S4 classes will use S4 methods, except when the function's default definition is wanted. For example, if an S4 class extends one of the basic object types the base code for that type may do what we want. Objects not from an S4 class will continue to follow S3 method selection.

The rest of this section describes S3 method selection in two special cases. In one case, the S4 class contains an S3 class (and has ensured that objects have all the structure needed for the S3 class). In the second case, S3 methods have been written for an S4 class; that is, a function `f.class`, where `f` is an S3 generic function and `class` is the name of an S4 class, other than a registered S3 class. The first case is now supported and recommended, the second case is discouraged, but occasionally needed (see section 4 of the paper in the references).

The following rules define selection of an S3 method for an S4 object. S4 objects are defined internally by a bit in the C structure. In practice, any object generated from an S4 class will be an S4 object, as well as the result of most computations on such objects. Older computations defined for non-S4 classes or object types may or may not return S4 objects when the arguments are such objects.

An S3 method will be selected applying the following criteria in order:

1. the `class` for the method matches the name of the S4 class exactly;
2. the object has a slot `".S3Class"` and `class` is selected by S3 inheritance, treating that slot as the S3 class of the object;

The second criterion will apply if either the S4 class contains an S3 class or the argument `S3methods=TRUE` was given to `setClass` for the class of the object or for one of its super-classes.

If an S4 class extends an S3 class, and if no S4 methods take precedence, we expect that the correct S3 method for the inherited S3 class will be chosen. This will happen, so long as the S3 class has been registered by a call to `setOldClass`. If so, the object from the S4 class will inherit a special slot that will be used as the class for S3 dispatch. Effectively, this slot is a proxy for the class attribute expected by S3 dispatch. It can even vary in its inheritance between objects, as happens with some S3 classes, such as `POSIXt`, if the replacement version of `S3Class` is used to set it. If the class so selected is one of the basic S3 classes, the object is converted to an S3 object with this vector as its class attribute.

A second nonstandard situation arises when an S3 method has been explicitly written for an S4 class. Versions of R up to and including 2.9.0 did not recognize S4 inheritance in dispatching S3 methods, so that subclasses of the S4 class would not then inherit the S3 method. The version of R accompanying this documentation fixes this problem, to the extent practical, as follows. S3 method selection will resemble S4 selection for the same class *if* the call to `setClass` has included the argument `S3methods = TRUE`. If not, the current behavior (R 2.9.1) is to select S3 methods defined for this class, but not for its subclasses (largely for back compatibility; in future versions of R, S3 methods may be ignored for S4 classes unless `S3methods` is set.) The implementation uses the same special slot as above for inheriting from an S3 class. Subclasses of a class set this way will inherit the same special slot and the same S3 method selection. It's even possible to set the slot in individual objects, as above, but the possibilities for confusion are serious.

Looking in the other direction, it remains true that S4 selection has no knowledge of S3 methods. This can cause problems when a class that expects to inherit the S3 method, "classA" in the example below, also inherits from another S4 class. If that class inherits an S4 method for a function, no matter how indirectly, that S4 method will be selected for an object from "classA", even though there is a directly defined S3 method. The S3 method can only be accessed through the default S4 method. These problems are relatively unlikely to occur, but anyone defining a class that extends both S3 and S4 classes needs to be careful.

### Method Selection and Dispatch: Details

When a call to a generic function is evaluated, a method is selected corresponding to the classes of the actual arguments in the signature. First, the cached methods table is searched for an exact match; that is, a method stored under the signature defined by the string value of `class(x)` for each non-missing argument, and "missing" for each missing argument. If no method is found directly for the actual arguments in a call to a generic function, an attempt is made to match the available methods to the arguments by using the superclass information about the actual classes.

Each class definition may include a list of one or more *superclasses* of the new class. The simplest and most common specification is by the `contains=` argument in the call to `setClass`. Each class named in this argument is a superclass of the new class. The S language has two additional mechanisms for defining superclasses. A call to `setIs` can create an inheritance relationship that is not the simple one of containing the superclass representation in the new class. In this case, explicit methods are defined to relate the subclass and the superclass. Also, a call to `setClassUnion` creates a union class that is a superclass of each of the members of the union. All three mechanisms are treated equivalently for purposes of method selection: they define the *direct* superclasses of a particular class. For more details on the mechanisms, see [Classes](#).

The direct superclasses themselves may have superclasses, defined by any of the same mechanisms, and similarly for further generations. Putting all this information together produces the full list of superclasses for this class. The superclass list is included in the definition of the class that is cached during the R session. Each element of the list describes the nature of the relationship (see [SClassExtension](#) for details). Included in the element is a `distance` slot giving a numeric distance between the two classes. The distance is the path length for the relationship: 1 for direct superclasses (regardless of which mechanism defined them), then 2 for the direct superclasses of



those classes, and so on. In addition, any class implicitly has class "ANY" as a superclass. The distance to "ANY" is treated as larger than the distance to any actual class. The special class "missing" corresponding to missing arguments has only "ANY" as a superclass, while "ANY" has no superclasses.

When a class definition is created or modified, the superclasses are ordered, first by a stable sort of the all superclasses by distance. If the set of superclasses has duplicates (that is, if some class is inherited through more than one relationship), these are removed, if possible, so that the list of superclasses is consistent with the superclasses of all direct superclasses. See the reference on inheritance for details.

The information about superclasses is summarized when a class definition is printed.

When a method is to be selected by inheritance, a search is made in the table for all methods directly corresponding to a combination of either the direct class or one of its superclasses, for each argument in the active signature. For an example, suppose there is only one argument in the signature and that the class of the corresponding object was "dgeMatrix" (from the recommended package `Matrix`). This class has two direct superclasses and through these 4 additional superclasses. Method selection finds all the methods in the table of directly specified methods labeled by one of these classes, or by "ANY".

When there are multiple arguments in the signature, each argument will generate a similar list of inherited classes. The possible matches are now all the combinations of classes from each argument (think of the function `outer` generating an array of all possible combinations). The search now finds all the methods matching any of this combination of classes. For each argument, the position in the list of superclasses of that argument's class defines which method or methods (if the same class appears more than once) match best. When there is only one argument, the best match is unambiguous. With more than one argument, there may be zero or one match that is among the best matches for *all* arguments.

If there is no best match, the selection is ambiguous and a message is printed noting which method was selected (the first method lexicographically in the ordering) and what other methods could have been selected. Since the ambiguity is usually nothing the end user could control, this is not a warning. Package authors should examine their package for possible ambiguous inheritance by calling `testInheritedMethods`.

When the inherited method has been selected, the selection is cached in the generic function so that future calls with the same class will not require repeating the search. Cached inherited selections are not themselves used in future inheritance searches, since that could result in invalid selections. If you want inheritance computations to be done again (for example, because a newly loaded package has a more direct method than one that has already been used in this session), call `resetGeneric`. Because classes and methods involving them tend to come from the same package, the current implementation does not reset all generics every time a new package is loaded.

Besides being initiated through calls to the generic function, method selection can be done explicitly by calling the function `selectMethod`.

Once a method has been selected, the evaluator creates a new context in which a call to the method is evaluated. The context is initialized with the arguments from the call to the generic function. These arguments are not rematched. All the arguments in the signature of the generic will have been evaluated (including any that are currently inactive); arguments that are not in the signature will obey the usual lazy evaluation rules of the language. If an argument was missing in the call, its default expression if any will *not* have been evaluated, since method dispatch always uses class `missing` for such arguments.

A call to a generic function therefore has two contexts: one for the function and a second for the method. The argument objects will be copied to the second context, but not any local objects created in a nonstandard generic function. The other important distinction is that the parent ("enclosing")

environment of the second context is the environment of the method as a function, so that all R programming techniques using such environments apply to method definitions as ordinary functions.

For further discussion of method selection and dispatch, see the first reference.

## Generic Functions

In principle, a generic function could be any function that evaluates a call to `standardGeneric()`, the internal function that selects a method and evaluates a call to the selected method. In practice, generic functions are special objects that in addition to being from a subclass of class `"function"` also extend the class `genericFunction`. Such objects have slots to define information needed to deal with their methods. They also have specialized environments, containing the tables used in method selection.

The slots `"generic"` and `"package"` in the object are the character string names of the generic function itself and of the package from which the function is defined. As with classes, generic functions are uniquely defined in R by the combination of the two names. There can be generic functions of the same name associated with different packages (although inevitably keeping such functions cleanly distinguished is not always easy). On the other hand, R will enforce that only one definition of a generic function can be associated with a particular combination of function and package name, in the current session or other active version of R.

Tables of methods for a particular generic function, in this sense, will often be spread over several other packages. The total set of methods for a given generic function may change during a session, as additional packages are loaded. Each table must be consistent in the signature assumed for the generic function.

R distinguishes *standard* and *nonstandard* generic functions, with the former having a function body that does nothing but dispatch a method. For the most part, the distinction is just one of simplicity: knowing that a generic function only dispatches a method call allows some efficiencies and also removes some uncertainties.

In most cases, the generic function is the visible function corresponding to that name, in the corresponding package. There are two exceptions, *implicit* generic functions and the special computations required to deal with R's *primitive* functions. Packages can contain a table of implicit generic versions of functions in the package, if the package wishes to leave a function non-generic but to constrain what the function would be like if it were generic. Such implicit generic functions are created during the installation of the package, essentially by defining the generic function and possibly methods for it, and then reverting the function to its non-generic form. (See `implicitGeneric` for how this is done.) The mechanism is mainly used for functions in the older packages in R, which may prefer to ignore S4 methods. Even in this case, the actual mechanism is only needed if something special has to be specified. All functions have a corresponding implicit generic version defined automatically (an implicit, implicit generic function one might say). This function is a standard generic with the same arguments as the non-generic function, with the non-generic version as the default (and only) method, and with the generic signature being all the formal arguments except . . . .

The implicit generic mechanism is needed only to override some aspect of the default definition. One reason to do so would be to remove some arguments from the signature. Arguments that may need to be interpreted literally, or for which the lazy evaluation mechanism of the language is needed, must *not* be included in the signature of the generic function, since all arguments in the signature will be evaluated in order to select a method. For example, the argument `expr` to the function `with` is treated literally and must therefore be excluded from the signature.

One would also need to define an implicit generic if the existing non-generic function were not suitable as the default method. Perhaps the function only applies to some classes of objects, and the package designer prefers to have no general default method. In the other direction, the package designer might have some ideas about suitable methods for some classes, if the function were

generic. With reasonably modern packages, the simple approach in all these cases is just to define the function as a generic. The implicit generic mechanism is mainly attractive for older packages that do not want to require the methods package to be available.

Generic functions will also be defined but not obviously visible for functions implemented as *primitive* functions in the base package. Primitive functions look like ordinary functions when printed but are in fact not function objects but objects of two types interpreted by the R evaluator to call underlying C code directly. Since their entire justification is efficiency, R refuses to hide primitives behind a generic function object. Methods may be defined for most primitives, and corresponding metadata objects will be created to store them. Calls to the primitive still go directly to the C code, which will sometimes check for applicable methods. The definition of “sometimes” is that methods must have been detected for the function in some package loaded in the session and `isS4(x)` is TRUE for the first argument (or for the second argument, in the case of binary operators). You can test whether methods have been detected by calling `isGeneric` for the relevant function and you can examine the generic function by calling `getGeneric`, whether or not methods have been detected. For more on generic functions, see the first reference and also section 2 of *R Internals*.

### Method Definitions

All method definitions are stored as objects from the `MethodDefinition` class. Like the class of generic functions, this class extends ordinary R functions with some additional slots: "generic", containing the name and package of the generic function, and two signature slots, "defined" and "target", the first being the signature supplied when the method was defined by a call to `setMethod`. The "target" slot starts off equal to the "defined" slot. When an inherited method is cached after being selected, as described above, a copy is made with the appropriate "target" signature. Output from `showMethods`, for example, includes both signatures.

Method definitions are required to have the same formal arguments as the generic function, since the method dispatch mechanism does not rematch arguments, for reasons of both efficiency and consistency.

### References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version: see section 10.6 for method selection and section 10.5 for generic functions).

Chambers, John M. (2009) *Developments in Class Inheritance and Method Selection* <http://stat.stanford.edu/~jmc4/classInheritance.pdf>.

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

### See Also

For more specific information, see `setGeneric`, `setMethod`, and `setClass`.

For the use of `...` in methods, see `dotsMethods`.

### Examples

```
## The rules for inheriting S3 methods.

f3 <- function(x)UseMethod("f3") # an S3 generic to illustrate inheritance

## A class that extends a registered S3 class inherits that class' S3
## methods. The S3 methods will be passed an object with the S3 class

setClass("myFrame", contains = "data.frame",
```

```

    representation(date = "POSIXt", type = "character"))

df1 <- data.frame(x = 1:10, y = rnorm(10), z = sample(letters,10))

mydf1 <- new("myFrame", df1, date = Sys.time())

## "myFrame" objects inherit "data.frame" S3 methods; e.g., for `[`

mydf1[1:2, ] # a data frame object (with extra attributes "date" and "type")

## Extending an S3 class with inconsistent (instance-based) inheritance
setClass("myDateTime", contains = "POSIXt")

now <- Sys.time() # class(now) is c("POSIXt", "POSIXct")
nowLt <- as.POSIXlt(now) # class(nowLt) is c("POSIXt", "POSIXlt")

mCt <- new("myDateTime", now)
mLt <- new("myDateTime", nowLt)

## S3 methods will be selected using instance-based information

f3.POSIXct <- function(x) "The POSIXct result"
f3.POSIXlt <- function(x) "The POSIXlt result"

stopifnot(identical(f3(mCt), f3.POSIXct(mCt)))
stopifnot(identical(f3(mLt), f3.POSIXlt(mLt)))

## An S4 class that does not contain a registered S3 class or object type
## selects S3 methods according to its S4 "inheritance"
## but only if the class definition requests this via S3methods=TRUE
## ( from version 2.9.1 on)

setClass("classA", contains = "numeric",
        representation(realData = "numeric"), S3methods = TRUE)

Math.classA <- function(x) {(getFunction(.Generic))(x@realData)}

x <- new("classA", log(1:10), realData = 1:10)

stopifnot(identical(abs(x), 1:10))

setClass("classB", contains = "classA")

y <- new("classB", x)

stopifnot(identical(abs(y), 1:10)) # (version 2.9.0 or earlier fails here)

## Note: with a class that tries to combine both S3 and S4 superclasses.
## The S3 inheritance is used and the S3 method for
## the S4 superclass will not be selected.

setClass("classC", representation(x = "numeric"))

```

```
# an S3 method for "[" (not a good idea, but it would work)
`[.classC` <- function(x, ..., drop = TRUE) {x@x[...]}

setClass("classD", contains = c("classC", "data.frame"))

## by the rule mentioned in the S3 method section, the
## S3 methods are selected from the S3 class defined; that is, "data.frame"
## If the user expected to inherit `[.classC`, no luck.
xd <- new("classD", df1, x = 1:50)

## Note the error from `[.data.frame`
try(xd[1:25])
```

---

MethodsList-class *Class MethodsList, Deprecated Representation of Methods*

---

## Description

This class of objects was used in the original implementation of the package to control method dispatch. Its use is now deprecated, but object appear as the default method slot in generic functions. This and any other remaining uses will be removed in the future.

For the modern alternative, see [listOfMethods](#).

The details in this documentation are retained to allow analysis of old-style objects.

## Details

Suppose a function  $f$  has formal arguments  $x$  and  $y$ . The methods list object for that function has the object `as.name("x")` as its argument slot. An element of the methods named "track" is selected if the actual argument corresponding to  $x$  is an object of class "track". If there is such an element, it can generally be either a function or another methods list object.

In the first case, the function defines the method to use for any call in which  $x$  is of class "track". In the second case, the new methods list object defines the available methods depending on the remaining formal arguments, in this example,  $y$ .

Each method corresponds conceptually to a *signature*; that is a named list of classes, with names corresponding to some or all of the formal arguments. In the previous example, if selecting class "track" for  $x$ , finding that the selection was another methods list and then selecting class "numeric" for  $y$  would produce a method associated with the signature  $x = \text{"track"}, y = \text{"numeric"}$ .

## Slots

**argument:** Object of class "name". The name of the argument being used for dispatch at this level.

**methods:** A named list of the methods (and method lists) defined *explicitly* for this argument. The names are the names of classes, and the corresponding element defines the method or methods to be used if the corresponding argument has that class. See the details below.

**allMethods:** A named list, contains all the directly defined methods from the `methods` slot, plus any inherited methods. Ignored when methods tables are used for dispatch (see [Methods](#))

**Extends**

Class "OptionalMethods", directly.

---

MethodWithNext-class

*Class MethodWithNext*

---

**Description**

Class of method definitions set up for callNextMethod

**Objects from the Class**

Objects from this class are generated as a side-effect of calls to [callNextMethod](#).

**Slots**

**.Data:** Object of class "function"; the actual function definition.

**nextMethod:** Object of class "PossibleMethod" the method to use in response to a [callNextMethod\(\)](#) call.

**excluded:** Object of class "list"; one or more signatures excluded in finding the next method.

**target:** Object of class "signature", from class "MethodDefinition"

**defined:** Object of class "signature", from class "MethodDefinition"

**generic:** Object of class "character"; the function for which the method was created.

**Extends**

Class "MethodDefinition", directly.

Class "function", from data part.

Class "PossibleMethod", by class "MethodDefinition".

Class "OptionalMethods", by class "MethodDefinition".

**Methods**

**findNextMethod** signature (method = "MethodWithNext"): used internally by method dispatch.

**loadMethod** signature (method = "MethodWithNext"): used internally by method dispatch.

**show** signature (object = "MethodWithNext")

**See Also**

[callNextMethod](#), and class [MethodDefinition](#).

---

 new

*Generate an Object from a Class*


---

**Description**

Given the name or the definition of a class, plus optionally data to be included in the object, `new` returns an object from that class.

**Usage**

```
new(Class, ...)
```

```
initialize(.Object, ...)
```

**Arguments**

Class	Either the name of a class (the usual case) or the object describing the class (e.g., the value returned by <code>getClass</code> ).
...	Data to include in the new object. Named arguments correspond to slots in the class definition. Unnamed arguments must be objects from classes that this class extends.
.Object	An object: see the Details section.

**Details**

The function `new` begins by copying the prototype object from the class definition. Then information is inserted according to the `...` arguments, if any. As of version 2.4 of R, the type of the prototype object, and therefore of all objects returned by `new()`, is "S4" except for classes that extend one of the basic types, where the prototype has that basic type. User functions that depend on `typeof(object)` should be careful to handle "S4" as a possible type.

The interpretation of the `...` arguments can be specialized to particular classes, if an appropriate method has been defined for the generic function "initialize". The `new` function calls `initialize` with the object generated from the prototype as the `.Object` argument to `initialize`.

By default, unnamed arguments in the `...` are interpreted as objects from a superclass, and named arguments are interpreted as objects to be assigned into the correspondingly named slots. Thus, explicit slots override inherited information for the same slot, regardless of the order in which the arguments appear.

The `initialize` methods do not have to have `...` as their second argument (see the examples). Initialize methods are often written when the natural parameters describing the new object are not the names of the slots. If you do define such a method, note the implications for future subclasses of your class. If these have additional slots, and your `initialize` method has `...` as a formal argument, then your method should pass such arguments along via `callNextMethod`. If your method does not have this argument, then either a subclass must have its own method or else the added slots must be specified by users in some way other than as arguments to `new`.

For examples of `initialize` methods, see [initialize-methods](#) for existing methods for classes "traceable" and "environment", among others.

Methods for `initialize` can be inherited only by simple inheritance, since it is a requirement that the method return an object from the target class. See the `simpleInheritanceOnly` argument to `setGeneric` and the discussion in `setIs` for the general concept.

Note that the basic vector classes, "numeric", etc. are implicitly defined, so one can use `new` for these classes.

## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

## See Also

[Classes](#) for an overview of defining class, and [setOldClass](#) for the relation to S3 classes.

## Examples

```
## using the definition of class "track" from \link{Classes}

## a new object with two slots specified
t1 <- new("track", x = seq_along(ydata), y = ydata)

# a new object including an object from a superclass, plus a slot
t2 <- new("trackCurve", t1, smooth = ysmooth)

### define a method for initialize, to ensure that new objects have
### equal-length x and y slots.

setMethod("initialize",
  "track",
  function(.Object, x = numeric(0), y = numeric(0)) {
    if(nargs() > 1) {
      if(length(x) != length(y))
        stop("specified x and y of different lengths")
      .Object@x <- x
      .Object@y <- y
    }
    .Object
  })

### the next example will cause an error (x will be numeric(0)),
### because we didn't build in defaults for x,
### although we could with a more elaborate method for initialize

try(new("track", y = sort(stats::rnorm(10))))

## a better way to implement the previous initialize method.
## Why? By using callNextMethod to call the default initialize method
## we don't inhibit classes that extend "track" from using the general
## form of the new() function. In the previous version, they could only
## use x and y as arguments to new, unless they wrote their own
## initialize method.

setMethod("initialize", "track", function(.Object, ...) {
  .Object <- callNextMethod()
  if(length(.Object@x) != length(.Object@y))
```



```
    stop("specified x and y of different lengths")
  }.Object
})
```

---

nonStructure-class *A non-structure S4 Class for basic types*

---

### Description

S4 classes that are defined to extend one of the basic vector classes should contain the class `structure` if they behave like structures; that is, if they should retain their class behavior under math functions or operators, so long as their length is unchanged. On the other hand, if their class depends on the values in the object, not just its structure, then they should lose that class under any such transformations. In the latter case, they should be defined to contain `nonStructure`.

If neither of these strategies applies, the class likely needs some methods of its own for `Ops`, `Math`, and/or other generic functions. What is not usually a good idea is to allow such computations to drop down to the default, base code. This is inconsistent with most definitions of such classes.

### Methods

Methods are defined for operators and math functions (groups `Ops`, `Math` and `Math2`). In all cases the result is an ordinary vector of the appropriate type.

### References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer.

### See Also

[structure](#)

### Examples

```
setClass("NumericNotStructure", contains = c("numeric", "nonStructure"))
xx <- new("NumericNotStructure", 1:10)
xx + 1 # vector
log(xx) # vector
sample(xx) # vector
```

---

 ObjectsWithPackage-class

*A Vector of Object Names, with associated Package Names*


---

### Description

This class of objects is used to represent ordinary character string object names, extended with a package slot naming the package associated with each object.

### Objects from the Class

The function `getGenerics` returns an object of this class.

### Slots

`.Data`: Object of class "character": the object names.

`package`: Object of class "character" the package names.

### Extends

Class "character", from data part.

Class "vector", by class "character".

### See Also

Methods for general background.

---

 promptClass

*Generate a Shell for Documentation of a Formal Class*


---

### Description

Assembles all relevant slot and method information for a class, with minimal markup for Rd processing; no QC facilities at present.

### Usage

```
promptClass(clName, filename = NULL, type = "class",
            keywords = "classes", where = toplevelenv(parent.frame()))
```

### Arguments

<code>clName</code>	a character string naming the class to be documented.
<code>filename</code>	usually, a connection or a character string giving the name of the file to which the documentation shell should be written. The default corresponds to a file whose name is the topic name for the class documentation, followed by ".Rd". Can also be NA (see below).
<code>type</code>	the documentation type to be declared in the output file.
<code>keywords</code>	the keywords to include in the shell of the documentation. The keyword "classes" should be one of them.
<code>where</code>	where to look for the definition of the class and of methods that use it.

## Details

The class definition is found on the search list. Using that definition, information about classes extended and slots is determined.

In addition, the currently available generics with methods for this class are found (using [getGenerics](#)). Note that these methods need not be in the same environment as the class definition; in particular, this part of the output may depend on which packages are currently in the search list.

As with other prompt-style functions, unless `filename` is `NA`, the documentation shell is written to a file, and a message about this is given. The file will need editing to give information about the *meaning* of the class. The output of `promptClass` can only contain information from the metadata about the formal definition and how it is used.

If `filename` is `NA`, a list-style representation of the documentation shell is created and returned. Writing the shell to a file amounts to `cat(unlist(x), file = filename, sep = "\n")`, where `x` is the list-style representation.

## Value

If `filename` is `NA`, a list-style representation of the documentation shell. Otherwise, the name of the file written to is returned invisibly.

## Author(s)

VJ Carey <stvjc@channing.harvard.edu> and John Chambers

## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

## See Also

[prompt](#) for documentation of functions, [promptMethods](#) for documentation of method definitions.

For processing of the edited documentation, either use R CMD [Rdconv](#), or include the edited file in the ‘man’ subdirectory of a package.

## Examples

```
## Not run: > promptClass("track")
A shell of class documentation has been written to the
file "track-class.Rd".

## End(Not run)
```

---

`promptMethods`*Generate a Shell for Documentation of Formal Methods*

---

### Description

Generates a shell of documentation for the methods of a generic function.

### Usage

```
promptMethods(f, filename = NULL, methods)
```

### Arguments

<code>f</code>	a character string naming the generic function whose methods are to be documented.
<code>filename</code>	usually, a connection or a character string giving the name of the file to which the documentation shell should be written. The default corresponds to the coded topic name for these methods (currently, <code>f</code> followed by <code>"-methods.Rd"</code> ). Can also be <code>FALSE</code> or <code>NA</code> (see below).
<code>methods</code>	Optional methods list object giving the methods to be documented. By default, the first methods object for this generic is used (for example, if the current global environment has some methods for <code>f</code> , these would be documented). If this argument is supplied, it is likely to be <code>getMethods(f, where)</code> , with <code>where</code> some package containing methods for <code>f</code> .

### Details

If `filename` is `FALSE`, the text created is returned, presumably to be inserted some other documentation file, such as the documentation of the generic function itself (see [prompt](#)).

If `filename` is `NA`, a list-style representation of the documentation shell is created and returned. Writing the shell to a file amounts to `cat(unlist(x), file = filename, sep = "\n")`, where `x` is the list-style representation.

Otherwise, the documentation shell is written to the file specified by `filename`.

### Value

If `filename` is `FALSE`, the text generated; if `filename` is `NA`, a list-style representation of the documentation shell. Otherwise, the name of the file written to is returned invisibly.

### References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

### See Also

[prompt](#) and [promptClass](#)

---

`representation`*Construct a Representation or a Prototype for a Class Definition*

---

## Description

In calls to `setClass`, these two functions construct, respectively, the `representation` and `prototype` arguments. They do various checks and handle special cases. You're encouraged to use them when defining classes that, for example, extend other classes as a data part or have multiple superclasses, or that combine extending a class and slots.

## Usage

```
representation(...)  
prototype(...)
```

## Arguments

...           The call to `representation` takes arguments that are single character strings. Unnamed arguments are classes that a newly defined class extends; named arguments name the explicit slots in the new class, and specify what class each slot should have.

In the call to `prototype`, if an unnamed argument is supplied, it unconditionally forms the basis for the prototype object. Remaining arguments are taken to correspond to slots of this object. It is an error to supply more than one unnamed argument.

## Details

The `representation` function applies tests for the validity of the arguments. Each must specify the name of a class.

The classes named don't have to exist when `representation` is called, but if they do, then the function will check for any duplicate slot names introduced by each of the inherited classes.

The arguments to `prototype` are usually named initial values for slots, plus an optional first argument that gives the object itself. The unnamed argument is typically useful if there is a data part to the definition (see the examples below).

## Value

The value of `representation` is just the list of arguments, after these have been checked for validity.

The value of `prototype` is the object to be used as the prototype. Slots will have been set consistently with the arguments, but the construction does *not* use the class definition to test validity of the contents (it hardly can, since the prototype object is usually supplied to create the definition).

## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

**See Also**

[setClass](#)

**Examples**

```
## representation for a new class with a directly define slot "smooth"
## which should be a "numeric" object, and extending class "track"
representation("track", smooth = "numeric")

setClass("Character", representation("character"))
setClass("TypedCharacter", representation("Character", type="character"),
         prototype(character(0), type="plain"))
ttt <- new("TypedCharacter", "foo", type = "character")

setClass("num1", representation(comment = "character"),
         contains = "numeric",
         prototype = prototype(pi, comment = "Start with pi"))
```

---

S3Part

*S3-style Objects and S4-class Objects*

---

**Description**

Old-style (S3) classes may be registered as S4 classes (by calling [setOldClass](#), and many have been. These classes can then be contained in (that is, superclasses of) regular S4 classes, allowing formal methods and slots to be added to the S3 behavior. The function `S3Part` extracts or replaces the S3 part of such an object. `S3Class` extracts or replaces the S3-style class. `S3Class` also applies to object from an S4 class with `S3methods=TRUE` in the call to [setClass](#).

See the details below. Also discussed are S3 <-> S4 coercion; see the section “S3 and S4 objects”

**Usage**

```
S3Part(object, strictS3 = FALSE, S3Class)

S3Part(object, strictS3 = FALSE, needClass = ) <- value

S3Class(object)

S3Class(object) <- value

isXS3Class(classDef)

slotsFromS3(object)
```

**Arguments**

<code>object</code>	An object from some class that extends a registered S3 class, usually because the class has as one of its superclasses an S3 class registered by a call to <code>setOldClass</code> , or from a class that extends a basic vector, matrix or array object type. See the details. For most of the functions, an S3 object can also be supplied, with the interpretation that it is its own S3 part.
<code>strictS3</code>	If <code>TRUE</code> , the value returned by <code>S3Part</code> will be an S3 object, with all the S4 slots removed. Otherwise, an S4 object will always be returned; for example, from the S4 class created by <code>setOldClass</code> as a proxy for an S3 class, rather than the underlying S3 object.
<code>S3Class</code>	The character vector to be stored as the S3 class slot in the object. Usually, and by default, retains the slot from <code>object</code> .
<code>needClass</code>	Require that the replacement value be this class or a subclass of it.
<code>value</code>	For <code>S3Part&lt;-</code> , the replacement value for the S3 part of the object. This does <i>not</i> need to be an S4 object; in fact, the usual way to create objects from these classes is by giving an S3 object of the right class as an argument to <code>new</code> . For <code>S3Class&lt;-</code> , the character vector that will be used as a proxy for <code>class(x)</code> in S3 method dispatch. This replacement function can be used to control S3 per-object method selection.
<code>classDef</code>	A class definition object, as returned by <code>getClass</code> .

**Details**

Classes that register S3 classes by a call to `setOldClass` have slot `".S3Class"` to hold the corresponding S3 vector of class strings. The prototype of such a class has the value for this slot determined by the argument to `setOldClass`. Other S4 classes will have the same slot if the argument `S3methods = TRUE` is supplied to `setClass`; in this case, the slot is set to the S4 inheritance of the class.

New S4 classes that extend (contain) such classes also have the same slot, and by default the prototype has the value determined by the `contains=` argument to `setClass`. Individual objects from the S4 class may have an S3 class corresponding to the value in the prototype or to an (S3) subclass of that value. See the examples below.

`S3Part()` with `strictS3 = TRUE` constructs the underlying S3 object by eliminating all the formally defined slots and turning off the S4 bit of the object. With `strictS3 = FALSE` the object returned is from the corresponding S4 class. For consistency and generality, `S3Part()` works also for classes that extend the basic vector, matrix and array classes. Since R is somewhat arbitrary about what it treats as an S3 class ("`ts`" is, but "`matrix`" is not), `S3Part()` tries to return an S3 (that is, non-S4) object whenever the S4 class has a suitable superclass, of either S3 or basic object type.

One general application that relies on this generality is to use `S3Part()` to get a superclass object that is guaranteed not to be an S4 object. If you are calling some function that checks for S4 objects, you need to be careful not to end up in a closed loop (`fooS4` calls `fooS3`, which checks for an S4 object and calls `fooS4` again, maybe indirectly). Using `S3Part()` with `strictS3 = TRUE` is a mechanism to avoid such loops.

Because the contents of S3 class objects have no definition or guarantee, the computations involving S3 parts do *not* check for slot validity. Slots are implemented internally in R as attributes, which are copied when present in the S3 part. Grave problems can occur if an S4 class extending an S3

class uses the name of an S3 attribute as the name of an S4 slot, and S3 code sets the attribute to an object from an invalid class according to the S4 definition.

Frequently, `S3Part` can and should be avoided by simply coercing objects to the desired class; methods are automatically defined to deal correctly with the slots when `as` is called to extract or replace superclass objects.

The function `slotsFromS3()` is a generic function used internally to access the slots associated with the S3 part of the object. Methods for this function are created automatically when `setOldClass` is called with the `S4Class` argument. Usually, there is only one S3 slot, containing the S3 class, but the `S4Class` argument may provide additional slots, in the case that the S3 class has some guaranteed attributes that can be used as formal S4 slots. See the corresponding section in the documentation of `setOldClass`.

## Value

`S3Part`: Returns or sets the S3 information (and possibly some S4 slots as well, depending on arguments `S3Class` and `keepSlots`). See the discussion of argument `strict` above. If it is `TRUE` the value returned is an S3 object.

`S3Class`: Returns or sets the character vector of S3 class(es) stored in the object, if the class has the corresponding `.S3Class` slot. Currently, the function defaults to `class` otherwise.

`isXS3Class`: Returns `TRUE` or `FALSE` according to whether the class defined by `ClassDef` extends S3 classes (specifically, whether it has the slot for holding the S3 class).

`slotsFromS3`: returns a list of the relevant slot classes, or an empty list for any other object.

## S3 and S4 Objects: Conversion Mechanisms

Objects in `R` have an internal bit that indicates whether or not to treat the object as coming from an S4 class. This bit is tested by `isS4` and can be set on or off by `asS4`. The latter function, however, does no checking or interpretation; you should only use it if you are very certain every detail has been handled correctly.

As a friendlier alternative, methods have been defined for coercing to the virtual classes "S3" and "S4". The expressions `as(object, "S3")` and `as(object, "S4")` return S3 and S4 objects, respectively. In addition, they attempt to do conversions in a valid way, and also check validity when coercing to S4.

The expression `as(object, "S3")` can be used in two ways. For objects from one of the registered S3 classes, the expression will ensure that the class attribute is the full multi-string S3 class implied by `class(object)`. If the registered class has known attribute/slots, these will also be provided.

Another use of `as(object, "S3")` is to take an S4 object and turn it into an S3 object with corresponding attributes. This is only meaningful with S4 classes that have a data part. If you want to operate on the object without invoking S4 methods, this conversion is usually the safest way.

The expression `as(object, "S4")` will use the attributes in the object to create an object from the S4 definition of `class(object)`. This is a general mechanism to create partially defined version of S4 objects via S3 computations (not much different from invoking `new` with corresponding arguments, but usable in this form even if the S4 object has an `initialize` method with different arguments).

## References

- Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version).
- Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)



**See Also**[setOldClass](#)**Examples**

```
## two examples extending S3 class "lm", class "xlm" directly and "ylm" indirectly
setClass("xlm", representation(eps = "numeric"), contains = "lm")
setClass("ylm", representation(header = "character"), contains = "xlm")

## lm.D9 is as computed in the example for stats::lm
y1 = new("ylm", lm.D9, header = "test", eps = .1)
xx = new("xlm", lm.D9, eps = .1)
y2 = new("ylm", xx, header = "test")
stopifnot(inherits(y2, "lm"))
stopifnot(identical(y1, y2))
stopifnot(identical(S3Part(y1, strict = TRUE), lm.D9))

## note the these classes can insert an S3 subclass of "lm" as the S3 part:
myData <- data.frame(time = 1:10, y = (1:10)^.5)
myLm <- lm(cbind(y, y^3) ~ time, myData) # S3 class: c("mlm", "lm")
ym1 = new("ylm", myLm, header = "Example", eps = 0.)

##similar classes to "xlm" and "ylm", but extending S3 class c("mlm", "lm")
setClass("xmm", representation(eps = "numeric"), contains = "mlm")
setClass("ymm", representation(header="character"), contains = "xmm")

ym2 <- new("ymm", myLm, header = "Example2", eps = .001)

# but for class "ymm", an S3 part of class "lm" is an error:
try(new("ymm", lm.D9, header = "Example2", eps = .001))

setClass("dataFramed", representation(date = "Date"), contains = "data.frame")
myDD <- new("dataFramed", myData, date = Sys.Date())

## S3Part() applied to classes with a data part (.Data slot)

setClass("NumX", contains="numeric", representation(id="character"))
nn = new("NumX", 1:10, id="test")
stopifnot(identical(1:10, S3Part(nn, strict = TRUE)))

m1 = cbind(group, weight)
setClass("MatX", contains = "matrix", representation(date = "Date"))
mx1 = new("MatX", m1, date = Sys.Date())
stopifnot(identical(m1, S3Part(mx1, strict = TRUE)))
```

**Description**

Methods can be defined for *group generic functions*. Each group generic function has a number of *member generic functions* associated with it.

Methods defined for a group generic function cause the same method to be defined for each member of the group, but a method explicitly defined for a member of the group takes precedence over a method defined, with the same signature, for the group generic.

The functions shown in this documentation page all reside in the **methods** package, but the mechanism is available to any programmer, by calling `setGroupGeneric`.

## Usage

```
## S4 group generics:
Arith(e1, e2)
Compare(e1, e2)
Ops(e1, e2)
Logic(e1, e2)
Math(x)
Math2(x, digits)
Summary(x, ..., na.rm = FALSE)
Complex(z)
```

## Arguments

`x`, `z`, `e1`, `e2` objects.

`digits` number of digits to be used in `round` or `signif`.

`...` further arguments passed to or from methods.

`na.rm` logical: should missing values be removed?

## Details

Methods can be defined for the group generic functions by calls to `setMethod` in the usual way. Note that the group generic functions should never be called directly – a suitable error message will result if they are. When metadata for a group generic is loaded, the methods defined become methods for the members of the group, but only if no method has been specified directly for the member function for the same signature. The effect is that group generic definitions are selected before inherited methods but after directly specified methods. For more on method selection, see [Methods](#).

There are also S3 groups `Math`, `Ops`, `Summary` and `Complex`, see [?S3groupGeneric](#), with no corresponding R objects, but these are irrelevant for S4 group generic functions.

The members of the group defined by a particular generic can be obtained by calling `getGroupMembers`. For the group generic functions currently defined in this package the members are as follows:

```
Arith "+", "-", "*", "^", "%%", "%/%", "/"
Compare "==", ">", "<", "!=", "<=", ">="
Logic "&", "|".
Ops "Arith", "Compare", "Logic"
Math "abs", "sign", "sqrt", "ceiling", "floor", "trunc", "cummax",
     "cummin", "cumprod", "cumsum", "log", "log10", "log2", "loglp", "acos",
     "acosh", "asin", "asinh", "atan", "atanh", "exp", "expm1", "cos",
     "cosh", "sin", "sinh", "tan", "tanh", "gamma", "lgamma", "digamma",
     "trigamma"
Math2 "round", "signif"
```

Summary "max", "min", "range", "prod", "sum", "any", "all"

Complex "Arg", "Conj", "Im", "Mod", "Re"

Note that Ops merely consists of three sub groups.

All the functions in these groups (other than the group generics themselves) are basic functions in R. They are not by default S4 generic functions, and many of them are defined as primitives. However, you can still define formal methods for them, both individually and via the group generics. It all works more or less as you might expect, admittedly via a bit of trickery in the background. See [Methods](#) for details.

Note that two members of the Math group, `log` and `trunc`, have ... as an extra formal argument. Since methods for Math will have only one formal argument, you must set a specific method for these functions in order to call them with the extra argument(s).

For further details about group generic functions see section 10.5 of *Software for Data Analysis*.

## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version).

## See Also

The function `callGeneric` is nearly always relevant when writing a method for a group generic. See the examples below and in section 10.5 of *Software for Data Analysis*.

See `S3groupGeneric` for S3 group generics.

## Examples

```
setClass("testComplex", representation(zz = "complex"))
## method for whole group "Complex"
setMethod("Complex", "testComplex",
          function(z) c("groupMethod", callGeneric(z@zz)))
## exception for Arg() :
setMethod("Arg", "testComplex",
          function(z) c("ArgMethod", Arg(z@zz)))
z1 <- 1+2i
z2 <- new("testComplex", zz = z1)
stopifnot(identical(Mod(z2), c("groupMethod", Mod(z1))))
stopifnot(identical(Arg(z2), c("ArgMethod", Arg(z1))))
```

---

SClassExtension-class

*Class to Represent Inheritance (Extension) Relations*

---

## Description

An object from this class represents a single 'is' relationship; lists of these objects are used to represent all the extensions (superclasses) and subclasses for a given class. The object contains information about how the relation is defined and methods to coerce, test, and replace correspondingly.

## Objects from the Class

Objects from this class are generated by `setIs`, from direct calls and from the `contains=` information in a call to `setClass`, and from class unions created by `setClassUnion`. In the last case, the information is stored in defining the *subclasses* of the union class (allowing unions to contain sealed classes).

## Slots

`subClass, superClass`: The classes being extended: corresponding to the `from`, and to arguments to `setIs`.

`package`: The package to which that class belongs.

`coerce`: A function to carry out the `as()` computation implied by the relation. Note that these functions should *not* be used directly. They only deal with the `strict=TRUE` calls to the `as` function, with the full method constructed from this mechanically.

`test`: The function that would test whether the relation holds. Except for explicitly specified `test` arguments to `setIs`, this function is trivial.

`replace`: The method used to implement `as(x, Class) <- value`.

`simple`: A "logical" flag, `TRUE` if this is a simple relation, either because one class is contained in the definition of another, or because a class has been explicitly stated to extend a virtual class. For simple extensions, the three methods are generated automatically.

`by`: If this relation has been constructed transitively, the first intermediate class from the subclass.

`dataPart`: A "logical" flag, `TRUE` if the extended class is in fact the data part of the subclass. In this case the extended class is a basic class (i.e., a type).

`distance`: The distance between the two classes, 1 for directly contained classes, plus the number of generations between otherwise.

## Methods

No methods defined with class "SClassExtension" in the signature.

## See Also

`is`, `as`, and the `classRepresentation` class.

---

`selectSuperClasses` *Super Classes (of Specific Kinds) of a Class*

---

## Description

Return superclasses of `ClassDef`, possibly only non-virtual or direct or simple ones.

These functions are designed to be fast, and consequently only work with the `contains` slot of the corresponding class definitions.

## Usage

```
selectSuperClasses(Class, dropVirtual = FALSE, namesOnly = TRUE,
  directOnly = TRUE, simpleOnly = directOnly,
  where = topenv(parent.frame()))
```

```
.selectSuperClasses(ext, dropVirtual = FALSE, namesOnly = TRUE,
  directOnly = TRUE, simpleOnly = directOnly)
```

**Arguments**

Class	name of the class or (more efficiently) the class definition object (see <a href="#">getClass</a> ).
dropVirtual	logical indicating if only non-virtual superclasses should be returned.
namesOnly	logical indicating if only a vector names instead of a named list class-extensions should be returned.
directOnly	logical indicating if only a <i>direct</i> super classes should be returned.
simpleOnly	logical indicating if only simple class extensions should be returned.
where	(only used when Class is not a class definition) environment where the class definition of Class is found.
ext	for <code>.selectSuperClasses()</code> only, a <a href="#">list</a> of class extensions, typically <code>getClassDef(..)@contains</code> .

**Value**

a [character](#) vector (if `namesOnly` is true, as per default) or a list of class extensions (as the `contains` slot in the result of [getClass](#)).

**Note**

The typical user level function is `selectSuperClasses()` which calls `.selectSuperClasses()`; i.e., the latter should only be used for efficiency reasons by experienced users.

**See Also**

is, [getClass](#); further, the more technical class [classRepresentation](#) documentation.

**Examples**

```
setClass("Root")
setClass("Base", contains = "Root", representation(length = "integer"))
setClass("A", contains = "Base", representation(x = "numeric"))
setClass("B", contains = "Base", representation(y = "character"))
setClass("C", contains = c("A", "B"))

extends("C") #--> "C" "A" "B" "Base" "Root"
selectSuperClasses("C") # "A" "B"
selectSuperClasses("C", direct=FALSE) # "A" "B" "Base" "Root"
selectSuperClasses("C", dropVirt = TRUE, direct=FALSE) # ditto w/o "Root"
```

---

setClass

---

*Create a Class Definition*


---

**Description**

Create a class definition, specifying the representation (the slots) and/or the classes contained in this one (the superclasses), plus other optional details.

**Usage**

```
setClass(Class, representation, prototype, contains=character(),
         validity, access, where, version, sealed, package,
         S3methods = FALSE)
```

**Arguments**

Class	character string name for the class.
representation	a named list of the slots that the new class should have, the names giving the names of the slots and the corresponding elements being the character string names of the corresponding classes. Usually a call to the <a href="#">representation</a> function. Backward compatibility and compatibility with S-Plus allows unnamed elements for superclasses, but the recommended style is to use the <code>contains=</code> argument instead.
prototype	an object providing the default data for the slots in this class. Usually and preferably the result of a call to <a href="#">prototype</a> .
contains	what classes does this class extend? (These are called <i>superclasses</i> in some languages.) When these classes have slots, all their slots will be contained in the new class as well.
where	the environment in which to store or remove the definition. Defaults to the top-level environment of the calling function (the global environment for ordinary computations, and the environment or name space of a package in the source code for that package).
validity	if supplied, should be a validity-checking method for objects from this class (a function that returns <code>TRUE</code> if its argument is a valid object of this class and one or more strings describing the failures otherwise). See <a href="#">validObject</a> for details.
access, version	access and version, included for compatibility with S-Plus, but currently ignored.
sealed	if <code>TRUE</code> , the class definition will be sealed, so that another call to <code>setClass</code> will fail on this class name.
package	an optional package name for the class. By default (and usually) the name of the package in which the class definition is assigned.
S3methods	if <code>TRUE</code> , S3 methods may be written for this class. S3 generic functions and primitives will dispatch an S3 method defined for this class, given an S4 object from the class or from a subclass of it, provided no S4 method and no more direct S3 method is found. Writing S3 methods for S4 classes is somewhat deprecated (see <a href="#">Methods</a> ), but if you do write them, the class should be created with this argument <code>TRUE</code> , so inheritance will work. By default, the current implementation takes no special action, so that methods will be dispatched for this class but <i>not</i> for subclasses. Note that future versions may revoke this and dispatch no S3 methods other than the default unless <code>S3methods</code> is <code>TRUE</code> .

**Basic Use: Slots and Inheritance**

The two essential arguments, other than the class name are `representation` and `contains`, defining the explicit slots and the inheritance (superclasses). Together, these arguments define all

the information in an object from this class; that is, the names of all the slots and the classes required for each of them.

The name of the class determines which methods apply directly to objects from this class. The inheritance information specifies which methods apply indirectly, through inheritance. See [Methods](#).

The slots in a class definition will be the union of all the slots specified directly by `representation` and all the slots in all the contained classes. There can only be one slot with a given name; specifically, the direct and inherited slot names must be unique. That does not, however, prevent the same class from being inherited via more than one path.

One kind of element in the `contains=` argument is special, specifying one of the R object types or one of a few other special R types (`matrix` and `array`). See the section on inheriting from object types, below.

Certain slot names are not allowed in the current implementation, as they correspond to [attributes](#) which are treated specially. These are `class`, `comment`, `dim`, `dimnames`, `names`, `row.names` and `tsp`. Some other slot names have special meaning; these names start with the "." character. To be safe, you should define all of your own slots with names starting with an alphabetic character.

### Inheriting from Object Types

In addition to containing other S4 classes, a class definition can contain either an S3 class (see the next section) or a built-in R pseudo-class—one of the R object types or one of the special R pseudo-classes `"matrix"` and `"array"`. A class can contain at most one of the object types, directly or indirectly. When it does, that contained class determines the “data part” of the class.

Objects from the new class try to inherit the built in behavior of the contained type. In the case of normal R data types, including vectors, functions and expressions, the implementation is relatively straightforward. For any object `x` from the class, `typeof(x)` will be the contained basic type; and a special pseudo-slot, `.Data`, will be shown with the corresponding class. See the `"numWithId"` example below.

For an object from any class that does *not* contain such a type, `typeof(x)` will be `"S4"`.

Some R data types do not behave normally, in the sense that they are non-local references or other objects that are not duplicated. Examples include those corresponding to classes `"environment"`, `"externalptr"`, and `"name"`. These can not be the types for objects with user-defined classes (either S4 or S3) because setting an attribute overwrites the object in all contexts. It is possible to define a class that inherits from such types, through an indirect mechanism that stores the inherited object in a reserved slot. The implementation tries to make such classes behave as if the object had a data part of the corresponding object type. Methods defined with the object type in the signature should work as should core code that coerces an object to the type in an internal or primitive calculation. There is no guarantee, however, because C-level code may switch directly on the object type, which in this case will be `"S4"`. The cautious mechanism is to use `as(x, "environment")` or something similar before doing the low-level computation. See the example for class `"stampedEnv"` below.

Also, keep in mind that the object passed to the low-level computation will be the underlying object type, *without* any of the slots defined in the class. To return the full information, you will usually have to define a method that sets the data part.

Note that, in the current implementation, the interpretation of the `".Data"` pseudo-slot includes all of the object types above, as well as the special pseudo-classes `"matrix"` and `"array"`, which R treats internally as if they were object types (they have no explicit class and `is.object` returns `FALSE` for such objects). Some of this implementation is still experimental, so a wise policy is to use standard tools, such as `as(object, type)`, to convert to the underlying data type, rather than the pseudo-slot, when possible.

## Inheriting from S3 Classes

Old-style S3 classes have no formal definition. Objects are “from” the class when their class attribute contains the character string considered to be the class name.

Using such classes with formal classes and methods is necessarily a risky business, since there are no guarantees about the content of the objects or about consistency of inherited methods. Given that, it is still possible to define a class that inherits from an S3 class, providing that class has been registered as an old class (see [setOldClass](#)). The essential result is that S3 method dispatch will use the S3 class as registered when dispatching.

Some additional options are planned, to control whether the object is converted to an S3 class before dispatch. In the present implementation, it is not, which causes some S3 computations to misbehave, since they are not seeing the S3 class explicitly.

## Classes and Packages

Class definitions normally belong to packages (but can be defined in the global environment as well, by evaluating the expression on the command line or in a file sourced from the command line). The corresponding package name is part of the class definition; that is, part of the `classRepresentation` object holding that definition. Thus, two classes with the same name can exist in different packages, for most purposes.

When a class name is supplied for a slot or a superclass, a corresponding class definition will be found, looking from the name space or environment of the current package, assuming the call to `setClass` in question appears directly in the source for the package. That’s where it should appear, to avoid ambiguity.

In particular, if the current package has a name space then the class must be found in the current package itself, in the imports defined by that name space, or in the base package.

When this rule does not identify a class uniquely (because it appears in more than one imported package) then the `packageSlot` of the character string name needs to be supplied with the name. This should be a rare occurrence.

## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

## See Also

[Classes](#) for a general discussion of classes, [Methods](#) for an analogous discussion of methods, [makeClassRepresentation](#)

## Examples

```
## A simple class with two slots
setClass("track",
  representation(x="numeric", y="numeric"))
## A class extending the previous, adding one more slot
setClass("trackCurve",
  representation(smooth = "numeric"),
  contains = "track")
## A class similar to "trackCurve", but with different structure
## allowing matrices for the "y" and "smooth" slots
setClass("trackMultiCurve",
```



```

      representation(x="numeric", y="matrix", smooth="matrix"),
      prototype = list(x=numeric(), y=matrix(0,0,0),
                      smooth= matrix(0,0,0)))
##
## Suppose we want trackMultiCurve to be like trackCurve when there's
## only one column.
## First, the wrong way.
try(setIs("trackMultiCurve", "trackCurve",
        test = function(obj) {ncol(slot(obj, "y")) == 1}))

## Why didn't that work? You can only override the slots "x", "y",
## and "smooth" if you provide an explicit coerce function to correct
## any inconsistencies:

setIs("trackMultiCurve", "trackCurve",
      test = function(obj) {ncol(slot(obj, "y")) == 1},
      coerce = function(obj) {
        new("trackCurve",
            x = slot(obj, "x"),
            y = as.numeric(slot(obj, "y")),
            smooth = as.numeric(slot(obj, "smooth")))
      })

## A class that extends the built-in data type "numeric"

setClass("numWithId", representation(id = "character"),
        contains = "numeric")

new("numWithId", 1:3, id = "An Example")

## inherit from reference object of type "environment"
setClass("stampedEnv", contains = "environment",
        representation(update = "POSIXct"))

e1 <- new("stampedEnv", new.env(), update = Sys.time())

setMethod("[[<-", c("stampedEnv", "character", "missing"),
  function(x, i, j, ..., value) {
    ev <- as(x, "environment")
    ev[[i]] <- value #update the object in the environment
    x@update <- Sys.time() # and the update time
    x})

e1[["noise"]] <- rnorm(10)

```

---

setClassUnion

*Classes Defined as the Union of Other Classes*


---

## Description

A class may be defined as the *union* of other classes; that is, as a virtual class defined as a superclass of several other classes. Class unions are useful in method signatures or as slots in other classes, when we want to allow one of several classes to be supplied.

**Usage**

```
setClassUnion(name, members, where)
isClassUnion(Class)
```

**Arguments**

name	the name for the new union class.
members	the classes that should be members of this union.
where	where to save the new class definition; by default, the environment of the package in which the <code>setClassUnion</code> call appears, or the global environment if called outside of the source of a package.
Class	the name or definition of a class.

**Details**

The classes in `members` must be defined before creating the union. However, members can be added later on to an existing union, as shown in the example below. Class unions can be members of other class unions.

Class unions are the only way to create a class that is extended by a class whose definition is sealed (for example, the basic datatypes or other classes defined in the base or methods package in R are sealed). You cannot say `setIs("function", "other")` unless "other" is a class union. In general, a `setIs` call of this form changes the definition of the first class mentioned (adding "other" to the list of superclasses contained in the definition of "function").

Class unions get around this by not modifying the first class definition, relying instead on storing information in the subclasses slot of the class union. In order for this technique to work, the internal computations for expressions such as `extends(class1, class2)` work differently for class unions than for regular classes; specifically, they test whether any class is in common between the superclasses of `class1` and the subclasses of `class2`.

The different behavior for class unions is made possible because the class definition object for class unions has itself a special class, "ClassUnionRepresentation", an extension of class `classRepresentation`.

**References**

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

**Examples**

```
## a class for either numeric or logical data
setClassUnion("maybeNumber", c("numeric", "logical"))

## use the union as the data part of another class
setClass("withId", representation("maybeNumber", id = "character"))

w1 <- new("withId", 1:10, id = "test 1")
w2 <- new("withId", sqrt(w1)%%1 < .01, id = "Perfect squares")

## add class "complex" to the union "maybeNumber"
setIs("complex", "maybeNumber")
```

```
w3 <- new("withId", complex(real = 1:10, imaginary = sqrt(1:10)))

## a class union containing the existing class union "OptionalFunction"
setClassUnion("maybeCode",
  c("expression", "language", "OptionalFunction"))

is(quote(sqrt(1:10)), "maybeCode") ## TRUE
```

---

 setGeneric

*Define a New Generic Function*


---

### Description

Create a new generic function of the given name, that is, a function that dispatches methods according to the classes of the arguments, from among the formal methods defined for this function.

### Usage

```
setGeneric(name, def= , group=list(), valueClass=character(),
  where= , package= , signature= , useAsDefault= ,
  genericFunction= , simpleInheritanceOnly = )

setGroupGeneric(name, def= , group=list(), valueClass=character(),
  knownMembers=list(), package= , where= )
```

### Arguments

name	The character string name of the generic function. The simplest (and recommended) call, <code>setGeneric(name)</code> , looks for a function with this name and creates a corresponding generic function, if the function found was not generic.
def	An optional function object, defining the generic. Don't supply this argument if you want an existing non-generic function to supply the arguments. Do supply it if there is no current function of this name, or if you want the generic function to have different arguments. In that case, the formal arguments and default values for the generic are taken from <code>def</code> . You can also supply this argument if you want the generic function to do something other than just dispatch methods. Note that <code>def</code> is <i>not</i> the default method; use argument <code>useAsDefault</code> if you want to specify the default separately.
group	Optionally, a character string giving the name of the group generic function to which this function belongs. See <a href="#">Methods</a> for details of group generic functions in method selection.
valueClass	An optional character vector of one or more class names. The value returned by the generic function must have (or extend) this class, or one of the classes; otherwise, an error is generated.
package	The name of the package with which this function is associated. Usually determined automatically (as the package containing the non-generic version if there is one, or else the package where this generic is to be saved).
where	Where to store the resulting initial methods definition, and possibly the generic function; by default, stored into the top-level environment.

- `signature` Optionally, the vector of names, from among the formal arguments to the function, that can appear in the signature of methods for this function, in calls to `setMethod`. If `...` is one of the formal arguments, it is treated specially. Starting with version 2.8.0 of R, `...` may be signature of the generic function. Methods will then be selected if their signature matches all the `...` arguments. See the documentation for topic `dotsMethods` for details. In the present version, it is not possible to mix `...` and other arguments in the signature (this restriction may be lifted in later versions).
- By default, the signature is inferred from the implicit generic function corresponding to a non-generic function. If no implicit generic function has been defined, the default is all the formal arguments except `...`, in the order they appear in the function definition. In the case that `...` is the only formal argument, that is also the default signature. To use `...` as the signature in a function that has any other arguments, you must supply the signature argument explicitly. See the “Implicit Generic” section below for more details.
- `useAsDefault` Override the usual choice of default argument (an existing non-generic function or no default if there is no such function). Argument `useAsDefault` can be supplied, either as a function to use for the default, or as a logical value. `FALSE` says not to have a default method at all, so that an error occurs if there is not an explicit or inherited method for a call. `TRUE` says to use the existing function as default, unconditionally (hardly ever needed as an explicit argument). See the section on details.
- `simpleInheritanceOnly` Supply this argument as `TRUE` to require that methods selected be inherited through simple inheritance only; that is, from superclasses specified in the `contains=` argument to `setClass`, or by simple inheritance to a class union or other virtual class. Generic functions should require simple inheritance if they need to be assured that they get the complete original object, not one that has been transformed. Examples of functions requiring simple inheritance are `initialize`, because by definition it must return an object from the same class as its argument, and `show`, because it claims to give a full description of the object provided as its argument.
- `genericFunction` Don't use; for (possible) internal use only.
- `knownMembers` (For `setGroupGeneric` only.) The names of functions that are known to be members of this group. This information is used to reset cached definitions of the member generics when information about the group generic is changed.

## Value

The `setGeneric` function exists for its side effect: saving the generic function to allow methods to be specified later. It returns `name`.

## Basic Use

The `setGeneric` function is called to initialize a generic function as preparation for defining some methods for that function.

The simplest and most common situation is that `name` is already an ordinary non-generic non-primitive function, and you now want to turn this function into a generic. In this case you will most often supply only `name`, for example:

```
setGeneric("colSums")
```

There must be an existing function of this name, on some attached package (in this case package "base"). A generic version of this function will be created in the current package (or in the global environment if the call to `setGeneric()` is from an ordinary source file or is entered on the command line). The existing function becomes the default method, and the package slot of the new generic function is set to the location of the original function ("base" in the example). It's an important feature that the same generic function definition is created each time, depending in the example only on the definition of `print` and where it is found. The signature of the generic function, defining which of the formal arguments can be used in specifying methods, is set by default to all the formal arguments except ...

Note that calling `setGeneric()` in this form is not strictly necessary before calling `setMethod()` for the same function. If the function specified in the call to `setMethod` is not generic, `setMethod` will execute the call to `setGeneric` itself. Declaring explicitly that you want the function to be generic can be considered better programming style; the only difference in the result, however, is that not doing so produces a message noting the creation of the generic function.

You cannot (and never need to) create an explicit generic version of the primitive functions in the base package. Those which can be treated as generic functions have methods selected and dispatched from the internal C code, to satisfy concerns for efficiency, and the others cannot be made generic. See the section on Primitive Functions below.

The description above is the effect when the package that owns the non-generic function has not created an implicit generic version. Otherwise, it is this implicit generic function that is used. See the section on Implicit Generic Functions below. Either way, the essential result is that the *same* version of the generic function will be created each time.

The second common use of `setGeneric()` is to create a new generic function, unrelated to any existing function, and frequently having no default method. In this case, you need to supply a skeleton of the function definition, to define the arguments for the function. The body of a generic function is usually a standard form, `standardGeneric(name)` where `name` is the quoted name of the generic function. When calling `setGeneric` in this form, you would normally supply the `def` argument as a function of this form. See the second and third examples below.

The `useAsDefault` argument controls the default method for the new generic. If not told otherwise, `setGeneric` will try to find a non-generic version of the function to use as a default. So, if you do have a suitable default method, it is often simpler to first set this up as a non-generic function, and then use the one-argument call to `setGeneric` at the beginning of this section. See the first example in the Examples section below.

If you *don't* want the existing function to be taken as default, supply the argument `useAsDefault`. That argument can be the function you want to be the default method, or `FALSE` to force no default (i.e., to cause an error if there is no direct or inherited method selected for a call to the function).

## Details

If you want to change the behavior of an existing function (typically, one in another package) when you create a generic version, you must supply arguments to `setGeneric` correspondingly. Whatever changes are made, the new generic function will be assigned with a package slot set to the *current* package, not the one in which the non-generic version of the function is found. This step is required because the version you are creating is no longer the same as that implied by the function in the other package. A message will be printed to indicate that this has taken place and noting one of the differences between the two functions.

The body of a generic function usually does nothing except for dispatching methods by a call to `standardGeneric`. Under some circumstances you might just want to do some additional computation in the generic function itself. As long as your function eventually calls

standardGeneric that is permissible (though perhaps not a good idea, in that it may make the behavior of your function less easy to understand). If your explicit definition of the generic function does *not* call standardGeneric you are in trouble, because none of the methods for the function will ever be dispatched.

By default, the generic function can return any object. If valueClass is supplied, it should be a vector of class names; the value returned by a method is then required to satisfy is(object, Class) for one of the specified classes. An empty (i.e., zero length) vector of classes means anything is allowed. Note that more complicated requirements on the result can be specified explicitly, by defining a non-standard generic function.

The setGroupGeneric function behaves like setGeneric except that it constructs a group generic function, differing in two ways from an ordinary generic function. First, this function cannot be called directly, and the body of the function created will contain a stop call with this information. Second, the group generic function contains information about the known members of the group, used to keep the members up to date when the group definition changes, through changes in the search list or direct specification of methods, etc.

### Implicit Generic Functions

Saying that a non-generic function “is converted to a generic” is more precisely state that the function is converted to the corresponding *implicit* generic function. If no special action has been taken, any function corresponds implicitly to a generic function with the same arguments, in which all arguments other than ... can be used. The signature of this generic function is the vector of formal arguments, in order, except for ...

The source code for a package can define an implicit generic function version of any function in that package (see [implicitGeneric](#) for the mechanism). You can not, generally, define an implicit generic function in someone else’s package. The usual reason for defining an implicit generic is to prevent certain arguments from appearing in the signature, which you must do if you want the arguments to be used literally or if you want to enforce lazy evaluation for any reason. An implicit generic can also contain some methods that you want to be predefined; in fact, the implicit generic can be any generic version of the non-generic function. The implicit generic mechanism can also be used to prohibit a generic version (see [prohibitGeneric](#)).

Whether defined or inferred automatically, the implicit generic will be compared with the generic function that setGeneric creates, when the implicit generic is in another package. If the two functions are identical, then the package slot of the created generic will have the name of the package containing the implicit generic. Otherwise, the slot will be the name of the package in which the generic is assigned.

The purpose of this rule is to ensure that all methods defined for a particular combination of generic function and package names correspond to a single, consistent version of the generic function. Calling setGeneric with only name and possibly package as arguments guarantees getting the implicit generic version, if one exists.

Including any of the other arguments can force a new, local version of the generic function. If you don’t want to create a new version, don’t use the extra arguments.

### Generic Functions and Primitive Functions

A number of the basic R functions are specially implemented as primitive functions, to be evaluated directly in the underlying C code rather than by evaluating an R language definition. Most have implicit generics (see [implicitGeneric](#)), and become generic as soon as methods (including group methods) are defined on them. Others cannot be made generic.

Even when methods are defined for such functions, the generic version is not visible on the search list, in order that the C version continues to be called. Method selection will be initiated in the C

code. Note, however, that the result is to restrict methods for primitive functions to signatures in which at least one of the classes in the signature is a formal S4 class.

To see the generic version of a primitive function, use `getGeneric(name)`. The function `isGeneric` will tell you whether methods are defined for the function in the current session.

Note that S4 methods can only be set on those primitives which are ‘`internal generic`’, plus `%*%`.

## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

## See Also

`Methods` and the links there for a general discussion, `dotsMethods` for methods that dispatch on “...”, and `setMethod` for method definitions.

## Examples

```
## create a new generic function, with a default method
props <- function(object) attributes(object)
setGeneric("props")

## A new generic function with no default method
setGeneric("increment",
  function(object, step, ...)
    standardGeneric("increment")
)

### A non-standard generic function. It insists that the methods
### return a non-empty character vector (a stronger requirement than
### valueClass = "character" in the call to setGeneric)

setGeneric("authorNames",
  function(text) {
    value <- standardGeneric("authorNames")
    if(!(is(value, "character") && any(nchar(value)>0)))
      stop("authorNames methods must return non-empty strings")
    value
  })

## An example of group generic methods, using the class
## "track"; see the documentation of setClass for its definition

## define a method for the Arith group

setMethod("Arith", c("track", "numeric"),
  function(e1, e2) {
    e1@y <- callGeneric(e1@y, e2)
    e1
  })
```

```

setMethod("Arith", c("numeric", "track"),
  function(e1, e2) {
    e2@y <- callGeneric(e1, e2@y)
    e2
  })

## now arithmetic operators will dispatch methods:

t1 <- new("track", x=1:10, y=sort(stats::rnorm(10)))

t1 - 100
1/t1

```

---

setMethod

---

*Create and Save a Method*


---

## Description

Create and save a formal method for a given function and list of classes.

## Usage

```

setMethod(f, signature=character(), definition,
  where = topenv(parent.frame()),
  valueClass = NULL, sealed = FALSE)

removeMethod(f, signature, where)

```

## Arguments

<code>f</code>	A generic function or the character-string name of the function.
<code>signature</code>	A match of formal argument names for <code>f</code> with the character-string names of corresponding classes. See the details below; however, if the signature is not trivial, you should use <code>method.skeleton</code> to generate a valid call to <code>setMethod</code> .
<code>definition</code>	A function definition, which will become the method called when the arguments in a call to <code>f</code> match the classes in <code>signature</code> , directly or through inheritance.
<code>where</code>	the environment in which to store the definition of the method. For <code>setMethod</code> , it is recommended to omit this argument and to include the call in source code that is evaluated at the top level; that is, either in an R session by something equivalent to a call to <code>source</code> , or as part of the R source code for a package. For <code>removeMethod</code> , the default is the location of the (first) instance of the method for this signature.
<code>valueClass</code>	Obsolete and unused, but see the same argument for <code>setGeneric</code> .
<code>sealed</code>	If <code>TRUE</code> , the method so defined cannot be redefined by another call to <code>setMethod</code> (although it can be removed and then re-assigned).



## Details

The call to `setMethod` stores the supplied method definition in the metadata table for this generic function in the environment, typically the global environment or the name space of a package. In the case of a package, the table object becomes part of the name space or environment of the package. When the package is loaded into a later session, the methods will be merged into the table of methods in the corresponding generic function object.

Generic functions are referenced by the combination of the function name and the package name; for example, the function `"show"` from the package `"methods"`. Metadata for methods is identified by the two strings; in particular, the generic function object itself has slots containing its name and its package name. The package name of a generic is set according to the package from which it originally comes; in particular, and frequently, the package where a non-generic version of the function originated. For example, generic functions for all the functions in package `base` will have `"base"` as the package name, although none of them is an S4 generic on that package. These include most of the base functions that are primitives, rather than true functions; see the section on primitive functions in the documentation for `setGeneric` for details.

Multiple packages can have methods for the same generic function; that is, for the same combination of generic function name and package name. Even though the methods are stored in separate tables in separate environments, loading the corresponding packages adds the methods to the table in the generic function itself, for the duration of the session.

The class names in the signature can be any formal class, including basic classes such as `"numeric"`, `"character"`, and `"matrix"`. Two additional special class names can appear: `"ANY"`, meaning that this argument can have any class at all; and `"missing"`, meaning that this argument *must not* appear in the call in order to match this signature. Don't confuse these two: if an argument isn't mentioned in a signature, it corresponds implicitly to class `"ANY"`, not to `"missing"`. See the example below. Old-style ('S3') classes can also be used, if you need compatibility with these, but you should definitely declare these classes by calling `setOldClass` if you want S3-style inheritance to work.

Method definitions can have default expressions for arguments, but a current limitation is that the generic function must have *some* default expression for the same argument in order for the method's defaults to be used. If so, and if the corresponding argument is missing in the call to the generic function, the default expression in the method is used. If the method definition has no default for the argument, then the expression supplied in the definition of the generic function itself is used, but note that this expression will be evaluated using the enclosing environment of the method, not of the generic function. Note also that specifying class `"missing"` in the signature does not require any default expressions, and method selection does not evaluate default expressions. All actual (non-missing) arguments in the signature of the generic function will be evaluated when a method is selected—when the call to `standardGeneric(f)` occurs.

It is possible to have some differences between the formal arguments to a method supplied to `setMethod` and those of the generic. Roughly, if the generic has `...` as one of its arguments, then the method may have extra formal arguments, which will be matched from the arguments matching `...` in the call to `f`. (What actually happens is that a local function is created inside the method, with the modified formal arguments, and the method is re-defined to call that local function.)

Method dispatch tries to match the class of the actual arguments in a call to the available methods collected for `f`. If there is a method defined for the exact same classes as in this call, that method is used. Otherwise, all possible signatures are considered corresponding to the actual classes or to superclasses of the actual classes (including `"ANY"`). The method having the least distance from the actual classes is chosen; if more than one method has minimal distance, one is chosen (the lexicographically first in terms of superclasses) but a warning is issued. All inherited methods chosen are stored in another table, so that the inheritance calculations only need to be done once per session per sequence of actual classes. See [Methods](#) for more details.

The function `removeMethod` removes the specified method from the metadata table in the corresponding environment. It's not a function that is used much, since one normally wants to redefine a method rather than leave no definition.

### Value

These functions exist for their side-effect, in setting or removing a method in the object defining methods for the specified generic.

The value returned by `removeMethod` is `TRUE` if a method was found to be removed.

### References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

### See Also

[method.skeleton](#), which is the recommended way to generate a skeleton of the call to `setMethod`, with the correct formal arguments and other details.

[Methods](#) and the links there for a general discussion, [dotsMethods](#) for methods that dispatch on "...", and [setGeneric](#) for generic functions.

### Examples

```
require(graphics)
## methods for plotting track objects (see the example for \link{setClass})
##
## First, with only one object as argument:
setMethod("plot", signature(x="track", y="missing"),
  function(x, y, ...) plot(slot(x, "x"), slot(x, "y"), ...)
)
## Second, plot the data from the track on the y-axis against anything
## as the x data.
setMethod("plot", signature(y = "track"),
  function(x, y, ...) plot(x, slot(y, "y"), ...)
)
## and similarly with the track on the x-axis (using the short form of
## specification for signatures)
setMethod("plot", "track",
  function(x, y, ...) plot(slot(x, "y"), y, ...)
)
t1 <- new("track", x=1:20, y=(1:20)^2)
tc1 <- new("trackCurve", t1)
slot(tc1, "smooth") <- smooth.spline(slot(tc1, "x"), slot(tc1, "y"))$y # $
plot(tc1)
plot(qnorm(ppoints(20)), t1)
## An example of inherited methods, and of conforming method arguments
## (note the dotCurve argument in the method, which will be pulled out
## of ... in the generic.
setMethod("plot", c("trackCurve", "missing"),
function(x, y, dotCurve = FALSE, ...) {
  plot(as(x, "track"))
  if(length(slot(x, "smooth") > 0))
```

```

        lines(slot(x, "x"), slot(x, "smooth"),
              lty = if(dotCurve) 2 else 1)
      }
    )
## the plot of tcl alone has an added curve; other uses of tcl
## are treated as if it were a "track" object.
plot(tcl, dotCurve = TRUE)
plot(qnorm(ppoints(20)), tcl)

## defining methods for a special function.
## Although "[" and "length" are not ordinary functions
## methods can be defined for them.
setMethod("[", "track",
  function(x, i, j, ..., drop) {
    x@x <- x@x[i]; x@y <- x@y[i]
    x
  })
plot(t1[1:15])

setMethod("length", "track", function(x)length(x@y))
length(t1)

## methods can be defined for missing arguments as well
setGeneric("summary") ## make the function into a generic

## A method for summary()
## The method definition can include the arguments, but
## if they're omitted, class "missing" is assumed.

setMethod("summary", "missing", function() "<No Object>")

```

---

setOldClass

*Register Old-Style (S3) Classes and Inheritance*


---

## Description

Register an old-style (a.k.a. ‘S3’) class as a formally defined class. The `Classes` argument is the character vector used as the `class` attribute; in particular, if there is more than one string, old-style class inheritance is mimicked. Registering via `setOldClass` allows S3 classes to appear in method signatures, as a slot in an S4 class, or as a superclass of an S4 class.

## Usage

```
setOldClass(Classes, prototype, where, test = FALSE, S4Class)
```

## Arguments

<code>Classes</code>	A character vector, giving the names for S3 classes, as they would appear on the right side of an assignment of the <code>class</code> attribute in S3 computations. In addition to S3 classes, an object type or other valid data part can be specified, if the S3 class is known to require its data to be of that form.
----------------------	--

<code>prototype</code>	An optional object to use as the prototype. This should be provided as the default S3 object for the class. If omitted, the S4 class created to register the S3 class is <code>VIRTUAL</code> . See the details.
<code>where</code>	Where to store the class definitions, the global or top-level environment by default. (When either function is called in the source for a package, the class definitions will be included in the package's environment by default.)
<code>test</code>	flag, if <code>TRUE</code> , arrange to test inheritance explicitly for each object, needed if the S3 class can have a different set of class strings, with the same first string. This is a different mechanism in implementation and should be specified separately for each pair of classes that have an optional inheritance. See the details below.
<code>S4Class</code>	optionally, the class definition or the class name of an S4 class. The new class will have all the slots and other properties of this class, plus its S3 inheritance as defined by the <code>Classes</code> argument. Arguments <code>prototype</code> and <code>test</code> must not be supplied in this case. See the section on "S3 classes with known attributes" below.

## Details

Each of the names will be defined as an S4 class, extending the remaining classes in `Classes`, and the class `oldClass`, which is the 'root' of all old-style classes. S3 classes have no formal definition, and therefore no formally defined slots. If a `prototype` argument is supplied in the call to `setOldClass()`, objects from the class can be generated, by a call to `new`; however, this usually not as relevant as generating objects from subclasses (see the section on extending S3 classes below). If a prototype is not provided, the class will be created as a virtual S4 class. The main disadvantage is that the prototype object in an S4 class that uses this class as a slot will have a `NULL` object in that slot, which can sometimes lead to confusion.

Beginning with version 2.8.0 of R, support is provided for using a (registered) S3 class as a super class of a new S4 class. See the section on extending S3 classes below, and the examples.

See [Methods](#) for the details of method dispatch and inheritance.

Some S3 classes cannot be represented as an ordinary combination of S4 classes and superclasses, because objects from the S3 class can have a variable set of strings in the class. It is still possible to register such classes as S4 classes, but now the inheritance has to be verified for each object, and you must call `setOldClass` with argument `test=TRUE` once for each superclass.

For example, ordered factors *always* have the S3 class `c("ordered", "factor")`. This is proper behavior, and maps simply into two S4 classes, with "ordered" extending "factor".

But objects whose class attribute has "POSIXt" as the first string may have either (or neither) of "POSIXct" or "POSIXlt" as the second string. This behavior can be mapped into S4 classes but now to evaluate `is(x, "POSIXlt")`, for example, requires checking the S3 class attribute on each object. Supplying the `test=TRUE` argument to `setOldClass` causes an explicit test to be included in the class definitions. It's never wrong to have this test, but since it adds significant overhead to methods defined for the inherited classes, you should only supply this argument if it's known that object-specific tests are needed.

The list `.OldClassesList` contains the old-style classes that are defined by the methods package. Each element of the list is a character vector, with multiple strings if inheritance is included.

Each element of the list was passed to `setOldClass` when creating the **methods** package; therefore, these classes can be used in `setMethod` calls, with the inheritance as implied by the list.

## Extending S3 classes

A call to `setOldClass` creates formal classes corresponding to S3 classes, allows these to be used as slots in other classes or in a signature in `setMethod`, and mimics the S3 inheritance.

In documentation for the initial implementation of S4 classes in R, users were warned against defining S4 classes that contained S3 classes, even if those had been registered. The warning was based mainly on two points. 1: The S3 behavior of the objects would fail because the S3 class would not be visible, for example, when S3 methods are dispatched. 2: Because S3 classes have no formal definition, nothing can be asserted in general about the S3 part of an object from such a class. (The warning was repeated as recently as the first reference below.)

Nevertheless, defining S4 classes to contain an S3 class and extend its behavior is attractive in many applications. The alternative is to be stuck with S3 programming, without the flexibility and security of formal class and method definitions.

Beginning with version 2.8.0, R provides support for extending registered S3 classes; that is, for new classes defined by a call to `setClass` in which the `contains=` argument includes an S3 class. See the examples below. The support is aimed primarily at providing the S3 class information for all classes that extend class `oldClass`, in particular by ensuring that all objects from such classes contain the S3 class in a special slot.

There are three different ways to indicate an extension to an existing S3 class: `setOldClass()`, `setClass()` and `setIs()`. In most cases, calling `setOldClass` is the best approach, but the alternatives may be preferred in the special circumstances described below.

Suppose "A" is any class extending "oldClass". then

```
setOldClass(c("B", "A"))
```

creates a new class "B" whose S3 class concatenates "B" with `S3Class("A")`. The new class is a virtual class. If "A" was defined with known attribute/slots, then "B" has these slots also; therefore, you must believe that the corresponding S3 objects from class "B" do indeed have the claimed attributes. Notice that you can supply an S4 definition for the new class to specify additional attributes (as described in the next section.) The first alternative call produces a non-virtual class.

```
setClass("B", contains = "A")
```

This creates a non-virtual class with the same slots and superclasses as class "A". However, class "B" is not included in the S3 class slot of the new class, unless you provide it explicitly in the prototype.

```
setClass("B"); setIs("B", "A", .....)
```

This creates a virtual class that extends "A", but does not contain the slots of "A". The additional arguments to `setIs` should provide a coerce and replacement method. In order for the new class to inherit S3 methods, the coerce method must ensure that the class "A" object produced has a suitable S3 class. The only likely reason to prefer this third approach is that class "B" is not consistent with known attributes in class "A".

Beginning with version 2.9.0 of R, objects from a class extending an S3 class will be converted to the corresponding S3 class when being passed to an S3 method defined for that class (that is, for one of the strings in the S3 class attribute). This is intended to ensure, as far as possible, that such methods will work if they work for ordinary S3 objects. See [Classes](#) for details.

### S3 Classes with known attributes

A further specification of an S3 class can be made *if* the class is guaranteed to have some attributes of known class (where as with slots, "known" means that the attribute is an object of a specified class, or a subclass of that class).

In this case, the call to `setOldClass()` can supply an S4 class definition representing the known structure. Since S4 slots are implemented as attributes (largely for just this reason), the known attributes can be specified in the representation of the S4 class. The usual technique will be to create an S4 class with the desired structure, and then supply the class name or definition as the argument `S4Class` to `setOldClass()`.

See the definition of class "ts" in the examples below. The call to `setClass` to create the S4 class can use the same class name, as here, so long as the class definition is not sealed. In the example, we define "ts" as a vector structure with a numeric slot for "tsp". The validity of this definition relies on an assertion that all the S3 code for this class is consistent with that definition; specifically, that all "ts" objects will behave as vector structures and will have a numeric "tsp" attribute. We believe this to be true of all the base code in R, but as always with S3 classes, no guarantee is possible.

The S4 class definition can have virtual superclasses (as in the "ts" case) if the S3 class is asserted to behave consistently with these (in the example, time-series objects are asserted to be consistent with the `structure` class).

For another example, look at the S4 class definition for "data.frame".

Be warned that failures of the S3 class to live up to its asserted behavior will usually go uncorrected, since S3 classes inherently have no definition, and the resulting invalid S4 objects can cause all sorts of grief. Many S3 classes are not candidates for known slots, either because the presence or class of the attributes are not guaranteed (e.g., `dimnames` in arrays, although these are not even S3 classes), or because the class uses named components of a list rather than attributes (e.g., "lm"). An attribute that is sometimes missing cannot be represented as a slot, not even by pretending that it is present with class "NULL", because attributes unlike slots can not have value NULL.

One irregularity that is usually tolerated, however, is to optionally add other attributes to those guaranteed to exist (for example, "terms" in "data.frame" objects returned by `model.frame`). As of version 2.8.0, validity checks by `validObject` ignore extra attributes; even if this check is tightened in the future, classes extending S3 classes would likely be exempted because extra attributes are so common.

## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version: see section 10.6 for method selection and section 13.4 for generic functions).

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

## See Also

[setClass](#), [setMethod](#)

## Examples

```
require(stats)
setOldClass(c("mlm", "lm"))
setGeneric("dfResidual", function(model) standardGeneric("dfResidual"))
setMethod("dfResidual", "lm", function(model) model$df.residual)

## dfResidual will work on mlm objects as well as lm objects
myData <- data.frame(time = 1:10, y = (1:10)^.5)
myLm <- lm(cbind(y, y^3) ~ time, myData)

showClass("data.frame")# to see the predefined S4 "oldClass"

## two examples extending S3 class "lm", class "xlm" directly and "ylm" indirectly
setClass("xlm", representation(eps = "numeric"), contains = "lm")
setClass("ylm", representation(header = "character"), contains = "xlm")
yml = new("ylm", myLm, header = "Example", eps = 0.)
## for more examples, see ?\link{S3Class}.
```

```

utils::str(.OldClassesList)

## Examples of S3 classes with guaranteed attributes
## an S3 class "stamped" with a vector and a "date" attribute
## Here is a generator function and an S3 print method.
## NOTE: it's essential that the generator checks the attribute classes
stamped <- function(x, date = Sys.time()) {
  if(!inherits(date, "POSIXt"))
    stop("bad date argument")
  if(!is.vector(x))
    stop("x must be a vector")
  attr(x, "date") <- date
  class(x) <- "stamped"
  x
}

print.stamped <- function(x, ...) {
  print(as.vector(x))
  cat("Date: ", format(attr(x,"date")), "\n")
}

## Now, an S4 class with the same structure:
setClass("stamped4", contains = "vector", representation(date = "POSIXt"))

## We can use the S4 class to register "stamped", with its attributes:
setOldClass("stamped", S4Class = "stamped4")
selectMethod("show", "stamped")
## and then remove "stamped4" to clean up
removeClass("stamped4")

someLetters <- stamped(sample(letters, 10), ISOdatetime(2008, 10, 15, 12, 0, 0))

st <- new("stamped", someLetters)
st # show() method prints the object's class, then calls the S3 print method.

stopifnot(identical(S3Part(st, TRUE), someLetters))

# creating the S4 object directly from its data part and slots
new("stamped", 1:10, date = ISOdatetime(1976, 5, 5, 15, 10, 0))

## Not run:
## The code in R that defines "ts" as an S4 class
setClass("ts", contains = "structure",
  representation(tsp = "numeric"),
  prototype(NA, tsp = rep(1,3))) # prototype to be a legal S3 time-series
## and now registers it as an S3 class
setOldClass("ts", S4Class = "ts", where = envir)

## End(Not run)

```

---

`show`*Show an Object*

---

## Description

Display the object, by printing, plotting or whatever suits its class. This function exists to be specialized by methods. The default method calls `showDefault`.

Formal methods for `show` will usually be invoked for automatic printing (see the details).

## Usage

```
show(object)
```

## Arguments

`object` Any R object

## Details

Objects from an S4 class (a class defined by a call to `setClass`) will be displayed automatically if by a call to `show`. S4 objects that occur as attributes of S3 objects will also be displayed in this form; conversely, S3 objects encountered as slots in S4 objects will be printed using the S3 convention, as if by a call to `print`.

Methods defined for `show` will only be inherited by simple inheritance, since otherwise the method would not receive the complete, original object, with misleading results. See the `simpleInheritanceOnly` argument to `setGeneric` and the discussion in `setIs` for the general concept.

## Value

`show` returns an invisible `NULL`.

## See Also

`showMethods` prints all the methods for one or more functions; `showMlist` prints individual methods lists; `showClass` prints class definitions. Neither of the latter two normally needs to be called directly.

## Examples

```
## following the example shown in the setMethod documentation ...
setClass("track",
         representation(x="numeric", y="numeric"))
setClass("trackCurve",
         representation("track", smooth = "numeric"))

t1 <- new("track", x=1:20, y=(1:20)^2)

tc1 <- new("trackCurve", t1)

setMethod("show", "track",
         function(object)print(rbind(x = object@x, y=object@y)))
```



```

)
## The method will now be used for automatic printing of t1

t1

## Not run:  [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
x   1   2   3   4   5   6   7   8   9  10  11  12
y   1   4   9  16  25  36  49  64  81 100 121 144
  [,13] [,14] [,15] [,16] [,17] [,18] [,19] [,20]
x   13  14  15  16  17  18  19  20
y  169 196 225 256 289 324 361 400

## End(Not run)
## and also for tcl, an object of a class that extends "track"
tcl

## Not run:  [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
x   1   2   3   4   5   6   7   8   9  10  11  12
y   1   4   9  16  25  36  49  64  81 100 121 144
  [,13] [,14] [,15] [,16] [,17] [,18] [,19] [,20]
x   13  14  15  16  17  18  19  20
y  169 196 225 256 289 324 361 400

## End(Not run)

```

---

```
showMethods
```

*Show all the methods for the specified function(s)*

---

## Description

Show a summary of the methods for one or more generic functions, possibly restricted to those involving specified classes.

## Usage

```

showMethods(f = character(), where = topenv(parent.frame()),
            classes = NULL, includeDefs = FALSE,
            inherited = !includeDefs,
            showEmpty, printTo = stdout(), fdef)

```

## Arguments

**f** one or more function names. If omitted, all functions will be shown that match the other arguments.  
 The argument can also be an expression that evaluates to a single generic function, in which case argument `fdef` is ignored. Providing an expression for the function allows examination of hidden or anonymous functions; see the example for `isDiagonal()`.

**where** Where to find the generic function, if not supplied as an argument. When `f` is missing, or length 0, this also determines which generic functions to examine. If `where` is supplied, only the generic functions returned by `getGenerics(where)` are eligible for printing. If `where` is also missing, all the cached generic functions are considered.

<code>classes</code>	If argument <code>classes</code> is supplied, it is a vector of class names that restricts the displayed results to those methods whose signatures include one or more of those classes.
<code>includeDefs</code>	If <code>includeDefs</code> is TRUE, include the definitions of the individual methods in the printout.
<code>inherited</code>	logical indicating if methods that have been found by inheritance, so far in the session, will be included and marked as inherited. Note that an inherited method will not usually appear until it has been used in this session. See <a href="#">selectMethod</a> if you want to know what method would be dispatched for particular classes of arguments.
<code>showEmpty</code>	logical indicating whether methods with no defined methods matching the other criteria should be shown at all. By default, TRUE if and only if argument <code>f</code> is not missing.
<code>printTo</code>	The connection on which the information will be shown; by default, on standard output.
<code>fdef</code>	Optionally, the generic function definition to use; if missing, one is found, looking in <code>where</code> if that is specified. See also comment in ‘Details’.

### Details

The name and package of the generic are followed by the list of signatures for which methods are currently defined, according to the criteria determined by the various arguments. Note that the package refers to the source of the generic function. Individual methods for that generic can come from other packages as well.

When more than one generic function is involved, either as specified or because `f` was missing, the functions are found and `showMethods` is recalled for each, including the generic as the argument `fdef`. In complicated situations, this can avoid some anomalous results.

### Value

If `printTo` is FALSE, the character vector that would have been printed is returned; otherwise the value is the connection or filename, via [invisible](#).

### References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

### See Also

[setMethod](#), and [GenericFunctions](#) for other tools involving methods; [selectMethod](#) will show you the method dispatched for a particular function and signature of classes for the arguments.

### Examples

```
require(graphics)

## Assuming the methods for plot
## are set up as in the example of help(setMethod),
## print (without definitions) the methods that involve class "track":
```

```

showMethods("plot", classes = "track")
## Not run:
# Function "plot":
# x = ANY, y = track
# x = track, y = missing
# x = track, y = ANY

require("Matrix")
showMethods("%*%")# many!
  methods(class = "Matrix")# nothing
showMethods(class = "Matrix")# everything
showMethods(Matrix:::isDiagonal) # a non-exported generic

## End(Not run)

not.there <- !any("package:stats4" == search())
if(not.there) library(stats4)
showMethods(classes = "mle")
if(not.there) detach("package:stats4")

```

---

signature-class      *Class "signature" For Method Definitions*

---

## Description

This class represents the mapping of some of the formal arguments of a function onto the names of some classes. It is used as one of two slots in the [MethodDefinition](#) class.

## Objects from the Class

Objects can be created by calls of the form `new("signature", functionDef, ...)`. The `functionDef` argument, if it is supplied as a function object, defines the formal names. The other arguments define the classes.

## Slots

`.Data`: Object of class "character" the classes.

`names`: Object of class "character" the corresponding argument names.

## Extends

Class "character", from data part. Class "vector", by class "character".

## Methods

**initialize** signature(object = "signature"): see the discussion of objects from the class, above.

## See Also

class [MethodDefinition](#) for the use of this class.

---

`slot`*The Slots in an Object from a Formal Class*

---

## Description

These functions return or set information about the individual slots in an object.

## Usage

```
object@name
object@name <- value

slot(object, name)
slot(object, name, check = TRUE) <- value

slotNames(x)
getSlots(x)
```

## Arguments

<code>object</code>	An object from a formally defined class.
<code>name</code>	The name of the slot. The operator takes a fixed name, which can be unquoted if it is syntactically a name in the language. A slot name can be any non-empty string, but if the name is not made up of letters, numbers, and <code>.</code> , it needs to be quoted (by backticks or single or double quotes). In the case of the <code>slot</code> function, <code>name</code> can be any expression that evaluates to a valid slot in the class definition. Generally, the only reason to use the functional form rather than the simpler operator is <i>because</i> the slot name has to be computed.
<code>value</code>	A new value for the named slot. The value must be valid for this slot in this object's class.
<code>check</code>	In the replacement version of <code>slot</code> , a flag. If <code>TRUE</code> , check the assigned value for validity as the value of this slot. User's coded should not set this to <code>FALSE</code> in normal use, since the resulting object can be invalid.
<code>x</code>	either the name of a class (as character string), or a class definition. If given an argument that is neither a character string nor a class definition, <code>slotNames</code> (only) uses <code>class(x)</code> instead.

## Details

The definition of the class specifies all slots directly and indirectly defined for that class. Each slot has a name and an associated class. Extracting a slot returns an object from that class. Setting a slot first coerces the value to the specified slot and then stores it.

Unlike general attributes, slots are not partially matched, and asking for (or trying to set) a slot with an invalid name for that class generates an error.

The `@` extraction operator and `slot` function themselves do no checking against the class definition, simply matching the name in the object itself. The replacement forms do check (except for `slot`

in the case `check=FALSE`). So long as slots are set without cheating, the extracted slots will be valid.

Be aware that there are two ways to cheat, both to be avoided but with no guarantees. The obvious way is to assign a slot with `check=FALSE`. Also, slots in `R` are implemented as attributes, for the sake of some back compatibility. The current implementation does not prevent attributes being assigned, via `attr<-`, and such assignments are not checked for legitimate slot names.

### Value

The `@` operator and the `slot` function extract or replace the formally defined slots for the object.

Functions `slotNames` and `getSlots` return respectively the names of the slots and the classes associated with the slots in the specified class definition. Except for its extended interpretation of `x` (above), `slotNames(x)` is just `names(getSlots(x))`.

### References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

### See Also

[@](#), [Classes](#), [Methods](#), [getClass](#)

### Examples

```
setClass("track", representation(x="numeric", y="numeric"))
myTrack <- new("track", x = -4:4, y = exp(-4:4))
slot(myTrack, "x")
slot(myTrack, "y") <- log(slot(myTrack, "y"))
utils::str(myTrack)

getSlots("track") # or
getSlots(getClass("track"))
slotNames(class(myTrack)) # is the same as
slotNames(myTrack)
```

---

StructureClasses      *Classes Corresponding to Basic Structures*

---

### Description

The virtual class `structure` and classes that extend it are formal classes analogous to S language structures such as arrays and time-series.

## Usage

```
## The following class names can appear in method signatures,  
## as the class in as() and is() expressions, and, except for  
## the classes commented as VIRTUAL, in calls to new()  
  
"matrix"  
"array"  
"ts"  
  
"structure" ## VIRTUAL
```

## Objects from the Classes

Objects can be created by calls of the form `new(Class, ...)`, where `Class` is the quoted name of the specific class (e.g., `"matrix"`), and the other arguments, if any, are interpreted as arguments to the corresponding function, e.g., to function `matrix()`. There is no particular advantage over calling those functions directly, unless you are writing software designed to work for multiple classes, perhaps with the class name and the arguments passed in.

Objects created from the classes `"matrix"` and `"array"` are unusual, to put it mildly, and have been for some time. Although they may appear to be objects from these classes, they do not have the internal structure of either an S3 or S4 class object. In particular, they have no `"class"` attribute and are not recognized as objects with classes (that is, both `is.object` and `isS4` will return `FALSE` for such objects).

That the objects still behave as if they came from the corresponding class (most of the time, anyway) results from special code recognizing such objects being built into the base code of R. For most purposes, treating the classes in the usual way will work, fortunately. One consequence of the special treatment is that these two classes may be used as the data part of an S4 class; for example, you can get away with `contains = "matrix"` in a call to `setGeneric` to create an S4 class that is a subclass of `"matrix"`. There is no guarantee that everything will work perfectly, but a number of classes have been written in this form successfully.

The class `"ts"` is basically an S3 class that has been registered with S4, using the `setOldClass` mechanism. Versions of R through 2.7.0 treated this class as a pure S4 class, which was in principal a good idea, but in practice did not allow subclasses to be defined and had other intrinsic problems. (For example, setting the `"tsp"` parameters as a slot often fails because the built-in implementation does not allow the slot to be temporarily inconsistent with the length of the data. Also, the S4 class prevented the correct specification of the S3 inheritance for class `"mts"`.)

The current behavior (beginning with version 2.8.0 of R) registers `"ts"` as an S3 class, using an S4-style definition (see the documentation for `setOldClass` in the examples section for an abbreviated listing of how this is done. The S3 inheritance of `"mts"` in package `stats` is also registered. These classes, as well as `"matrix"` and `"array"` should be valid in most examples as superclasses for new S4 class definitions.

## Extends

The specific classes all extend class `"structure"`, directly, and class `"vector"`, by class `"structure"`.

## Methods

**coerce** Methods are defined to coerce arbitrary objects to these classes, by calling the corresponding basic function, for example, `as(x, "matrix")` calls `as.matrix(x)`. If `strict`

= TRUE in the call to `as()`, the method goes on to delete all other slots and attributes other than the `dim` and `dimnames`.

**Ops** Group methods (see, e.g., [S4groupGeneric](#)) are defined for combinations of structures and vectors (including special cases for array and matrix), implementing the concept of vector structures as in the reference. Essentially, structures combined with vectors retain the structure as long as the resulting object has the same length. Structures combined with other structures remove the structure, since there is no automatic way to determine what should happen to the slots defining the structure.

Note that these methods will be activated when a package is loaded containing a class that inherits from any of the structure classes or class `"vector"`.

## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole (for the original vector structures).

## See Also

Class [nonStructure](#), which enforces the alternative model, in which all slots are dropped if any math transformation or operation is applied to an object from a class extending one of the basic classes.

## Examples

```
showClass("structure")

## explore a bit :
showClass("ts")
(ts0 <- new("ts"))
str(ts0)

showMethods("Ops") # six methods from these classes, but maybe many more
```

---

```
testInheritedMethods
```

*Test for and Report about Selection of Inherited Methods*

---

## Description

A set of distinct inherited signatures is generated to test inheritance for all the methods of a specified generic function. If method selection is ambiguous for some of these, a summary of the ambiguities is attached to the returned object. This test should be performed by package authors *before* releasing a package.

## Usage

```
testInheritedMethods(f, signatures, test = TRUE, virtual = FALSE,
                    groupMethods = TRUE, where = .GlobalEnv)
```

**Arguments**

<code>f</code>	a generic function or the character string name of one. By default, all currently defined subclasses of all the method signatures for this generic will be examined. The other arguments are mainly options to modify which inheritance patterns will be examined.
<code>signatures</code>	An optional set of subclass signatures to use instead of the relevant subclasses computed by <code>testInheritedMethods</code> . See the Details for how this is done. This argument might be supplied after a call with <code>test = FALSE</code> , to test selection in batches.
<code>test</code>	optional flag to control whether method selection is actually tested. If <code>FALSE</code> , returns just the list of relevant signatures for subclasses, without calling <code>selectMethod</code> for each signature. If there are a very large number of signatures, you may want to collect the full list and then test them in batches.
<code>virtual</code>	should virtual classes be included in the relevant subclasses. Normally not, since only the classes of actual arguments will trigger the inheritance calculation in a call to the generic function. Including virtual classes may be useful if the class has no current non-virtual subclasses but you anticipate your users may define such classes in the future.
<code>groupMethods</code>	should methods for the group generic function be included?
<code>where</code>	the environment in which to look for class definitions. Nearly always, use the default global environment after attaching all the packages with relevant methods and/or class definitions.

**Details**

The following description applies when the optional arguments are omitted, the usual case. First, the defining signatures for all methods are computed by calls to `findMethodSignatures`. From these all the known non-virtual subclasses are found for each class that appears in the signature of some method. These subclasses are split into groups according to which class they inherit from, and only one subclass from each group is retained (for each argument in the generic signature). So if a method was defined with class `"vector"` for some argument, one actual vector class is chosen arbitrarily. The case of `"ANY"` is dealt with specially, since all classes extend it. A dummy, nonvirtual class, `".Other"`, is used to correspond to all classes that have no superclasses among those being tested.

All combinations of retained subclasses for the arguments in the generic signature are then computed. Each row of the resulting matrix is a signature to be tested by a call to `selectMethod`. To collect information on ambiguous selections, `testInheritedMethods` establishes a calling handler for the special signal `"ambiguousMethodSelection"`, by setting the corresponding option.

**Value**

An object of class `"methodSelectionReport"`. The details of this class are currently subject to change. It has slots `"target"`, `"selected"`, `"candidates"`, and `"note"`, all referring to the ambiguous cases (and so of length 0 if there were none). These slots are intended to be examined by the programmer to detect and preferably fix ambiguous method selections. The object contains in addition slots `"generic"`, the name of the generic function, and `"allSelections"`, giving the vector of labels for all the signatures tested.



## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (Section 10.6 for basics of method selection.)

Chambers, John M. (2009) *Class Inheritance in R* <http://stat.stanford.edu/~jmc4/classInheritance.pdf> (to be submitted to the R Journal).

## Examples

```
## if no other attached packages have methods for `+` or its group generic
## functions, this returns a 16 by 2 matrix of selection patterns (in R 2.9.0)
testInheritedMethods("+")
```

---

TraceClasses

*Classes Used Internally to Control Tracing*

---

## Description

The classes described here are used by the R function `trace` to create versions of functions and methods including browser calls, etc., and also to `untrace` the same objects.

## Usage

```
### Objects from the following classes are generated
### by calling trace() on an object from the corresponding
### class without the "WithTrace" in the name.

"functionWithTrace"
"MethodDefinitionWithTrace"
"MethodWithNextWithTrace"
"genericFunctionWithTrace"
"groupGenericFunctionWithTrace"

### the following is a virtual class extended by each of the
### classes above

"traceable"
```

## Objects from the Class

Objects will be created from these classes by calls to `trace`. (There is an `initialize` method for class `"traceable"`, but you are unlikely to need it directly.)

## Slots

`.Data`: The data part, which will be `"function"` for class `"functionWithTrace"`, and similarly for the other classes.

`original`: Object of the original class; e.g., `"function"` for class `"functionWithTrace"`.

**Extends**

Each of the classes extends the corresponding untraced class, from the data part; e.g., "functionWithTrace" extends "function". Each of the specific classes extends "traceable", directly, and class "VIRTUAL", by class "traceable".

**Methods**

The point of the specific classes is that objects generated from them, by function `trace()`, remain callable or dispatchable, in addition to their new trace information.

**See Also**

function `trace`

---

validObject	<i>Test the Validity of an Object</i>
-------------	---------------------------------------

---

**Description**

The validity of `object` related to its class definition is tested. If the object is valid, `TRUE` is returned; otherwise, either a vector of strings describing validity failures is returned, or an error is generated (according to whether `test` is `TRUE`). Optionally, all slots in the object can also be validated.

The function `setValidity` sets the validity method of a class (but more normally, this method will be supplied as the `validity` argument to `setClass`). The method should be a function of one object that returns `TRUE` or a description of the non-validity.

**Usage**

```
validObject(object, test = FALSE, complete = FALSE)
```

```
setValidity(Class, method, where = toparent(parent.frame()) )
```

```
getValidity(ClassDef)
```

**Arguments**

<code>object</code>	any object, but not much will happen unless the object's class has a formal definition.
<code>test</code>	logical; if <code>TRUE</code> and validity fails, the function returns a vector of strings describing the problems. If <code>test</code> is <code>FALSE</code> (the default) validity failure generates an error.
<code>complete</code>	logical; if <code>TRUE</code> , validity methods will be applied recursively to any of the slots that have such methods.
<code>Class</code>	the name or class definition of the class whose validity method is to be set.
<code>ClassDef</code>	a class definition object, as from <code>getClassDef</code> .
<code>method</code>	a validity method; that is, either <code>NULL</code> or a function of one argument ( <code>object</code> ). Like <code>validObject</code> , the function should return <code>TRUE</code> if the object is valid, and one or more descriptive strings if any problems are found. Unlike <code>validObject</code> , it should never generate an error.

where

the modified class definition will be stored in this environment.

Note that validity methods do not have to check validity of superclasses: the logic of `validObject` ensures these tests are done once only. As a consequence, if one validity method wants to use another, it should extract and call the method from the other definition of the other class by calling `getValidity()`: it should *not* call `validObject`.

## Details

Validity testing takes place ‘bottom up’: Optionally, if `complete=TRUE`, the validity of the object’s slots, if any, is tested. Then, in all cases, for each of the classes that this class extends (the ‘superclasses’), the explicit validity method of that class is called, if one exists. Finally, the validity method of object’s class is called, if there is one.

Testing generally stops at the first stage of finding an error, except that all the slots will be examined even if a slot has failed its validity test.

The standard validity test (with `complete=FALSE`) is applied when an object is created via `new` with any optional arguments (without the extra arguments the result is just the class prototype object).

An attempt is made to fix up the definition of a validity method if its argument is not `object`.

## Value

`validObject` returns `TRUE` if the object is valid. Otherwise a vector of strings describing problems found, except that if `test` is `FALSE`, validity failure generates an error, with the corresponding strings in the error message.

## References

Chambers, John M. (2008) *Software for Data Analysis: Programming with R* Springer. (For the R version.)

Chambers, John M. (1998) *Programming with Data* Springer (For the original S4 version.)

## See Also

[setClass](#); class [classRepresentation](#).

## Examples

```
setClass("track",
         representation(x="numeric", y = "numeric"))
t1 <- new("track", x=1:10, y=sort(stats::rnorm(10)))
## A valid "track" object has the same number of x, y values
validTrackObject <- function(object) {
  if(length(object@x) == length(object@y)) TRUE
  else paste("Unequal x,y lengths: ", length(object@x), ", ",
            length(object@y), sep="")
}
## assign the function as the validity method for the class
setValidity("track", validTrackObject)
## t1 should be a valid "track" object
validObject(t1)
## Now we do something bad
t2 <- t1
```

```
t2@x <- 1:20
## This should generate an error
## Not run: try(validObject(t2))

setClass("trackCurve",
         representation("track", smooth = "numeric"))

## all superclass validity methods are used when validObject
## is called from initialize() with arguments, so this fails
## Not run: trynew("trackCurve", t2)

setClass("twoTrack", representation(tr1 = "track", tr2 = "track"))

## validity tests are not applied recursively by default,
## so this object is created (invalidly)
tT <- new("twoTrack", tr2 = t2)

## A stricter test detects the problem
## Not run: try(validObject(tT, complete = TRUE))
```



## Chapter 7

# The stats package

---

stats-package

*The R Stats Package*

---

### Description

R statistical functions

### Details

This package contains functions for statistical calculations and random number generation.

For a complete list of functions, use `library(help="stats")`.

### Author(s)

R Development Core Team and contributors worldwide

Maintainer: R Core Team <R-core@r-project.org>

---

.checkMFClasses

*Functions to Check the Type of Variables passed to Model Frames*

---

### Description

`.checkMFClasses` checks if the variables used in a predict method agree in type with those used for fitting.

`.MFclass` categorizes variables for this purpose.

### Usage

```
.checkMFClasses(cl, m, ordNotOK = FALSE)
.MFclass(x)
.getXlevels(Terms, m)
```

**Arguments**

<code>cl</code>	a character vector of class descriptions to match.
<code>m</code>	a model frame.
<code>x</code>	any R object.
<code>ordNotOK</code>	logical: are ordered factors different?
<code>Terms</code>	a terms object.

**Details**

For applications involving `model.matrix` such as linear models we do not need to differentiate between ordered factors and factors as although these affect the coding, the coding used in the fit is already recorded and imposed during prediction. However, other applications may treat ordered factors differently: `rpart` does, for example.

**Value**

`.MFclass` returns a character string, one of "logical", "ordered", "factor", "numeric", "nmatrix.\*" (a numeric matrix with a number of columns appended) or "other".

`.getXlevels` returns a named character vector, or NULL.

---

 acf

---

*Auto- and Cross- Covariance and -Correlation Function Estimation*


---

**Description**

The function `acf` computes (and by default plots) estimates of the autocovariance or autocorrelation function. Function `pacf` is the function used for the partial autocorrelations. Function `ccf` computes the cross-correlation or cross-covariance of two univariate series.

**Usage**

```
acf(x, lag.max = NULL,
    type = c("correlation", "covariance", "partial"),
    plot = TRUE, na.action = na.fail, demean = TRUE, ...)

pacf(x, lag.max, plot, na.action, ...)

## Default S3 method:
pacf(x, lag.max = NULL, plot = TRUE, na.action = na.fail,
     ...)

ccf(x, y, lag.max = NULL, type = c("correlation", "covariance"),
    plot = TRUE, na.action = na.fail, ...)

## S3 method for class 'acf':
x[i, j]
```

**Arguments**

<code>x, y</code>	a univariate or multivariate (not <code>ccf</code> ) numeric time series object or a numeric vector or matrix, or an "acf" object.
<code>lag.max</code>	maximum lag at which to calculate the acf. Default is $10 \log_{10}(N/m)$ where $N$ is the number of observations and $m$ the number of series. Will be automatically limited to one less than the number of observations in the series.
<code>type</code>	character string giving the type of acf to be computed. Allowed values are "correlation" (the default), "covariance" or "partial".
<code>plot</code>	logical. If TRUE (the default) the acf is plotted.
<code>na.action</code>	function to be called to handle missing values. <code>na.pass</code> can be used.
<code>demean</code>	logical. Should the covariances be about the sample means?
<code>...</code>	further arguments to be passed to <code>plot.acf</code> .
<code>i</code>	a set of lags (time differences) to retain.
<code>j</code>	a set of series (names or numbers) to retain.

**Details**

For `type = "correlation"` and `"covariance"`, the estimates are based on the sample covariance. (The lag 0 autocorrelation is fixed at 1 by convention.)

By default, no missing values are allowed. If the `na.action` function passes through missing values (as `na.pass` does), the covariances are computed from the complete cases. This means that the estimate computed may well not be a valid autocorrelation sequence, and may contain missing values. Missing values are not allowed when computing the PACF of a multivariate time series.

The partial correlation coefficient is estimated by fitting autoregressive models of successively higher orders up to `lag.max`.

The generic function `plot` has a method for objects of class "acf".

The lag is returned and plotted in units of time, and not numbers of observations.

There are `print` and subsetting methods for objects of class "acf".

**Value**

An object of class "acf", which is a list with the following elements:

<code>lag</code>	A three dimensional array containing the lags at which the acf is estimated.
<code>acf</code>	An array with the same dimensions as <code>lag</code> containing the estimated acf.
<code>type</code>	The type of correlation (same as the <code>type</code> argument).
<code>n.used</code>	The number of observations in the time series.
<code>series</code>	The name of the series $x$ .
<code>snames</code>	The series names for a multivariate time series.

The lag  $k$  value returned by `ccf(x, y)` estimates the correlation between  $x[t+k]$  and  $y[t]$ .

The result is returned invisibly if `plot` is TRUE.

**Author(s)**

Original: Paul Gilbert, Martyn Plummer. Extensive modifications and univariate case of `pacf` by B. D. Ripley.



## References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth Edition. Springer-Verlag.

(This contains the exact definitions used.)

## See Also

[plot.acf](#), [ARMAacf](#) for the exact autocorrelations of a given ARMA process.

## Examples

```
require(graphics)

## Examples from Venables & Ripley
acf(lh)
acf(lh, type = "covariance")
pacf(lh)

acf(ldeaths)
acf(ldeaths, ci.type = "ma")
acf(ts.union(mdeaths, fdeaths))
ccf(mdeaths, fdeaths, ylab = "cross-correlation")
# (just the cross-correlations)

presidents # contains missing values
acf(presidents, na.action = na.pass)
pacf(presidents, na.action = na.pass)
```

---

acf2AR

*Compute an AR Process Exactly Fitting an ACF*

---

## Description

Compute an AR process exactly fitting an autocorrelation function.

## Usage

```
acf2AR(acf)
```

## Arguments

`acf`                    An autocorrelation or autocovariance sequence.

## Value

A matrix, with one row for the computed AR(p) coefficients for  $1 \leq p \leq \text{length}(\text{acf})$ .

## See Also

[ARMAacf](#), [ar.yw](#) which does this from an empirical ACF.

**Examples**

```
(Acf <- ARMAacf(c(0.6, 0.3, -0.2)))
acf2AR(Acf)
```

---

add1

---

*Add or Drop All Possible Single Terms to a Model*


---

**Description**

Compute all the single terms in the `scope` argument that can be added to or dropped from the model, fit those models and compute a table of the changes in fit.

**Usage**

```
add1(object, scope, ...)

## Default S3 method:
add1(object, scope, scale = 0, test = c("none", "Chisq"),
      k = 2, trace = FALSE, ...)

## S3 method for class 'lm':
add1(object, scope, scale = 0, test = c("none", "Chisq", "F"),
      x = NULL, k = 2, ...)

## S3 method for class 'glm':
add1(object, scope, scale = 0, test = c("none", "Chisq", "F"),
      x = NULL, k = 2, ...)

drop1(object, scope, ...)

## Default S3 method:
drop1(object, scope, scale = 0, test = c("none", "Chisq"),
       k = 2, trace = FALSE, ...)

## S3 method for class 'lm':
drop1(object, scope, scale = 0, all.cols = TRUE,
       test = c("none", "Chisq", "F"), k = 2, ...)

## S3 method for class 'glm':
drop1(object, scope, scale = 0, test = c("none", "Chisq", "F"),
       k = 2, ...)
```

**Arguments**

<code>object</code>	a fitted model object.
<code>scope</code>	a formula giving the terms to be considered for adding or dropping.
<code>scale</code>	an estimate of the residual mean square to be used in computing $C_p$ . Ignored if 0 or NULL.

<code>test</code>	should the results include a test statistic relative to the original model? The F test is only appropriate for <code>lm</code> and <code>aoV</code> models or perhaps for <code>glm</code> fits with estimated dispersion. The $\chi^2$ test can be an exact test ( <code>lm</code> models with known scale) or a likelihood-ratio test or a test of the reduction in scaled deviance depending on the method.
<code>k</code>	the penalty constant in AIC / $C_p$ .
<code>trace</code>	if TRUE, print out progress reports.
<code>x</code>	a model matrix containing columns for the fitted model and all terms in the upper scope. Useful if <code>add1</code> is to be called repeatedly. <b>Warning:</b> no checks are done on its validity.
<code>all.cols</code>	(Provided for compatibility with S.) Logical to specify whether all columns of the design matrix should be used. If FALSE then non-estimable columns are dropped, but the result is not usually statistically meaningful.
<code>...</code>	further arguments passed to or from other methods.

### Details

For `drop1` methods, a missing `scope` is taken to be all terms in the model. The hierarchy is respected when considering terms to be added or dropped: all main effects contained in a second-order interaction must remain, and so on.

In a `scope` formula `.` means ‘what is already there’.

The methods for `lm` and `glm` are more efficient in that they do not recompute the model matrix and call the `fit` methods directly.

The default output table gives AIC, defined as minus twice log likelihood plus  $2p$  where  $p$  is the rank of the model (the number of effective parameters). This is only defined up to an additive constant (like log-likelihoods). For linear Gaussian models with fixed scale, the constant is chosen to give Mallows’  $C_p$ ,  $RSS/scale + 2p - n$ . Where  $C_p$  is used, the column is labelled as  $C_p$  rather than AIC.

The F tests for the "`glm`" methods are based on analysis of deviance tests, so if the dispersion is estimated it is based on the residual deviance, unlike the F tests of `anova.glm`.

### Value

An object of class "`anova`" summarizing the differences in fit between the models.

### Warning

The model fitting must apply the models to the same dataset. Most methods will attempt to use a subset of the data with no missing values for any of the variables if `na.action=na.omit`, but this may give biased results. Only use these functions with data containing missing values with great care.

### Note

These are not fully equivalent to the functions in S. There is no `keep` argument, and the methods used are not quite so computationally efficient.

Their authors’ definitions of Mallows’  $C_p$  and Akaike’s AIC are used, not those of the authors of the models chapter of S.

**Author(s)**

The design was inspired by the S functions of the same names described in Chambers (1992).

**References**

Chambers, J. M. (1992) *Linear models*. Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

[step](#), [aov](#), [lm](#), [extractAIC](#), [anova](#)

**Examples**

```
require(graphics); require(utils)
example(step)#-> swiss
add1(lm1, ~ I(Education^2) + .^2)
drop1(lm1, test="F") # So called 'type II' anova

example(glm)
drop1(glm.D93, test="Chisq")
drop1(glm.D93, test="F")
```

---

 addmargins

*Puts Arbitrary Margins on Multidimensional Tables or Arrays*


---

**Description**

For a given table one can specify which of the classifying factors to expand by one or more levels to hold margins to be calculated. One may for example form sums and means over the first dimension and medians over the second. The resulting table will then have two extra levels for the first dimension and one extra level for the second. The default is to sum over all margins in the table. Other possibilities may give results that depend on the order in which the margins are computed. This is flagged in the printed output from the function.

**Usage**

```
addmargins(A, margin = seq_along(dim(A)), FUN = sum, quiet = FALSE)
```

**Arguments**

A	table or array. The function uses the presence of the "dim" and "dimnames" attributes of A.
margin	vector of dimensions over which to form margins. Margins are formed in the order in which dimensions are specified in margin.
FUN	list of the same length as margin, each element of the list being either a function or a list of functions. Names of the list elements will appear as levels in dimnames of the result. Unnamed list elements will have names constructed: the name of a function or a constructed name based on the position in the table.
quiet	logical which suppresses the message telling the order in which the margins were computed.

**Details**

If the functions used to form margins are not commutative the result depends on the order in which margins are computed. Annotation of margins is done via naming the FUN list.

**Value**

A table or array with the same number of dimensions as A, but with extra levels of the dimensions mentioned in margin. The number of levels added to each dimension is the length of the entries in FUN. A message with the order of computation of margins is printed.

**Author(s)**

Bendix Carstensen, Steno Diabetes Center & Department of Biostatistics, University of Copenhagen, <http://www.biostat.ku.dk/~bxc>, autumn 2003. Margin naming enhanced by Duncan Murdoch.

**See Also**

[table](#), [ftable](#), [margin.table](#).

**Examples**

```
Aye <- sample(c("Yes", "Si", "Oui"), 177, replace = TRUE)
Bee <- sample(c("Hum", "Buzz"), 177, replace = TRUE)
Sea <- sample(c("White", "Black", "Red", "Dead"), 177, replace = TRUE)
(A <- table(Aye, Bee, Sea))
addmargins(A)

ftable(A)
ftable(addmargins(A))

# Non-commutative functions - note differences between resulting tables:
ftable(addmargins(A, c(1,3),
  FUN = list(Sum = sum, list(Min = min, Max = max))))
ftable(addmargins(A, c(3,1),
  FUN = list(list(Min = min, Max = max), Sum = sum)))

# Weird function needed to return the N when computing percentages
sqsm <- function(x) sum(x)^2/100
B <- table(Sea, Bee)
round(sweep(addmargins(B, 1, list(list(All = sum, N = sqsm))), 2,
  apply(B, 2, sum)/100, "/"), 1)
round(sweep(addmargins(B, 2, list(list(All = sum, N = sqsm))), 1,
  apply(B, 1, sum)/100, "/"), 1)

# A total over Bee requires formation of the Bee-margin first:
mB <- addmargins(B, 2, FUN = list(list(Total = sum)))
round(ftable(sweep(addmargins(mB, 1, list(list(All = sum, N = sqsm))), 2,
  apply(mB, 2, sum)/100, "/")), 1)

## Zero.Printing table+margins:
set.seed(1)
x <- sample( 1:7, 20, replace=TRUE)
y <- sample( 1:7, 20, replace=TRUE)
tx <- addmargins( table(x, y) )
print(tx, zero.print = ".")
```

---

 aggregate

*Compute Summary Statistics of Data Subsets*


---

**Description**

Splits the data into subsets, computes summary statistics for each, and returns the result in a convenient form.

**Usage**

```
aggregate(x, ...)

## Default S3 method:
aggregate(x, ...)

## S3 method for class 'data.frame':
aggregate(x, by, FUN, ..., simplify = TRUE)

## S3 method for class 'formula':
aggregate(formula, data, FUN, ...,
          subset, na.action = na.omit)

## S3 method for class 'ts':
aggregate(x, nfrequency = 1, FUN = sum, ndeltat = 1,
          ts.eps = getOption("ts.eps"), ...)
```

**Arguments**

x	an R object.
by	a list of grouping elements, each as long as the variables in x.
FUN	a function to compute the summary statistics which can be applied to all data subsets.
simplify	a logical indicating whether results should be simplified to a vector or matrix if possible.
formula	a <a href="#">formula</a> , such as $y \sim x$ or $\text{cbind}(y1, y2) \sim x1 + x2$ , where the y variables are numeric data to be split into groups according to the grouping x variables (usually factors).
data	a data frame (or list) from which the variables in formula should be taken.
subset	an optional vector specifying a subset of observations to be used.
na.action	a function which indicates what should happen when the data contain NA values. The default is to ignore missing values in the given variables.
nfrequency	new number of observations per unit of time; must be a divisor of the frequency of x.
ndeltat	new fraction of the sampling period between successive observations; must be a divisor of the sampling interval of x.
ts.eps	tolerance used to decide if nfrequency is a sub-multiple of the original frequency.
...	further arguments passed to or used by methods.

## Details

`aggregate` is a generic function with methods for data frames and time series.

The default method `aggregate.default` uses the time series method if `x` is a time series, and otherwise coerces `x` to a data frame and calls the data frame method.

`aggregate.data.frame` is the data frame method. If `x` is not a data frame, it is coerced to one, which must have a non-zero number of rows. Then, each of the variables (columns) in `x` is split into subsets of cases (rows) of identical combinations of the components of `by`, and `FUN` is applied to each such subset with further arguments in `...` passed to it. The result is reformatted into a data frame containing the variables in `by` and `x`. The ones arising from `by` contain the unique combinations of grouping values used for determining the subsets, and the ones arising from `x` the corresponding summaries for the subset of the respective variables in `x`. If `simplify` is true, summaries are simplified to vectors or matrices if they have a common length of one or greater than one, respectively; otherwise, lists of summary results according to subsets are obtained. Rows with missing values in any of the `by` variables will be omitted from the result. (Note that versions of R prior to 2.11.0 required `FUN` to be a scalar function.)

`aggregate.formula` is a standard formula interface to `aggregate.data.frame`.

`aggregate.ts` is the time series method, and requires `FUN` to be a scalar function. If `x` is not a time series, it is coerced to one. Then, the variables in `x` are split into appropriate blocks of length `frequency(x) / nfrequency`, and `FUN` is applied to each such block, with further (named) arguments in `...` passed to it. The result returned is a time series with frequency `nfrequency` holding the aggregated values. Note that this make most sense for a quarterly or yearly result when the original series covers a whole number of quarters or years: in particular aggregating a monthly series to quarters starting in February does not give a conventional quarterly series.

`FUN` is passed to `match.fun`, and hence it can be a function or a symbol or character string naming a function.

## Value

For the time series method, a time series of class `"ts"` or class `c("mts", "ts")`.

For the data frame method, a data frame with columns corresponding to the grouping variables in `by` followed by aggregated columns from `x`. If the `by` has names, the non-empty times are used to label the columns in the results, with unnamed grouping variables being named `Group.i` for `by[[i]]`.

**Note:** prior to R 2.6.0 the grouping variables were reported as factors with levels in alphabetical order in the current locale. Now the variable in the result is found by subsetting the original variable.

## Author(s)

Kurt Hornik, with contributions by Arni Magnusson.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[apply](#), [lapply](#), [tapply](#).

**Examples**

```

## Compute the averages for the variables in 'state.x77', grouped
## according to the region (Northeast, South, North Central, West) that
## each state belongs to.
aggregate(state.x77, list(Region = state.region), mean)

## Compute the averages according to region and the occurrence of more
## than 130 days of frost.
aggregate(state.x77,
          list(Region = state.region,
               Cold = state.x77["Frost"] > 130),
          mean)
## (Note that no state in 'South' is THAT cold.)

## example with character variables and NAs
testDF <- data.frame(v1 = c(1,3,5,7,8,3,5,NA,4,5,7,9),
                    v2 = c(11,33,55,77,88,33,55,NA,44,55,77,99) )
by1 <- c("red","blue",1,2,NA,"big",1,2,"red",1,NA,12)
by2 <- c("wet","dry",99,95,NA,"damp",95,99,"red",99,NA,NA)
aggregate(x = testDF, by = list(by1, by2), FUN = "mean")

# and if you want to treat NAs as a group
fby1 <- factor(by1, exclude = "")
fby2 <- factor(by2, exclude = "")
aggregate(x = testDF, by = list(fby1, fby2), FUN = "mean")

## Formulas, one ~ one, one ~ many, many ~ one, and many ~ many:
aggregate(weight ~ feed, data = chickwts, mean)
aggregate(breaks ~ wool + tension, data = warpbreaks, mean)
aggregate(cbind(Ozone, Temp) ~ Month, data = airquality, mean)
aggregate(cbind(ncases, ncontrols) ~ alcgp + tobgp, data = esoph, sum)

## Dot notation:
aggregate(. ~ Species, data = iris, mean)
aggregate(len ~ ., data = ToothGrowth, mean)

## Often followed by xtabs():
ag <- aggregate(len ~ ., data = ToothGrowth, mean)
xtabs(len ~ ., data = ag)

## Compute the average annual approval ratings for American presidents.
aggregate(presidents, nfrequency = 1, FUN = mean)
## Give the summer less weight.
aggregate(presidents, nfrequency = 1,
          FUN = weighted.mean, w = c(1, 1, 0.5, 1))

```



## Description

Generic function calculating the Akaike information criterion for one or several fitted model objects for which a log-likelihood value can be obtained, according to the formula  $-2\log\text{-likelihood} + kn_{par}$ , where  $n_{par}$  represents the number of parameters in the fitted model, and  $k = 2$  for the usual AIC, or  $k = \log(n)$  ( $n$  the number of observations) for the so-called BIC or SBC (Schwarz's Bayesian criterion).

## Usage

```
AIC(object, ..., k = 2)
```

## Arguments

<code>object</code>	a fitted model object, for which there exists a <code>logLik</code> method to extract the corresponding log-likelihood, or an object inheriting from class <code>logLik</code> .
<code>...</code>	optionally more fitted model objects.
<code>k</code>	numeric, the <i>penalty</i> per parameter to be used; the default <code>k = 2</code> is the classical AIC.

## Details

The default method for AIC, `AIC.default()` entirely relies on the existence of a `logLik` method computing the log-likelihood for the given class.

When comparing fitted objects, the smaller the AIC, the better the fit.

The log-likelihood and hence the AIC is only defined up to an additive constant. Different constants have conventionally be used for different purposes and so `extractAIC` and `AIC` may give different values (and do for models of class `"lm"`: see the help for `extractAIC`).

## Value

If just one object is provided, returns a numeric value with the corresponding AIC (or BIC, or ..., depending on `k`); if multiple objects are provided, returns a `data.frame` with rows corresponding to the objects and columns representing the number of parameters in the model (`df`) and the AIC.

## Author(s)

José Pinheiro and Douglas Bates

## References

Sakamoto, Y., Ishiguro, M., and Kitagawa G. (1986). *Akaike Information Criterion Statistics*. D. Reidel Publishing Company.

## See Also

[extractAIC](#), [logLik](#).

**Examples**

```

lm1 <- lm(Fertility ~ . , data = swiss)
AIC(lm1)
stopifnot(all.equal(AIC(lm1),
                    AIC(logLik(lm1))))
## a version of BIC or Schwarz's BC :
AIC(lm1, k = log(nrow(swiss)))

```

alias

*Find Aliases (Dependencies) in a Model***Description**

Find aliases (linearly dependent terms) in a linear model specified by a formula.

**Usage**

```

alias(object, ...)

## S3 method for class 'formula':
alias(object, data, ...)

## S3 method for class 'lm':
alias(object, complete = TRUE, partial = FALSE,
      partial.pattern = FALSE, ...)

```

**Arguments**

object	A fitted model object, for example from <code>lm</code> or <code>aov</code> , or a formula for <code>alias.formula</code> .
data	Optionally, a data frame to search for the objects in the formula.
complete	Should information on complete aliasing be included?
partial	Should information on partial aliasing be included?
partial.pattern	Should partial aliasing be presented in a schematic way? If this is done, the results are presented in a more compact way, usually giving the deciles of the coefficients.
...	further arguments passed to or from other methods.

**Details**

Although the main method is for class "lm", `alias` is most useful for experimental designs and so is used with fits from `aov`. Complete aliasing refers to effects in linear models that cannot be estimated independently of the terms which occur earlier in the model and so have their coefficients omitted from the fit. Partial aliasing refers to effects that can be estimated less precisely because of correlations induced by the design.

**Value**

	A list (of class "listof") containing components
Model	Description of the model; usually the formula.
Complete	A matrix with columns corresponding to effects that are linearly dependent on the rows.
Partial	The correlations of the estimable effects, with a zero diagonal. An object of class "mtable" which has its own <code>print</code> method.

**Note**

The aliasing pattern may depend on the contrasts in use: Helmert contrasts are probably most useful. The defaults are different from those in S.

**Author(s)**

The design was inspired by the S function of the same name described in Chambers *et al.* (1992).

**References**

Chambers, J. M., Freeny, A and Heiberger, R. M. (1992) *Analysis of variance; designed experiments*. Chapter 5 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**Examples**

```
## From Venables and Ripley (2002) p.165.
utils::data(npk, package="MASS")

op <- options(contrasts=c("contr.helmert", "contr.poly"))
npk.aov <- aov(yield ~ block + N*P*K, npk)
alias(npk.aov)
options(op) # reset
```

---

 anova

*Anova Tables*


---

**Description**

Compute analysis of variance (or deviance) tables for one or more fitted model objects.

**Usage**

```
anova(object, ...)
```

**Arguments**

object	an object containing the results returned by a model fitting function (e.g., <code>lm</code> or <code>glm</code> ).
...	additional objects of the same type.

**Value**

This (generic) function returns an object of class `anova`. These objects represent analysis-of-variance and analysis-of-deviance tables. When given a single argument it produces a table which tests whether the model terms are significant.

When given a sequence of objects, `anova` tests the models against one another in the order specified.

The print method for `anova` objects prints tables in a ‘pretty’ form.

**Warning**

The comparison between two or more models will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values and R’s default of `na.action = na.omit` is used.

**References**

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*, Wadsworth & Brooks/Cole.

**See Also**

[coefficients](#), [effects](#), [fitted.values](#), [residuals](#), [summary](#), [drop1](#), [add1](#).

---

`anova.glm`*Analysis of Deviance for Generalized Linear Model Fits*

---

**Description**

Compute an analysis of deviance table for one or more generalized linear model fits.

**Usage**

```
## S3 method for class 'glm':  
anova(object, ..., dispersion = NULL, test = NULL)
```

**Arguments**

`object, ...` objects of class `glm`, typically the result of a call to [glm](#), or a list of objects for the `"glm.list"` method.

`dispersion` the dispersion parameter for the fitting family. By default it is obtained from the object(s).

`test` a character string, (partially) matching one of `"Chisq"`, `"F"` or `"Cp"`. See [stat.anova](#).

## Details

Specifying a single object gives a sequential analysis of deviance table for that fit. That is, the reductions in the residual deviance as each term of the formula is added in turn are given in as the rows of a table, plus the residual deviances themselves.

If more than one object is specified, the table has a row for the residual degrees of freedom and deviance for each model. For all but the first model, the change in degrees of freedom and deviance is also given. (This only makes statistical sense if the models are nested.) It is conventional to list the models from smallest to largest, but this is up to the user.

The table will optionally contain test statistics (and P values) comparing the reduction in deviance for the row to the residuals. For models with known dispersion (e.g., binomial and Poisson fits) the chi-squared test is most appropriate, and for those with dispersion estimated by moments (e.g., gaussian, quasibinomial and quasipoisson fits) the F test is most appropriate. Mallows'  $C_p$  statistic is the residual deviance plus twice the estimate of  $\sigma^2$  times the residual degrees of freedom, which is closely related to AIC (and a multiple of it if the dispersion is known).

The dispersion estimate will be taken from the largest model, using the value returned by [summary.glm](#). As this will in most cases use a Chisquared-based estimate, the F tests are not based on the residual deviance in the analysis of deviance table shown.

## Value

An object of class "anova" inheriting from class "data.frame".

## Warning

The comparison between two or more models by `anova` or `anova.glm` will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values and R's default of `na.action = na.omit` is used, and `anova.glm` will detect this with an error.

## References

Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models*. Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

## See Also

[glm](#), [anova](#).

[drop1](#) for so-called 'type II' anova where each term is dropped one at a time respecting their hierarchy.

## Examples

```
## --- Continuing the Example from '?glm':

anova(glm.D93)
anova(glm.D93, test = "Cp")
anova(glm.D93, test = "Chisq")
```

---

 anova.lm

ANOVA for Linear Model Fits

**Description**

Compute an analysis of variance table for one or more linear model fits.

**Usage**

```
## S3 method for class 'lm':
anova(object, ...)

anova.lmlist(object, ..., scale = 0, test = "F")
```

**Arguments**

`object, ...` objects of class `lm`, usually, a result of a call to `lm`.

`test` a character string specifying the test statistic to be used. Can be one of "F", "Chisq" or "Cp", with partial matching allowed, or NULL for no test.

`scale` numeric. An estimate of the noise variance  $\sigma^2$ . If zero this will be estimated from the largest model considered.

**Details**

Specifying a single object gives a sequential analysis of variance table for that fit. That is, the reductions in the residual sum of squares as each term of the formula is added in turn are given in as the rows of a table, plus the residual sum of squares.

The table will contain F statistics (and P values) comparing the mean square for the row to the residual mean square.

If more than one object is specified, the table has a row for the residual degrees of freedom and sum of squares for each model. For all but the first model, the change in degrees of freedom and sum of squares is also given. (This only make statistical sense if the models are nested.) It is conventional to list the models from smallest to largest, but this is up to the user.

Optionally the table can include test statistics. Normally the F statistic is most appropriate, which compares the mean square for a row to the residual sum of squares for the largest model considered. If `scale` is specified chi-squared tests can be used. Mallows'  $C_p$  statistic is the residual sum of squares plus twice the estimate of  $\sigma^2$  times the residual degrees of freedom.

**Value**

An object of class "anova" inheriting from class "data.frame".

**Warning**

The comparison between two or more models will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values and R's default of `na.action = na.omit` is used, and `anova.lmlist` will detect this with an error.

**Note**

Versions of R prior to 1.2.0 based F tests on pairwise comparisons, and this behaviour can still be obtained by a direct call to `anova.list.lm`.

**References**

Chambers, J. M. (1992) *Linear models*. Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

The model fitting function `lm`, `anova`.

`drop1` for so-called ‘type II’ anova where each term is dropped one at a time respecting their hierarchy.

**Examples**

```
## sequential table
fit <- lm(sr ~ ., data = LifeCycleSavings)
anova(fit)

## same effect via separate models
fit0 <- lm(sr ~ 1, data = LifeCycleSavings)
fit1 <- update(fit0, . ~ . + pop15)
fit2 <- update(fit1, . ~ . + pop75)
fit3 <- update(fit2, . ~ . + dpi)
fit4 <- update(fit3, . ~ . + ddpi)
anova(fit0, fit1, fit2, fit3, fit4, test="F")

anova(fit4, fit2, fit0, test="F") # unconventional order
```

---

 anova.mlm

---

*Comparisons between Multivariate Linear Models*


---

**Description**

Compute a (generalized) analysis of variance table for one or more multivariate linear models.

**Usage**

```
## S3 method for class 'mlm':
anova(object, ...,
       test =
         c("Pillai", "Wilks", "Hotelling-Lawley", "Roy", "Spherical"),
       Sigma = diag(nrow = p), T = Thin.row(proj(M) - proj(X)),
       M = diag(nrow = p), X = ~0,
       idata = data.frame(index = seq_len(p)), tol = 1e-7)
```

**Arguments**

object	an object of class "mlm".
...	further objects of class "mlm".
test	choice of test statistic (see below).
Sigma	(only relevant if <code>test == "Spherical"</code> ). Covariance matrix assumed proportional to Sigma.
T	transformation matrix. By default computed from M and X.
M	formula or matrix describing the outer projection (see below).
X	formula or matrix describing the inner projection (see below).
idata	data frame describing intra-block design.
tol	tolerance to be used in deciding if the residuals are rank-deficient: see <a href="#">qr</a> .

**Details**

The `anova.mlm` method uses either a multivariate test statistic for the summary table, or a test based on sphericity assumptions (i.e. that the covariance is proportional to a given matrix).

For the multivariate test, Wilks' statistic is most popular in the literature, but the default Pillai–Bartlett statistic is recommended by Hand and Taylor (1987). See [summary.manova](#) for further details.

For the "Spherical" test, proportionality is usually with the identity matrix but a different matrix can be specified using `Sigma`). Corrections for asphericity known as the Greenhouse–Geisser, respectively Huynh–Feldt, epsilons are given and adjusted  $F$  tests are performed.

It is common to transform the observations prior to testing. This typically involves transformation to intra-block differences, but more complicated within-block designs can be encountered, making more elaborate transformations necessary. A transformation matrix `T` can be given directly or specified as the difference between two projections onto the spaces spanned by `M` and `X`, which in turn can be given as matrices or as model formulas with respect to `idata` (the tests will be invariant to parametrization of the quotient space  $M/X$ ).

As with `anova.lm`, all test statistics use the SSD matrix from the largest model considered as the (generalized) denominator.

Contrary to other `anova` methods, the intercept is not excluded from the display in the single-model case. When contrast transformations are involved, it often makes good sense to test for a zero intercept.

**Value**

An object of class "anova" inheriting from class "data.frame"

**Note**

The Huynh–Feldt epsilon differs from that calculated by SAS (as of v. 8.2) except when the DF is equal to the number of observations minus one. This is believed to be a bug in SAS, not in R.

**References**

Hand, D. J. and Taylor, C. C. (1987) *Multivariate Analysis of Variance and Repeated Measures*. Chapman and Hall.



**See Also**

[summary.manova](#)

**Examples**

```
require(graphics)
utils::example(SSD) # Brings in the mlmfit and reacttime objects

mlmfit0 <- update(mlmfit, ~0)

### Traditional tests of intrasubj. contrasts
## Using MANOVA techniques on contrasts:
anova(mlmfit, mlmfit0, X=~1)

## Assuming sphericity
anova(mlmfit, mlmfit0, X=~1, test="Spherical")

### tests using intra-subject 3x2 design
idata <- data.frame(deg=gl(3,1,6,labels=c(0,4,8)),
                    noise=gl(2,3,6,labels=c("A","P")))

anova(mlmfit, mlmfit0, X = ~ deg + noise,
      idata = idata, test = "Spherical")
anova(mlmfit, mlmfit0, M = ~ deg + noise, X = ~ noise,
      idata = idata, test="Spherical" )
anova(mlmfit, mlmfit0, M = ~ deg + noise, X = ~ deg,
      idata = idata, test="Spherical" )

f <- factor(rep(1:2,5)) # bogus, just for illustration
mlmfit2 <- update(mlmfit, ~f)
anova(mlmfit2, mlmfit, mlmfit0, X = ~1, test = "Spherical")
anova(mlmfit2, X = ~1, test = "Spherical")
# one-model form, equiv. to previous

### There seems to be a strong interaction in these data
plot(colMeans(reacttime))
```

---

ansari.test

*Ansari-Bradley Test*

---

**Description**

Performs the Ansari-Bradley two-sample test for a difference in scale parameters.

**Usage**

```
ansari.test(x, ...)

## Default S3 method:
ansari.test(x, y,
            alternative = c("two.sided", "less", "greater"),
            exact = NULL, conf.int = FALSE, conf.level = 0.95,
```

```

... )

## S3 method for class 'formula':
ansari.test(formula, data, subset, na.action, ...)

```

### Arguments

<code>x</code>	numeric vector of data values.
<code>y</code>	numeric vector of data values.
<code>alternative</code>	indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter.
<code>exact</code>	a logical indicating whether an exact p-value should be computed.
<code>conf.int</code>	a logical, indicating whether a confidence interval should be computed.
<code>conf.level</code>	confidence level of the interval.
<code>formula</code>	a formula of the form <code>lhs ~ rhs</code> where <code>lhs</code> is a numeric variable giving the data values and <code>rhs</code> a factor with two levels giving the corresponding groups.
<code>data</code>	an optional matrix or data frame (or similar: see <code>model.frame</code> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>subset</code>	an optional vector specifying a subset of observations to be used.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. Defaults to <code>getOption("na.action")</code> .
<code>...</code>	further arguments to be passed to or from methods.

### Details

Suppose that  $x$  and  $y$  are independent samples from distributions with densities  $f((t - m)/s)/s$  and  $f(t - m)$ , respectively, where  $m$  is an unknown nuisance parameter and  $s$ , the ratio of scales, is the parameter of interest. The Ansari-Bradley test is used for testing the null that  $s$  equals 1, the two-sided alternative being that  $s \neq 1$  (the distributions differ only in variance), and the one-sided alternatives being  $s > 1$  (the distribution underlying  $x$  has a larger variance, "greater") or  $s < 1$  ("less").

By default (if `exact` is not specified), an exact p-value is computed if both samples contain less than 50 finite values and there are no ties. Otherwise, a normal approximation is used.

Optionally, a nonparametric confidence interval and an estimator for  $s$  are computed. If exact p-values are available, an exact confidence interval is obtained by the algorithm described in Bauer (1972), and the Hodges-Lehmann estimator is employed. Otherwise, the returned confidence interval and point estimate are based on normal approximations.

Note that mid-ranks are used in the case of ties rather than average scores as employed in Hollander & Wolfe (1973). See, e.g., Hajek, Sidak and Sen (1999), pages 131ff, for more information.

### Value

A list with class "htest" containing the following components:

<code>statistic</code>	the value of the Ansari-Bradley test statistic.
<code>p.value</code>	the p-value of the test.
<code>null.value</code>	the ratio of scales $s$ under the null, 1.
<code>alternative</code>	a character string describing the alternative hypothesis.

method	the string "Ansari-Bradley test".
data.name	a character string giving the names of the data.
conf.int	a confidence interval for the scale parameter. (Only present if argument conf.int = TRUE.)
estimate	an estimate of the ratio of scales. (Only present if argument conf.int = TRUE.)

### Note

To compare results of the Ansari-Bradley test to those of the F test to compare two variances (under the assumption of normality), observe that  $s$  is the ratio of scales and hence  $s^2$  is the ratio of variances (provided they exist), whereas for the F test the ratio of variances itself is the parameter of interest. In particular, confidence intervals are for  $s$  in the Ansari-Bradley test but for  $s^2$  in the F test.

### References

David F. Bauer (1972), Constructing confidence sets using rank statistics. *Journal of the American Statistical Association* **67**, 687–690.

Jaroslav Hajek, Zbynek Sidak and Pranab K. Sen (1999), *Theory of Rank Tests*. San Diego, London: Academic Press.

Myles Hollander and Douglas A. Wolfe (1973), *Nonparametric Statistical Methods*. New York: John Wiley & Sons. Pages 83–92.

### See Also

[fligner.test](#) for a rank-based (nonparametric)  $k$ -sample test for homogeneity of variances; [mood.test](#) for another rank-based two-sample test for a difference in scale parameters; [var.test](#) and [bartlett.test](#) for parametric tests for the homogeneity in variance.

[ansari\\_test](#) in package **coin** for exact and approximate *conditional* p-values for the Ansari-Bradley test, as well as different methods for handling ties.

### Examples

```
## Hollander & Wolfe (1973, p. 86f):
## Serum iron determination using Hyland control sera
ramsay <- c(111, 107, 100, 99, 102, 106, 109, 108, 104, 99,
           101, 96, 97, 102, 107, 113, 116, 113, 110, 98)
jung.parekh <- c(107, 108, 106, 98, 105, 103, 110, 105, 104,
                100, 96, 108, 103, 104, 114, 114, 113, 108, 106, 99)
ansari.test(ramsay, jung.parekh)

ansari.test(rnorm(10), rnorm(10, 0, 2), conf.int = TRUE)

## try more points - failed in 2.4.1
ansari.test(rnorm(100), rnorm(100, 0, 2), conf.int = TRUE)
```

---

aov

*Fit an Analysis of Variance Model*

---

## Description

Fit an analysis of variance model by a call to `lm` for each stratum.

## Usage

```
aov(formula, data = NULL, projections = FALSE, qr = TRUE,
     contrasts = NULL, ...)
```

## Arguments

<code>formula</code>	A formula specifying the model.
<code>data</code>	A data frame in which the variables specified in the formula will be found. If missing, the variables are searched for in the standard way.
<code>projections</code>	Logical flag: should the projections be returned?
<code>qr</code>	Logical flag: should the QR decomposition be returned?
<code>contrasts</code>	A list of contrasts to be used for some of the factors in the formula. These are not used for any <code>Error</code> term, and supplying contrasts for factors only in the <code>Error</code> term will give a warning.
<code>...</code>	Arguments to be passed to <code>lm</code> , such as <code>subset</code> or <code>na.action</code> . See ‘Details’ about <code>weights</code> .

## Details

This provides a wrapper to `lm` for fitting linear models to balanced or unbalanced experimental designs.

The main difference from `lm` is in the way `print`, `summary` and so on handle the fit: this is expressed in the traditional language of the analysis of variance rather than that of linear models.

If the formula contains a single `Error` term, this is used to specify error strata, and appropriate models are fitted within each error stratum.

The formula can specify multiple responses.

Weights can be specified by a `weights` argument, but should not be used with an `Error` term, and are incompletely supported (e.g., not by `model.tables`).

## Value

An object of class `c("aov", "lm")` or for multiple responses of class `c("maov", "aov", "mlm", "lm")` or for multiple error strata of class `"aovlist"`. There are `print` and `summary` methods available for these.

**Note**

`aov` is designed for balanced designs, and the results can be hard to interpret without balance: beware that missing values in the response(s) will likely lose the balance. If there are two or more error strata, the methods used are statistically inefficient without balance, and it may be better to use `lme` in package `nlme`.

Balance can be checked with the `replications` function.

The default ‘contrasts’ in R are not orthogonal contrasts, and `aov` and its helper functions will work better with such contrasts: see the examples for how to select these.

**Author(s)**

The design was inspired by the S function of the same name described in Chambers *et al.* (1992).

**References**

Chambers, J. M., Freeny, A and Heiberger, R. M. (1992) *Analysis of variance; designed experiments*. Chapter 5 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

[lm](#), [summary.aov](#), [replications](#), [alias](#), [proj](#), [model.tables](#), [TukeyHSD](#)

**Examples**

```
## From Venables and Ripley (2002) p.165.
utils::data(npk, package="MASS")

## Set orthogonal contrasts.
op <- options(contrasts=c("contr.helmert", "contr.poly"))
( npk.aov <- aov(yield ~ block + N*P*K, npk) )
summary(npk.aov)
coefficients(npk.aov)

## to show the effects of re-ordering terms contrast the two fits
aov(yield ~ block + N * P + K, npk)
aov(terms(yield ~ block + N * P + K, keep.order=TRUE), npk)

## as a test, not particularly sensible statistically
npk.aovE <- aov(yield ~ N*P*K + Error(block), npk)
npk.aovE
summary(npk.aovE)
options(op) # reset to previous
```

**Description**

Return a list of points which linearly interpolate given data points, or a function performing the linear (or constant) interpolation.

**Usage**

```
approx (x, y = NULL, xout, method="linear", n=50,
        yleft, yright, rule = 1, f = 0, ties = mean)

approxfun(x, y = NULL,          method="linear",
          yleft, yright, rule = 1, f = 0, ties = mean)
```

**Arguments**

<code>x, y</code>	vectors giving the coordinates of the points to be interpolated. Alternatively a single plotting structure can be specified: see <a href="#">xy.coords</a> .
<code>xout</code>	an optional set of values specifying where interpolation is to take place.
<code>method</code>	specifies the interpolation method to be used. Choices are "linear" or "constant".
<code>n</code>	If <code>xout</code> is not specified, interpolation takes place at <code>n</code> equally spaced points spanning the interval $[\min(x), \max(x)]$ .
<code>yleft</code>	the value to be returned when input <code>x</code> values are less than $\min(x)$ . The default is defined by the value of <code>rule</code> given below.
<code>yright</code>	the value to be returned when input <code>x</code> values are greater than $\max(x)$ . The default is defined by the value of <code>rule</code> given below.
<code>rule</code>	an integer (of length 1 or 2) describing how interpolation is to take place outside the interval $[\min(x), \max(x)]$ . If <code>rule</code> is 1 then NAs are returned for such points and if it is 2, the value at the closest data extreme is used. Use, e.g., <code>rule = 2:1</code> , if the left and right side extrapolation should differ.
<code>f</code>	for <code>method="constant"</code> a number between 0 and 1 inclusive, indicating a compromise between left- and right-continuous step functions. If <code>y0</code> and <code>y1</code> are the values to the left and right of the point then the value is $y0*(1-f) + y1*f$ so that <code>f=0</code> is right-continuous and <code>f=1</code> is left-continuous.
<code>ties</code>	Handling of tied <code>x</code> values. Either a function with a single vector argument returning a single number result or the string "ordered".

**Details**

The inputs can contain missing values which are deleted, so at least two complete (`x, y`) pairs are required (for `method = "linear"`, one otherwise). If there are duplicated (tied) `x` values and `ties` is a function it is applied to the `y` values for each distinct `x` value. Useful functions in this context include [mean](#), [min](#), and [max](#). If `ties="ordered"` the `x` values are assumed to be already ordered. The first `y` value will be used for interpolation to the left and the last one for interpolation to the right.

**Value**

`approx` returns a list with components `x` and `y`, containing `n` coordinates which interpolate the given data points according to the `method` (and `rule`) desired.

The function `approxfun` returns a function performing (linear or constant) interpolation of the given data points. For a given set of `x` values, this function will return the corresponding interpolated values. This is often more useful than `approx`.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[spline](#) and [splinefun](#) for spline interpolation.

## Examples

```
require(graphics)

x <- 1:10
y <- rnorm(10)
par(mfrow = c(2,1))
plot(x, y, main = "approx(.) and approxfun(.)")
points(approx(x, y), col = 2, pch = "*")
points(approx(x, y, method = "constant"), col = 4, pch = "*")

f <- approxfun(x, y)
curve(f(x), 0, 11, col = "green2")
points(x, y)
is.function(fc <- approxfun(x, y, method = "const")) # TRUE
curve(fc(x), 0, 10, col = "darkblue", add = TRUE)
## different extrapolation on left and right side :
plot(approxfun(x, y, rule = 2:1), 0, 11,
      col = "tomato", add = TRUE, lty = 3, lwd = 2)

## Show treatment of 'ties' :

x <- c(2,2:4,4,4,5,5,7,7,7)
y <- c(1:6, 5:4, 3:1)
approx(x,y, xout=x)$y # warning
(ay <- approx(x,y, xout=x, ties = "ordered"))$y
stopifnot(ay == c(2,2,3,6,6,6,4,4,1,1,1))
approx(x,y, xout=x, ties = min)$y
approx(x,y, xout=x, ties = max)$y
```

---

ar

*Fit Autoregressive Models to Time Series*

---

## Description

Fit an autoregressive time series model to the data, by default selecting the complexity by AIC.

## Usage

```
ar(x, aic = TRUE, order.max = NULL,
   method=c("yule-walker", "burg", "ols", "mle", "yw"),
   na.action, series, ...)
```

```

ar.burg(x, ...)
## Default S3 method:
ar.burg(x, aic = TRUE, order.max = NULL,
        na.action = na.fail, demean = TRUE, series,
        var.method = 1, ...)
## S3 method for class 'mts':
ar.burg(x, aic = TRUE, order.max = NULL,
        na.action = na.fail, demean = TRUE, series,
        var.method = 1, ...)

ar.yw(x, ...)
## Default S3 method:
ar.yw(x, aic = TRUE, order.max = NULL,
      na.action = na.fail, demean = TRUE, series, ...)
## S3 method for class 'mts':
ar.yw(x, aic = TRUE, order.max = NULL,
      na.action = na.fail, demean = TRUE, series,
      var.method = 1, ...)

ar.mle(x, aic = TRUE, order.max = NULL, na.action = na.fail,
       demean = TRUE, series, ...)

## S3 method for class 'ar':
predict(object, newdata, n.ahead = 1, se.fit = TRUE, ...)

```

## Arguments

x	A univariate or multivariate time series.
aic	Logical flag. If TRUE then the Akaike Information Criterion is used to choose the order of the autoregressive model. If FALSE, the model of order <code>order.max</code> is fitted.
order.max	Maximum order (or order) of model to fit. Defaults to the smaller of $N - 1$ and $10 \log_{10}(N)$ where $N$ is the number of observations except for <code>method="mle"</code> where it is the minimum of this quantity and 12.
method	Character string giving the method used to fit the model. Must be one of the strings in the default argument (the first few characters are sufficient). Defaults to "yule-walker".
na.action	function to be called to handle missing values.
demean	should a mean be estimated during fitting?
series	names for the series. Defaults to <code>deparse(substitute(x))</code> .
var.method	the method to estimate the innovations variance (see 'Details').
...	additional arguments for specific methods.
object	a fit from <code>ar</code> .
newdata	data to which to apply the prediction.
n.ahead	number of steps ahead at which to predict.
se.fit	logical: return estimated standard errors of the prediction error?



## Details

For definiteness, note that the AR coefficients have the sign in

$$x_t - \mu = a_1(x_{t-1} - \mu) + \cdots + a_p(x_{t-p} - \mu) + e_t$$

`ar` is just a wrapper for the functions `ar.yw`, `ar.burg`, `ar.ols` and `ar.mle`.

Order selection is done by AIC if `aic` is true. This is problematic, as of the methods here only `ar.mle` performs true maximum likelihood estimation. The AIC is computed as if the variance estimate were the MLE, omitting the determinant term from the likelihood. Note that this is not the same as the Gaussian likelihood evaluated at the estimated parameter values. In `ar.yw` the variance matrix of the innovations is computed from the fitted coefficients and the autocovariance of  $x$ .

`ar.burg` allows two methods to estimate the innovations variance and hence AIC. Method 1 is to use the update given by the Levinson-Durbin recursion (Brockwell and Davis, 1991, (8.2.6) on page 242), and follows S-PLUS. Method 2 is the mean of the sum of squares of the forward and backward prediction errors (as in Brockwell and Davis, 1996, page 145). Percival and Walden (1998) discuss both. In the multivariate case the estimated coefficients will depend (slightly) on the variance estimation method.

Remember that `ar` includes by default a constant in the model, by removing the overall mean of  $x$  before fitting the AR model, or (`ar.mle`) estimating a constant to subtract.

## Value

For `ar` and its methods a list of class "ar" with the following elements:

<code>order</code>	The order of the fitted model. This is chosen by minimizing the AIC if <code>aic=TRUE</code> , otherwise it is <code>order.max</code> .
<code>ar</code>	Estimated autoregression coefficients for the fitted model.
<code>var.pred</code>	The prediction variance: an estimate of the portion of the variance of the time series that is not explained by the autoregressive model.
<code>x.mean</code>	The estimated mean of the series used in fitting and for use in prediction.
<code>x.intercept</code>	( <code>ar.ols</code> only.) The intercept in the model for $x - x.mean$ .
<code>aic</code>	The differences in AIC between each model and the best-fitting model. Note that the latter can have an AIC of <code>-Inf</code> .
<code>n.used</code>	The number of observations in the time series.
<code>order.max</code>	The value of the <code>order.max</code> argument.
<code>partialacf</code>	The estimate of the partial autocorrelation function up to lag <code>order.max</code> .
<code>resid</code>	residuals from the fitted model, conditioning on the first <code>order</code> observations. The first <code>order</code> residuals are set to NA. If $x$ is a time series, so is <code>resid</code> .
<code>method</code>	The value of the <code>method</code> argument.
<code>series</code>	The name(s) of the time series.
<code>frequency</code>	The frequency of the time series.
<code>call</code>	The matched call.
<code>asy.var.coef</code>	(univariate case, <code>order &gt; 0</code> .) The asymptotic-theory variance matrix of the coefficient estimates.

For `predict.ar`, a time series of predictions, or if `se.fit = TRUE`, a list with components `pred`, the predictions, and `se`, the estimated standard errors. Both components are time series.

**Note**

Only the univariate case of `ar.mle` is implemented.

Fitting by `method="mle"` to long series can be very slow.

**Author(s)**

Martyn Plummer. Univariate case of `ar.yw`, `ar.mle` and C code for univariate case of `ar.burg` by B. D. Ripley.

**References**

Brockwell, P. J. and Davis, R. A. (1991) *Time Series and Forecasting Methods*. Second edition. Springer, New York. Section 11.4.

Brockwell, P. J. and Davis, R. A. (1996) *Introduction to Time Series and Forecasting*. Springer, New York. Sections 5.1 and 7.6.

Percival, D. P. and Walden, A. T. (1998) *Spectral Analysis for Physical Applications*. Cambridge University Press.

Whittle, P. (1963) On the fitting of multivariate autoregressions and the approximate canonical factorization of a spectral density matrix. *Biometrika* **40**, 129–134.

**See Also**

[ar.ols](#), [arima](#) for ARMA models; [acf2AR](#), for AR construction from the ACF.

[arima.sim](#) for simulation of AR processes.

**Examples**

```
ar(lh)
ar(lh, method="burg")
ar(lh, method="ols")
ar(lh, FALSE, 4) # fit ar(4)

(sunspot.ar <- ar(sunspot.year))
predict(sunspot.ar, n.ahead=25)
## try the other methods too

ar(ts.union(BJsales, BJsales.lead))
## Burg is quite different here, as is OLS (see ar.ols)
ar(ts.union(BJsales, BJsales.lead), method="burg")
```

---

ar.ols

*Fit Autoregressive Models to Time Series by OLS*


---

**Description**

Fit an autoregressive time series model to the data by ordinary least squares, by default selecting the complexity by AIC.

**Usage**

```
ar.ols(x, aic = TRUE, order.max = NULL, na.action = na.fail,
       demean = TRUE, intercept = demean, series, ...)
```

**Arguments**

<code>x</code>	A univariate or multivariate time series.
<code>aic</code>	Logical flag. If <code>TRUE</code> then the Akaike Information Criterion is used to choose the order of the autoregressive model. If <code>FALSE</code> , the model of order <code>order.max</code> is fitted.
<code>order.max</code>	Maximum order (or order) of model to fit. Defaults to $10 \log_{10}(N)$ where $N$ is the number of observations.
<code>na.action</code>	function to be called to handle missing values.
<code>demean</code>	should the AR model be for $x$ minus its mean?
<code>intercept</code>	should a separate intercept term be fitted?
<code>series</code>	names for the series. Defaults to <code>deparse(substitute(x))</code> .
<code>...</code>	further arguments to be passed to or from methods.

**Details**

`ar.ols` fits the general AR model to a possibly non-stationary and/or multivariate system of series  $x$ . The resulting unconstrained least squares estimates are consistent, even if some of the series are non-stationary and/or co-integrated. For definiteness, note that the AR coefficients have the sign in

$$x_t - \mu = a_0 + a_1(x_{t-1} - \mu) + \dots + a_p(x_{t-p} - \mu) + e_t$$

where  $a_0$  is zero unless `intercept` is true, and  $\mu$  is the sample mean if `demean` is true, zero otherwise.

Order selection is done by AIC if `aic` is true. This is problematic, as `ar.ols` does not perform true maximum likelihood estimation. The AIC is computed as if the variance estimate (computed from the variance matrix of the residuals) were the MLE, omitting the determinant term from the likelihood. Note that this is not the same as the Gaussian likelihood evaluated at the estimated parameter values.

Some care is needed if `intercept` is true and `demean` is false. Only use this if the series are roughly centred on zero. Otherwise the computations may be inaccurate or fail entirely.

**Value**

A list of class "ar" with the following elements:

<code>order</code>	The order of the fitted model. This is chosen by minimizing the AIC if <code>aic=TRUE</code> , otherwise it is <code>order.max</code> .
<code>ar</code>	Estimated autoregression coefficients for the fitted model.
<code>var.pred</code>	The prediction variance: an estimate of the portion of the variance of the time series that is not explained by the autoregressive model.
<code>x.mean</code>	The estimated mean (or zero if <code>demean</code> is false) of the series used in fitting and for use in prediction.
<code>x.intercept</code>	The intercept in the model for $x - x.mean$ , or zero if <code>intercept</code> is false.

aic	The differences in AIC between each model and the best-fitting model. Note that the latter can have an AIC of $-\text{Inf}$ .
n.used	The number of observations in the time series.
order.max	The value of the <code>order.max</code> argument.
partialacf	NULL. For compatibility with <code>ar</code> .
resid	residuals from the fitted model, conditioning on the first <code>order</code> observations. The first <code>order</code> residuals are set to NA. If <code>x</code> is a time series, so is <code>resid</code> .
method	The character string "Unconstrained LS".
series	The name(s) of the time series.
frequency	The frequency of the time series.
call	The matched call.
asy.se.coef	The asymptotic-theory standard errors of the coefficient estimates.

**Author(s)**

Adrian Trapletti, Brian Ripley.

**References**

Luetkepohl, H. (1991): *Introduction to Multiple Time Series Analysis*. Springer Verlag, NY, pp. 368–370.

**See Also**

[ar](#)

**Examples**

```
ar(lh, method="burg")
ar.ols(lh)
ar.ols(lh, FALSE, 4) # fit ar(4)

ar.ols(ts.union(BJsales, BJsales.lead))

x <- diff(log(EuStockMarkets))
ar.ols(x, order.max=6, demean=FALSE, intercept=TRUE)
```

---

arima

*ARIMA Modelling of Time Series*


---

**Description**

Fit an ARIMA model to a univariate time series.

**Usage**

```
arima(x, order = c(0, 0, 0),
      seasonal = list(order = c(0, 0, 0), period = NA),
      xreg = NULL, include.mean = TRUE,
      transform.pars = TRUE,
      fixed = NULL, init = NULL,
      method = c("CSS-ML", "ML", "CSS"),
      n.cond, optim.method = "BFGS",
      optim.control = list(), kappa = 1e6)
```

**Arguments**

<code>x</code>	a univariate time series
<code>order</code>	A specification of the non-seasonal part of the ARIMA model: the three components ( $p, d, q$ ) are the AR order, the degree of differencing, and the MA order.
<code>seasonal</code>	A specification of the seasonal part of the ARIMA model, plus the period (which defaults to <code>frequency(x)</code> ). This should be a list with components <code>order</code> and <code>period</code> , but a specification of just a numeric vector of length 3 will be turned into a suitable list with the specification as the <code>order</code> .
<code>xreg</code>	Optionally, a vector or matrix of external regressors, which must have the same number of rows as <code>x</code> .
<code>include.mean</code>	Should the ARMA model include a mean/intercept term? The default is <code>TRUE</code> for undifferenced series, and it is ignored for ARIMA models with differencing.
<code>transform.pars</code>	Logical. If true, the AR parameters are transformed to ensure that they remain in the region of stationarity. Not used for <code>method = "CSS"</code> .
<code>fixed</code>	optional numeric vector of the same length as the total number of parameters. If supplied, only NA entries in <code>fixed</code> will be varied. <code>transform.pars = TRUE</code> will be overridden (with a warning) if any AR parameters are fixed. It may be wise to set <code>transform.pars = FALSE</code> when fixing MA parameters, especially near non-invertibility.
<code>init</code>	optional numeric vector of initial parameter values. Missing values will be filled in, by zeroes except for regression coefficients. Values already specified in <code>fixed</code> will be ignored.
<code>method</code>	Fitting method: maximum likelihood or minimize conditional sum-of-squares. The default (unless there are missing values) is to use conditional-sum-of-squares to find starting values, then maximum likelihood.
<code>n.cond</code>	Only used if fitting by conditional-sum-of-squares: the number of initial observations to ignore. It will be ignored if less than the maximum lag of an AR term.
<code>optim.method</code>	The value passed as the <code>method</code> argument to <code>optim</code> .
<code>optim.control</code>	List of control parameters for <code>optim</code> .
<code>kappa</code>	the prior variance (as a multiple of the innovations variance) for the past observations in a differenced model. Do not reduce this.

## Details

Different definitions of ARMA models have different signs for the AR and/or MA coefficients. The definition used here has

$$X_t = a_1 X_{t-1} + \dots + a_p X_{t-p} + e_t + b_1 e_{t-1} + \dots + b_q e_{t-q}$$

and so the MA coefficients differ in sign from those of S-PLUS. Further, if `include.mean` is true (the default for an ARMA model), this formula applies to  $X - m$  rather than  $X$ . For ARIMA models with differencing, the differenced series follows a zero-mean ARMA model. If an `xreg` term is included, a linear regression (with a constant term if `include.mean` is true and there is no differencing) is fitted with an ARMA model for the error term.

The variance matrix of the estimates is found from the Hessian of the log-likelihood, and so may only be a rough guide.

Optimization is done by `optim`. It will work best if the columns in `xreg` are roughly scaled to zero mean and unit variance, but does attempt to estimate suitable scalings.

## Value

A list of class "Arima" with components:

<code>coef</code>	a vector of AR, MA and regression coefficients, which can be extracted by the <code>coef</code> method.
<code>sigma2</code>	the MLE of the innovations variance.
<code>var.coef</code>	the estimated variance matrix of the coefficients <code>coef</code> , which can be extracted by the <code>vcov</code> method.
<code>loglik</code>	the maximized log-likelihood (of the differenced data), or the approximation to it used.
<code>arma</code>	A compact form of the specification, as a vector giving the number of AR, MA, seasonal AR and seasonal MA coefficients, plus the period and the number of non-seasonal and seasonal differences.
<code>aic</code>	the AIC value corresponding to the log-likelihood. Only valid for <code>method = "ML"</code> fits.
<code>residuals</code>	the fitted innovations.
<code>call</code>	the matched call.
<code>series</code>	the name of the series <code>x</code> .
<code>code</code>	the convergence value returned by <code>optim</code> .
<code>n.cond</code>	the number of initial observations not used in the fitting.
<code>model</code>	A list representing the Kalman Filter used in the fitting. See <code>KalmanLike</code> .

## Fitting methods

The exact likelihood is computed via a state-space representation of the ARIMA process, and the innovations and their variance found by a Kalman filter. The initialization of the differenced ARMA process uses stationarity and is based on Gardner *et al.* (1980). For a differenced process the non-stationary components are given a diffuse prior (controlled by `kappa`). Observations which are still controlled by the diffuse prior (determined by having a Kalman gain of at least  $1e4$ ) are excluded from the likelihood calculations. (This gives comparable results to `arima0` in the absence of missing values, when the observations excluded are precisely those dropped by the differencing.)

Missing values are allowed, and are handled exactly in method "ML".

If `transform.pars` is true, the optimization is done using an alternative parametrization which is a variation on that suggested by Jones (1980) and ensures that the model is stationary. For an AR(p) model the parametrization is via the inverse tanh of the partial autocorrelations: the same procedure is applied (separately) to the AR and seasonal AR terms. The MA terms are not constrained to be invertible during optimization, but they will be converted to invertible form after optimization if `transform.pars` is true.

Conditional sum-of-squares is provided mainly for expositional purposes. This computes the sum of squares of the fitted innovations from observation `n.cond` on, (where `n.cond` is at least the maximum lag of an AR term), treating all earlier innovations to be zero. Argument `n.cond` can be used to allow comparability between different fits. The 'part log-likelihood' is the first term, half the log of the estimated mean square. Missing values are allowed, but will cause many of the innovations to be missing.

When regressors are specified, they are orthogonalized prior to fitting unless any of the coefficients is fixed. It can be helpful to roughly scale the regressors to zero mean and unit variance.

### Note

The results are likely to be different from S-PLUS's `arima.mle`, which computes a conditional likelihood and does not include a mean in the model. Further, the convention used by `arima.mle` reverses the signs of the MA coefficients.

`arima` is very similar to `arima0` for ARMA models or for differenced models without missing values, but handles differenced models with missing values exactly. It is somewhat slower than `arima0`, particularly for seasonally differenced models.

### References

- Brockwell, P. J. and Davis, R. A. (1996) *Introduction to Time Series and Forecasting*. Springer, New York. Sections 3.3 and 8.3.
- Durbin, J. and Koopman, S. J. (2001) *Time Series Analysis by State Space Methods*. Oxford University Press.
- Gardner, G, Harvey, A. C. and Phillips, G. D. A. (1980) Algorithm AS154. An algorithm for exact maximum likelihood estimation of autoregressive-moving average models by means of Kalman filtering. *Applied Statistics* **29**, 311–322.
- Harvey, A. C. (1993) *Time Series Models*, 2nd Edition, Harvester Wheatsheaf, sections 3.3 and 4.4.
- Jones, R. H. (1980) Maximum likelihood fitting of ARMA models to time series with missing observations. *Technometrics* **20** 389–395.

### See Also

[predict.Arima](#), [arima.sim](#) for simulating from an ARIMA model, [tsdiag](#), [arima0](#), [ar](#)

### Examples

```
arima(lh, order = c(1,0,0))
arima(lh, order = c(3,0,0))
arima(lh, order = c(1,0,1))

arima(lh, order = c(3,0,0), method = "CSS")

arima(USAccDeaths, order = c(0,1,1), seasonal = list(order=c(0,1,1)))
```

```

arima(USAccDeaths, order = c(0,1,1), seasonal = list(order=c(0,1,1)),
      method = "CSS") # drops first 13 observations.
# for a model with as few years as this, we want full ML

arima(LakeHuron, order = c(2,0,0), xreg = time(LakeHuron)-1920)

## presidents contains NAs
## graphs in example(acf) suggest order 1 or 3
require(graphics)
(fit1 <- arima(presidents, c(1, 0, 0)))
tsdiag(fit1)
(fit3 <- arima(presidents, c(3, 0, 0))) # smaller AIC
tsdiag(fit3)

```

arima.sim

*Simulate from an ARIMA Model*

## Description

Simulate from an ARIMA model.

## Usage

```

arima.sim(model, n, rand.gen = rnorm, innov = rand.gen(n, ...),
          n.start = NA, start.innov = rand.gen(n.start, ...),
          ...)

```

## Arguments

model	A list with component <code>ar</code> and/or <code>ma</code> giving the AR and MA coefficients respectively. Optionally a component <code>order</code> can be used. An empty list gives an ARIMA(0, 0, 0) model, that is white noise.
n	length of output series, before un-differencing.
rand.gen	optional: a function to generate the innovations.
innov	an optional times series of innovations. If not provided, <code>rand.gen</code> is used.
n.start	length of ‘burn-in’ period. If NA, the default, a reasonable value is computed.
start.innov	an optional times series of innovations to be used for the burn-in period. If supplied there must be at least <code>n.start</code> values (and <code>n.start</code> is by default computed inside the function).
...	additional arguments for <code>rand.gen</code> . Most usefully, the standard deviation of the innovations generated by <code>rnorm</code> can be specified by <code>sd</code> .

## Details

See [arima](#) for the precise definition of an ARIMA model.

The ARMA model is checked for stationarity.

ARIMA models are specified via the `order` component of `model`, in the same way as for [arima](#). Other aspects of the `order` component are ignored, but inconsistent specifications of the MA and AR orders are detected. The un-differencing assumes previous values of zero, and to remind the user of this, those values are returned.

Random inputs for the ‘burn-in’ period are generated by calling `rand.gen`.



**Value**

A time-series object of class "ts".

**See Also**

[arima](#)

**Examples**

```
require(graphics)

arima.sim(n = 63, list(ar = c(0.8897, -0.4858), ma = c(-0.2279, 0.2488)),
          sd = sqrt(0.1796))
# mildly long-tailed
arima.sim(n = 63, list(ar=c(0.8897, -0.4858), ma=c(-0.2279, 0.2488)),
          rand.gen = function(n, ...) sqrt(0.1796) * rt(n, df = 5))

# An ARIMA simulation
ts.sim <- arima.sim(list(order = c(1,1,0), ar = 0.7), n = 200)
ts.plot(ts.sim)
```

---

arima0

*ARIMA Modelling of Time Series – Preliminary Version*


---

**Description**

Fit an ARIMA model to a univariate time series, and forecast from the fitted model.

**Usage**

```
arima0(x, order = c(0, 0, 0),
       seasonal = list(order = c(0, 0, 0), period = NA),
       xreg = NULL, include.mean = TRUE, delta = 0.01,
       transform.pars = TRUE, fixed = NULL, init = NULL,
       method = c("ML", "CSS"), n.cond, optim.control = list())

## S3 method for class 'arima0':
predict(object, n.ahead = 1, newxreg, se.fit = TRUE, ...)
```

**Arguments**

x	a univariate time series
order	A specification of the non-seasonal part of the ARIMA model: the three components ( $p, d, q$ ) are the AR order, the degree of differencing, and the MA order.
seasonal	A specification of the seasonal part of the ARIMA model, plus the period (which defaults to <code>frequency(x)</code> ). This should be a list with components <code>order</code> and <code>period</code> , but a specification of just a numeric vector of length 3 will be turned into a suitable list with the specification as the <code>order</code> .
xreg	Optionally, a vector or matrix of external regressors, which must have the same number of rows as <code>x</code> .

<code>include.mean</code>	Should the ARIMA model include a mean term? The default is <code>TRUE</code> for undifferenced series, <code>FALSE</code> for differenced ones (where a mean would not affect the fit nor predictions).
<code>delta</code>	A value to indicate at which point ‘fast recursions’ should be used. See the ‘Details’ section.
<code>transform.pars</code>	Logical. If true, the AR parameters are transformed to ensure that they remain in the region of stationarity. Not used for <code>method = "CSS"</code> .
<code>fixed</code>	optional numeric vector of the same length as the total number of parameters. If supplied, only NA entries in <code>fixed</code> will be varied. <code>transform.pars = TRUE</code> will be overridden (with a warning) if any ARMA parameters are fixed.
<code>init</code>	optional numeric vector of initial parameter values. Missing values will be filled in, by zeroes except for regression coefficients. Values already specified in <code>fixed</code> will be ignored.
<code>method</code>	Fitting method: maximum likelihood or minimize conditional sum-of-squares.
<code>n.cond</code>	Only used if fitting by conditional-sum-of-squares: the number of initial observations to ignore. It will be ignored if less than the maximum lag of an AR term.
<code>optim.control</code>	List of control parameters for <code>optim</code> .
<code>object</code>	The result of an <code>arima0</code> fit.
<code>newxreg</code>	New values of <code>xreg</code> to be used for prediction. Must have at least <code>n.ahead</code> rows.
<code>n.ahead</code>	The number of steps ahead for which prediction is required.
<code>se.fit</code>	Logical: should standard errors of prediction be returned?
<code>...</code>	arguments passed to or from other methods.

## Details

Different definitions of ARMA models have different signs for the AR and/or MA coefficients. The definition here has

$$X_t = a_1 X_{t-1} + \dots + a_p X_{t-p} + e_t + b_1 e_{t-1} + \dots + b_q e_{t-q}$$

and so the MA coefficients differ in sign from those of S-PLUS. Further, if `include.mean` is true, this formula applies to  $X - m$  rather than  $X$ . For ARIMA models with differencing, the differenced series follows a zero-mean ARMA model.

The variance matrix of the estimates is found from the Hessian of the log-likelihood, and so may only be a rough guide, especially for fits close to the boundary of invertibility.

Optimization is done by `optim`. It will work best if the columns in `xreg` are roughly scaled to zero mean and unit variance, but does attempt to estimate suitable scalings.

Finite-history prediction is used. This is only statistically efficient if the MA part of the fit is invertible, so `predict.arima0` will give a warning for non-invertible MA models.

**Value**

For `arima0`, a list of class "arima0" with components:

<code>coef</code>	a vector of AR, MA and regression coefficients,
<code>sigma2</code>	the MLE of the innovations variance.
<code>var.coef</code>	the estimated variance matrix of the coefficients <code>coef</code> .
<code>loglik</code>	the maximized log-likelihood (of the differenced data), or the approximation to it used.
<code>arma</code>	A compact form of the specification, as a vector giving the number of AR, MA, seasonal AR and seasonal MA coefficients, plus the period and the number of non-seasonal and seasonal differences.
<code>aic</code>	the AIC value corresponding to the log-likelihood. Only valid for <code>method = "ML"</code> fits.
<code>residuals</code>	the fitted innovations.
<code>call</code>	the matched call.
<code>series</code>	the name of the series <code>x</code> .
<code>convergence</code>	the value returned by <code>optim</code> .
<code>n.cond</code>	the number of initial observations not used in the fitting.

For `predict.arima0`, a time series of predictions, or if `se.fit = TRUE`, a list with components `pred`, the predictions, and `se`, the estimated standard errors. Both components are time series.

**Fitting methods**

The exact likelihood is computed via a state-space representation of the ARMA process, and the innovations and their variance found by a Kalman filter based on Gardner *et al.* (1980). This has the option to switch to 'fast recursions' (assume an effectively infinite past) if the innovations variance is close enough to its asymptotic bound. The argument `delta` sets the tolerance: at its default value the approximation is normally negligible and the speed-up considerable. Exact computations can be ensured by setting `delta` to a negative value.

If `transform.pars` is true, the optimization is done using an alternative parametrization which is a variation on that suggested by Jones (1980) and ensures that the model is stationary. For an AR(p) model the parametrization is via the inverse tanh of the partial autocorrelations: the same procedure is applied (separately) to the AR and seasonal AR terms. The MA terms are also constrained to be invertible during optimization by the same transformation if `transform.pars` is true. Note that the MLE for MA terms does sometimes occur for MA polynomials with unit roots: such models can be fitted by using `transform.pars = FALSE` and specifying a good set of initial values (often obtainable from a fit with `transform.pars = TRUE`).

Missing values are allowed, but any missing values will force `delta` to be ignored and full recursions used. Note that missing values will be propagated by differencing, so the procedure used in this function is not fully efficient in that case.

Conditional sum-of-squares is provided mainly for expositional purposes. This computes the sum of squares of the fitted innovations from observation `n.cond` on, (where `n.cond` is at least the maximum lag of an AR term), treating all earlier innovations to be zero. Argument `n.cond` can be used to allow comparability between different fits. The 'part log-likelihood' is the first term, half the log of the estimated mean square. Missing values are allowed, but will cause many of the innovations to be missing.

When regressors are specified, they are orthogonalized prior to fitting unless any of the coefficients is fixed. It can be helpful to roughly scale the regressors to zero mean and unit variance.

**Note**

This is a preliminary version, and will be replaced by [arima](#).

The standard errors of prediction exclude the uncertainty in the estimation of the ARMA model and the regression coefficients.

The results are likely to be different from S-PLUS's `arima.mle`, which computes a conditional likelihood and does not include a mean in the model. Further, the convention used by `arima.mle` reverses the signs of the MA coefficients.

**References**

Brockwell, P. J. and Davis, R. A. (1996) *Introduction to Time Series and Forecasting*. Springer, New York. Sections 3.3 and 8.3.

Gardner, G, Harvey, A. C. and Phillips, G. D. A. (1980) Algorithm AS154. An algorithm for exact maximum likelihood estimation of autoregressive-moving average models by means of Kalman filtering. *Applied Statistics* **29**, 311–322.

Harvey, A. C. (1993) *Time Series Models*, 2nd Edition, Harvester Wheatsheaf, sections 3.3 and 4.4.

Harvey, A. C. and McKenzie, C. R. (1982) Algorithm AS182. An algorithm for finite sample prediction from ARIMA processes. *Applied Statistics* **31**, 180–187.

Jones, R. H. (1980) Maximum likelihood fitting of ARMA models to time series with missing observations. *Technometrics* **20** 389–395.

**See Also**

[arima](#), [ar](#), [tsdiag](#)

**Examples**

```
## Not run: arima0(lh, order = c(1,0,0))
arima0(lh, order = c(3,0,0))
arima0(lh, order = c(1,0,1))
predict(arima0(lh, order = c(3,0,0)), n.ahead = 12)

arima0(lh, order = c(3,0,0), method = "CSS")

# for a model with as few years as this, we want full ML
(fit <- arima0(USAccDeaths, order = c(0,1,1),
              seasonal = list(order=c(0,1,1)), delta = -1))
predict(fit, n.ahead = 6)

arima0(LakeHuron, order = c(2,0,0), xreg = time(LakeHuron)-1920)
## Not run:
## presidents contains NAs
## graphs in example(acf) suggest order 1 or 3
(fit1 <- arima0(presidents, c(1, 0, 0), delta = -1)) # avoid warning
tsdiag(fit1)
(fit3 <- arima0(presidents, c(3, 0, 0), delta = -1)) # smaller AIC
tsdiag(fit3)
## End(Not run)
```

ARMAacf

*Compute Theoretical ACF for an ARMA Process***Description**

Compute the theoretical autocorrelation function or partial autocorrelation function for an ARMA process.

**Usage**

```
ARMAacf(ar = numeric(0), ma = numeric(0), lag.max = r, pacf = FALSE)
```

**Arguments**

ar	numeric vector of AR coefficients
ma	numeric vector of MA coefficients
lag.max	integer. Maximum lag required. Defaults to $\max(p, q+1)$ , where $p$ , $q$ are the numbers of AR and MA terms respectively.
pacf	logical. Should the partial autocorrelations be returned?

**Details**

The methods used follow Brockwell & Davis (1991, section 3.3). Their equations (3.3.8) are solved for the autocovariances at lags  $0, \dots, \max(p, q+1)$ , and the remaining autocorrelations are given by a recursive filter.

**Value**

A vector of (partial) autocorrelations, named by the lags.

**References**

Brockwell, P. J. and Davis, R. A. (1991) *Time Series: Theory and Methods*, Second Edition. Springer.

**See Also**

[arima](#), [ARMAtoMA](#), [acf2AR](#) for inverting part of ARMAacf; further [filter](#).

**Examples**

```
ARMAacf(c(1.0, -0.25), 1.0, lag.max = 10)

## Example from Brockwell & Davis (1991, pp.92-4)
## answer 2^(-n) * (32/3 + 8 * n) / (32/3)
n <- 1:10; 2^(-n) * (32/3 + 8 * n) / (32/3)
ARMAacf(c(1.0, -0.25), 1.0, lag.max = 10, pacf = TRUE)
ARMAacf(c(1.0, -0.25), lag.max = 10, pacf = TRUE)

## Cov-Matrix of length-7 sub-sample of AR(1) example:
toeplitz(ARMAacf(0.8, lag.max = 7))
```

---

`ARMAtoMA`*Convert ARMA Process to Infinite MA Process*

---

**Description**

Convert ARMA process to infinite MA process.

**Usage**

```
ARMAtoMA(ar = numeric(0), ma = numeric(0), lag.max)
```

**Arguments**

<code>ar</code>	numeric vector of AR coefficients
<code>ma</code>	numeric vector of MA coefficients
<code>lag.max</code>	Largest MA(Inf) coefficient required.

**Value**

A vector of coefficients.

**References**

Brockwell, P. J. and Davis, R. A. (1991) *Time Series: Theory and Methods*, Second Edition. Springer.

**See Also**

[arima](#), [ARMAacf](#).

**Examples**

```
ARMAtoMA(c(1.0, -0.25), 1.0, 10)
## Example from Brockwell & Davis (1991, p.92)
## answer (1 + 3*n)*2^(-n)
n <- 1:10; (1 + 3*n)*2^(-n)
```

---

`as.hclust`*Convert Objects to Class hclust*

---

**Description**

Converts objects from other hierarchical clustering functions to class "hclust".

**Usage**

```
as.hclust(x, ...)
```

**Arguments**

`x` Hierarchical clustering object  
`...` further arguments passed to or from other methods.

**Details**

Currently there is only support for converting objects of class "twins" as produced by the functions `diana` and `agnes` from the package **cluster**. The default method throws an error unless passed an "hclust" object.

**Value**

An object of class "hclust".

**See Also**

[hclust](#), and from package **cluster**, [diana](#) and [agnes](#)

**Examples**

```
x <- matrix(rnorm(30), ncol=3)
hc <- hclust(dist(x), method="complete")

if(require(cluster, quietly=TRUE)) {# is a recommended package
  ag <- agnes(x, method="complete")
  hcag <- as.hclust(ag)
  ## The dendrograms order slightly differently:
  op <- par(mfrow=c(1,2))
  plot(hc) ; mtext("hclust", side=1)
  plot(hcag); mtext("agnes", side=1)
}
```

---

asOneSidedFormula *Convert to One-Sided Formula*

---

**Description**

Names, expressions, numeric values, and character strings are converted to one-sided formulae. If `object` is a formula, it must be one-sided, in which case it is returned unaltered.

**Usage**

```
asOneSidedFormula(object)
```

**Arguments**

`object` a one-sided formula, an expression, a numeric value, or a character string.

**Value**

a one-sided formula representing `object`

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

[formula](#)

**Examples**

```
asOneSidedFormula("age")
asOneSidedFormula(~ age)
```

---

 ave

*Group Averages Over Level Combinations of Factors*

---

**Description**

Subsets of `x[]` are averaged, where each subset consist of those observations with the same factor levels.

**Usage**

```
ave(x, ..., FUN = mean)
```

**Arguments**

<code>x</code>	A numeric.
<code>...</code>	Grouping variables, typically factors, all of the same length as <code>x</code> .
<code>FUN</code>	Function to apply for each factor level combination.

**Value**

A numeric vector, say `y` of length `length(x)`. If `...` is `g1, g2`, e.g., `y[i]` is equal to `FUN(x[j], for all j with g1[j] == g1[i] and g2[j] == g2[i])`.

**See Also**

[mean](#), [median](#).

**Examples**

```
require(graphics)

ave(1:3) # no grouping -> grand mean

attach(warpbreaks)
ave(breaks, wool)
ave(breaks, tension)
ave(breaks, tension, FUN = function(x)mean(x, trim=.1))
plot(breaks, main =
      "ave( Warpbreaks ) for wool x tension combinations")
lines(ave(breaks, wool, tension
          ), type='s', col = "blue")
```



```
lines(ave(breaks, wool, tension, FUN=median), type='s', col = "green")
legend(40, 70, c("mean", "median"), lty=1, col=c("blue", "green"), bg="gray90")
detach()
```

bandwidth

*Bandwidth Selectors for Kernel Density Estimation***Description**

Bandwidth selectors for Gaussian kernels in `density`.

**Usage**

```
bw.nrd0(x)

bw.nrd(x)

bw.ucv(x, nb = 1000, lower = 0.1 * hmax, upper = hmax, tol = 0.1 * lower)

bw.bcv(x, nb = 1000, lower = 0.1 * hmax, upper = hmax, tol = 0.1 * lower)

bw.SJ(x, nb = 1000, lower = 0.1 * hmax, upper = hmax,
      method = c("ste", "dpi"), tol = 0.1 * lower)
```

**Arguments**

<code>x</code>	numeric vector.
<code>nb</code>	number of bins to use.
<code>lower, upper</code>	range over which to minimize. The default is almost always satisfactory. <code>hmax</code> is calculated internally from a normal reference bandwidth.
<code>method</code>	either "ste" ("solve-the-equation") or "dpi" ("direct plug-in").
<code>tol</code>	for method "ste", the convergence tolerance for <code>uniroot</code> . The default leads to bandwidth estimates with only slightly more than one digit accuracy, which is sufficient for practical density estimation, but possibly not for theoretical simulation studies.

**Details**

`bw.nrd0` implements a rule-of-thumb for choosing the bandwidth of a Gaussian kernel density estimator. It defaults to 0.9 times the minimum of the standard deviation and the interquartile range divided by 1.34 times the sample size to the negative one-fifth power (= Silverman's 'rule of thumb', Silverman (1986, page 48, eqn (3.31)) *unless* the quartiles coincide when a positive result will be guaranteed.

`bw.nrd` is the more common variation given by Scott (1992), using factor 1.06.

`bw.ucv` and `bw.bcv` implement unbiased and biased cross-validation respectively.

`bw.SJ` implements the methods of Sheather & Jones (1991) to select the bandwidth using pilot estimation of derivatives.

The algorithm for method "ste" solves an equation (via `uniroot`) and because of that, enlarges the interval `c(lower, upper)` when the boundaries were not user-specified and do not bracket the root.

**Value**

A bandwidth on a scale suitable for the `bw` argument of `density`.

**References**

- Scott, D. W. (1992) *Multivariate Density Estimation: Theory, Practice, and Visualization*. Wiley.
- Sheather, S. J. and Jones, M. C. (1991) A reliable data-based bandwidth selection method for kernel density estimation. *Journal of the Royal Statistical Society series B*, **53**, 683–690.
- Silverman, B. W. (1986) *Density Estimation*. London: Chapman and Hall.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Springer.

**See Also**

[density](#).

[bandwidth.nrd](#), [ucv](#), [bcv](#) and [width.SJ](#) in package **MASS**, which are all scaled to the `width` argument of `density` and so give answers four times as large.

**Examples**

```
require(graphics)

plot(density(precip, n = 1000))
rug(precip)
lines(density(precip, bw="nrd"), col = 2)
lines(density(precip, bw="ucv"), col = 3)
lines(density(precip, bw="bcv"), col = 4)
lines(density(precip, bw="SJ-ste"), col = 5)
lines(density(precip, bw="SJ-dpi"), col = 6)
legend(55, 0.035,
      legend = c("nrd0", "nrd", "ucv", "bcv", "SJ-ste", "SJ-dpi"),
      col = 1:6, lty = 1)
```

---

 bartlett.test

*Bartlett Test of Homogeneity of Variances*


---

**Description**

Performs Bartlett's test of the null that the variances in each of the groups (samples) are the same.

**Usage**

```
bartlett.test(x, ...)

## Default S3 method:
bartlett.test(x, g, ...)

## S3 method for class 'formula':
bartlett.test(formula, data, subset, na.action, ...)
```

**Arguments**

<code>x</code>	a numeric vector of data values, or a list of numeric data vectors representing the respective samples, or fitted linear model objects (inheriting from class "lm").
<code>g</code>	a vector or factor object giving the group for the corresponding elements of <code>x</code> . Ignored if <code>x</code> is a list.
<code>formula</code>	a formula of the form <code>lhs ~ rhs</code> where <code>lhs</code> gives the data values and <code>rhs</code> the corresponding groups.
<code>data</code>	an optional matrix or data frame (or similar: see <code>model.frame</code> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>subset</code>	an optional vector specifying a subset of observations to be used.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. Defaults to <code>getOption("na.action")</code> .
<code>...</code>	further arguments to be passed to or from methods.

**Details**

If `x` is a list, its elements are taken as the samples or fitted linear models to be compared for homogeneity of variances. In this case, the elements must either all be numeric data vectors or fitted linear model objects, `g` is ignored, and one can simply use `bartlett.test(x)` to perform the test. If the samples are not yet contained in a list, use `bartlett.test(list(x, ...))`.

Otherwise, `x` must be a numeric data vector, and `g` must be a vector or factor object of the same length as `x` giving the group for the corresponding elements of `x`.

**Value**

A list of class "htest" containing the following components:

<code>statistic</code>	Bartlett's K-squared test statistic.
<code>parameter</code>	the degrees of freedom of the approximate chi-squared distribution of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>method</code>	the character string "Bartlett test of homogeneity of variances".
<code>data.name</code>	a character string giving the names of the data.

**References**

Bartlett, M. S. (1937). Properties of sufficiency and statistical tests. *Proceedings of the Royal Society of London Series A* **160**, 268–282.

**See Also**

`var.test` for the special case of comparing variances in two samples from normal distributions; `fligner.test` for a rank-based (nonparametric)  $k$ -sample test for homogeneity of variances; `ansari.test` and `mood.test` for two rank based two-sample tests for difference in scale.

**Examples**

```
require(graphics)

plot(count ~ spray, data = InsectSprays)
bartlett.test(InsectSprays$count, InsectSprays$spray)
bartlett.test(count ~ spray, data = InsectSprays)
```

Beta

*The Beta Distribution***Description**

Density, distribution function, quantile function and random generation for the Beta distribution with parameters `shapel` and `shape2` (and optional non-centrality parameter `ncp`).

**Usage**

```
dbeta(x, shapel, shape2, ncp = 0, log = FALSE)
pbeta(q, shapel, shape2, ncp = 0, lower.tail = TRUE, log.p = FALSE)
qbeta(p, shapel, shape2, ncp = 0, lower.tail = TRUE, log.p = FALSE)
rbeta(n, shapel, shape2, ncp = 0)
```

**Arguments**

`x`, `q`            vector of quantiles.  
`p`                 vector of probabilities.  
`n`                 number of observations. If `length(n) > 1`, the length is taken to be the number required.  
`shapel`, `shape2`    positive parameters of the Beta distribution.  
`ncp`               non-centrality parameter.  
`log`, `log.p`       logical; if TRUE, probabilities `p` are given as `log(p)`.  
`lower.tail`       logical; if TRUE (default), probabilities are  $P[X \leq x]$ , otherwise,  $P[X > x]$ .

**Details**

The Beta distribution with parameters `shapel = a` and `shape2 = b` has density

$$f(x) = \frac{\Gamma(a+b)}{\Gamma(a)\Gamma(b)} x^a (1-x)^b$$

for  $a > 0$ ,  $b > 0$  and  $0 \leq x \leq 1$  where the boundary values at  $x = 0$  or  $x = 1$  are defined as by continuity (as limits).

The mean is  $a/(a+b)$  and the variance is  $ab/((a+b)^2(a+b+1))$ .

`pbeta` is closely related to the incomplete beta function. As defined by Abramowitz and Stegun 6.6.1

$$B_x(a, b) = \int_0^x t^{a-1} (1-t)^{b-1} dt,$$

and 6.6.2  $I_x(a, b) = B_x(a, b)/B(a, b)$  where  $B(a, b) = B_1(a, b)$  is the Beta function (`beta`).

$I_x(a, b)$  is `pbeta(x, a, b)`.

The noncentral Beta distribution (with `ncp = λ`) is defined (Johnson et al, 1995, pp. 502) as the distribution of  $X/(X+Y)$  where  $X \sim \chi_{2a}^2(\lambda)$  and  $Y \sim \chi_{2b}^2$ .

**Value**

`dbeta` gives the density, `pbeta` the distribution function, `qbeta` the quantile function, and `rbeta` generates random deviates.

Invalid arguments will result in return value `NaN`, with a warning.

**Source**

The central `dbeta` is based on a binomial probability, using code contributed by Catherine Loader (see `dbinom`) if either shape parameter is larger than one, otherwise directly from the definition. The non-central case is based on the derivation as a Poisson mixture of betas (Johnson *et al*, 1995, pp. 502–3).

The central `pbeta` uses a C translation (and enhancement for `log_p=TRUE`) of

Didonato, A. and Morris, A., Jr. (1992) Algorithm 708: Significant digit computation of the incomplete beta function ratios, *ACM Transactions on Mathematical Software*, **18**, 360–373. (See also Brown, B. and Lawrence Levy, L. (1994) Certification of algorithm 708: Significant digit computation of the incomplete beta, *ACM Transactions on Mathematical Software*, **20**, 393–397.)

The non-central `pbeta` uses a C translation of

Lenth, R. V. (1987) Algorithm AS226: Computing noncentral beta probabilities. *Appl. Statist*, **36**, 241–244, incorporating

Frick, H. (1990)'s AS R84, *Appl. Statist*, **39**, 311–2, and

Lam, M.L. (1995)'s AS R95, *Appl. Statist*, **44**, 551–2.

This computes the lower tail only, so the upper tail suffers from cancellation and a warning will be given when this is likely to be significant.

`qbeta` is based on a C translation of

Cran, G. W., K. J. Martin and G. E. Thomas (1977). Remark AS R19 and Algorithm AS 109, *Applied Statistics*, **26**, 111–114, and subsequent remarks (AS83 and correction).

`rbeta` is based on a C translation of

R. C. H. Cheng (1978). Generating beta variates with nonintegral shape parameters. *Communications of the ACM*, **21**, 317–322.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Abramowitz, M. and Stegun, I. A. (1972) *Handbook of Mathematical Functions*. New York: Dover. Chapter 6: Gamma and Related Functions.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 2, especially chapter 25. Wiley, New York.

**See Also**

[beta](#) for the Beta function, and [dgamma](#) for the Gamma distribution.

**Examples**

```
x <- seq(0, 1, length=21)
dbeta(x, 1, 1)
pbeta(x, 1, 1)
```

---

binom.test	<i>Exact Binomial Test</i>
------------	----------------------------

---

### Description

Performs an exact test of a simple null hypothesis about the probability of success in a Bernoulli experiment.

### Usage

```
binom.test(x, n, p = 0.5,  
           alternative = c("two.sided", "less", "greater"),  
           conf.level = 0.95)
```

### Arguments

x	number of successes, or a vector of length 2 giving the numbers of successes and failures, respectively.
n	number of trials; ignored if x has length 2.
p	hypothesized probability of success.
alternative	indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter.
conf.level	confidence level for the returned confidence interval.

### Details

Confidence intervals are obtained by a procedure first given in Clopper and Pearson (1934). This guarantees that the confidence level is at least `conf.level`, but in general does not give the shortest-length confidence intervals.

### Value

A list with class "htest" containing the following components:

statistic	the number of successes.
parameter	the number of trials.
p.value	the p-value of the test.
conf.int	a confidence interval for the probability of success.
estimate	the estimated probability of success.
null.value	the probability of success under the null, p.
alternative	a character string describing the alternative hypothesis.
method	the character string "Exact binomial test".
data.name	a character string giving the names of the data.

## References

Clopper, C. J. & Pearson, E. S. (1934). The use of confidence or fiducial limits illustrated in the case of the binomial. *Biometrika*, **26**, 404–413.

William J. Conover (1971), *Practical nonparametric statistics*. New York: John Wiley & Sons. Pages 97–104.

Myles Hollander & Douglas A. Wolfe (1973), *Nonparametric Statistical Methods*. New York: John Wiley & Sons. Pages 15–22.

## See Also

[prop.test](#) for a general (approximate) test for equal or given proportions.

## Examples

```
## Conover (1971), p. 97f.
## Under (the assumption of) simple Mendelian inheritance, a cross
## between plants of two particular genotypes produces progeny 1/4 of
## which are "dwarf" and 3/4 of which are "giant", respectively.
## In an experiment to determine if this assumption is reasonable, a
## cross results in progeny having 243 dwarf and 682 giant plants.
## If "giant" is taken as success, the null hypothesis is that p =
## 3/4 and the alternative that p != 3/4.
binom.test(c(682, 243), p = 3/4)
binom.test(682, 682 + 243, p = 3/4) # The same.
## => Data are in agreement with the null hypothesis.
```

---

Binomial

*The Binomial Distribution*

---

## Description

Density, distribution function, quantile function and random generation for the binomial distribution with parameters `size` and `prob`.

## Usage

```
dbinom(x, size, prob, log = FALSE)
pbinom(q, size, prob, lower.tail = TRUE, log.p = FALSE)
qbinom(p, size, prob, lower.tail = TRUE, log.p = FALSE)
rbinom(n, size, prob)
```

## Arguments

<code>x, q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
<code>size</code>	number of trials (zero or more).
<code>prob</code>	probability of success on each trial.
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$ .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .

**Details**

The binomial distribution with `size = n` and `prob = p` has density

$$p(x) = \binom{n}{x} p^x (1-p)^{n-x}$$

for  $x = 0, \dots, n$ .

If an element of `x` is not integer, the result of `dbinom` is zero, with a warning.  $p(x)$  is computed using Loader's algorithm, see the reference below.

The quantile is defined as the smallest value  $x$  such that  $F(x) \geq p$ , where  $F$  is the distribution function.

**Value**

`dbinom` gives the density, `pbinom` gives the distribution function, `qbinom` gives the quantile function and `rbinom` generates random deviates.

If `size` is not an integer, NaN is returned.

**Source**

For `dbinom` a saddle-point expansion is used: see

Catherine Loader (2000). *Fast and Accurate Computation of Binomial Probabilities*; available from <http://www.herine.net/stat/software/dbinom.html>.

`pbinom` uses `pbeta`.

`qbinom` uses the Cornish–Fisher Expansion to include a skewness correction to a normal approximation, followed by a search.

`rbinom` (for `size < .Machine$integer.max`) is based on

Kachitvichyanukul, V. and Schmeiser, B. W. (1988) Binomial random variate generation. *Communications of the ACM*, **31**, 216–222.

**See Also**

`dnbinom` for the negative binomial, and `dpois` for the Poisson distribution.

**Examples**

```
require(graphics)
# Compute P(45 < X < 55) for X Binomial(100,0.5)
sum(dbinom(46:54, 100, 0.5))

## Using "log = TRUE" for an extended range :
n <- 2000
k <- seq(0, n, by = 20)
plot(k, dbinom(k, n, pi/10, log=TRUE), type='l', ylab="log density",
      main = "dbinom(*, log=TRUE) is better than log(dbinom(*))")
lines(k, log(dbinom(k, n, pi/10)), col='red', lwd=2)
## extreme points are omitted since dbinom gives 0.
mtext("dbinom(k, log=TRUE)", adj=0)
mtext("extended range", adj=0, line = -1, font=4)
mtext("log(dbinom(k))", col="red", adj=1)
```



---

 biplot

*Biplot of Multivariate Data*


---

### Description

Plot a biplot on the current graphics device.

### Usage

```
biplot(x, ...)
```

## Default S3 method:

```
biplot(x, y, var.axes = TRUE, col, cex = rep(par("cex"), 2),
       xlabs = NULL, ylabs = NULL, expand = 1,
       xlim = NULL, ylim = NULL, arrow.len = 0.1,
       main = NULL, sub = NULL, xlab = NULL, ylab = NULL, ...)
```

### Arguments

<code>x</code>	The <code>biplot</code> , a fitted object. For <code>biplot.default</code> , the first set of points (a two-column matrix), usually associated with observations.
<code>y</code>	The second set of points (a two-column matrix), usually associated with variables.
<code>var.axes</code>	If <code>TRUE</code> the second set of points have arrows representing them as (unscaled) axes.
<code>col</code>	A vector of length 2 giving the colours for the first and second set of points respectively (and the corresponding axes). If a single colour is specified it will be used for both sets. If missing the default colour is looked for in the <code>palette</code> : if there it and the next colour as used, otherwise the first two colours of the palette are used.
<code>cex</code>	The character expansion factor used for labelling the points. The labels can be of different sizes for the two sets by supplying a vector of length two.
<code>xlabs</code>	A vector of character strings to label the first set of points: the default is to use the row dimname of <code>x</code> , or <code>1:n</code> is the dimname is <code>NULL</code> .
<code>ylabs</code>	A vector of character strings to label the second set of points: the default is to use the row dimname of <code>y</code> , or <code>1:n</code> is the dimname is <code>NULL</code> .
<code>expand</code>	An expansion factor to apply when plotting the second set of points relative to the first. This can be used to tweak the scaling of the two sets to a physically comparable scale.
<code>arrow.len</code>	The length of the arrow heads on the axes plotted in <code>var.axes</code> is true. The arrow head can be suppressed by <code>arrow.len = 0</code> .
<code>xlim, ylim</code>	Limits for the x and y axes in the units of the first set of variables.
<code>main, sub, xlab, ylab, ...</code>	graphical parameters.

**Details**

A biplot is plot which aims to represent both the observations and variables of a matrix of multivariate data on the same plot. There are many variations on biplots (see the references) and perhaps the most widely used one is implemented by `biplot.princomp`. The function `biplot.default` merely provides the underlying code to plot two sets of variables on the same figure.

Graphical parameters can also be given to `biplot`: the size of `xlabs` and `ylabs` is controlled by `cex`.

**Side Effects**

a plot is produced on the current graphics device.

**References**

K. R. Gabriel (1971). The biplot graphical display of matrices with application to principal component analysis. *Biometrika* **58**, 453–467.

J.C. Gower and D. J. Hand (1996). *Biplots*. Chapman & Hall.

**See Also**

`biplot.princomp`, also for examples.

---

`biplot.princomp`      *Biplot for Principal Components*

---

**Description**

Produces a biplot (in the strict sense) from the output of `princomp` or `prcomp`

**Usage**

```
## S3 method for class 'prcomp':
biplot(x, choices = 1:2, scale = 1, pc.biplot = FALSE, ...)

## S3 method for class 'princomp':
biplot(x, choices = 1:2, scale = 1, pc.biplot = FALSE, ...)
```

**Arguments**

<code>x</code>	an object of class "princomp".
<code>choices</code>	length 2 vector specifying the components to plot. Only the default is a biplot in the strict sense.
<code>scale</code>	The variables are scaled by $\lambda^{\text{scale}}$ and the observations are scaled by $\lambda^{(1-\text{scale})}$ where $\lambda$ are the singular values as computed by <code>princomp</code> . Normally $0 \leq \text{scale} \leq 1$ , and a warning will be issued if the specified <code>scale</code> is outside this range.
<code>pc.biplot</code>	If true, use what Gabriel (1971) refers to as a "principal component biplot", with $\lambda = 1$ and observations scaled up by $\sqrt{n}$ and variables scaled down by $\sqrt{n}$ . Then inner products between variables approximate covariances and distances between observations approximate Mahalanobis distance.
<code>...</code>	optional arguments to be passed to <code>biplot.default</code> .

**Details**

This is a method for the generic function `biplot`. There is considerable confusion over the precise definitions: those of the original paper, Gabriel (1971), are followed here. Gabriel and Odoroff (1990) use the same definitions, but their plots actually correspond to `pc.biplot = TRUE`.

**Side Effects**

a plot is produced on the current graphics device.

**References**

- Gabriel, K. R. (1971). The biplot graphical display of matrices with applications to principal component analysis. *Biometrika*, **58**, 453–467.
- Gabriel, K. R. and Odoroff, C. L. (1990). Biplots in biomedical research. *Statistics in Medicine*, **9**, 469–485.

**See Also**

[biplot](#), [princomp](#).

**Examples**

```
require(graphics)
biplot(princomp(USArrests))
```

---

birthday

*Probability of coincidences*

---

**Description**

Computes approximate answers to a generalised *birthday paradox* problem. `pbirthday` computes the probability of a coincidence and `qbirthday` computes the number of observations needed to have a specified probability of coincidence.

**Usage**

```
qbirthday(prob = 0.5, classes = 365, coincident = 2)
pbirthday(n, classes = 365, coincident = 2)
```

**Arguments**

<code>classes</code>	How many distinct categories the people could fall into
<code>prob</code>	The desired probability of coincidence
<code>n</code>	The number of people
<code>coincident</code>	The number of people to fall in the same category

**Details**

The birthday paradox is that a very small number of people, 23, suffices to have a 50-50 chance that two of them have the same birthday. This function generalises the calculation to probabilities other than 0.5, numbers of coincident events other than 2, and numbers of classes other than 365.

This formula is approximate, as the example below shows. For `coincident=2` the exact computation is straightforward and may be preferable.

**Value**

`qbirthday`      Number of people needed for a probability `prob` that `k` of them have the same one out of `classes` equiprobable labels.

`pbirthday`      Probability of the specified coincidence

**References**

Diaconis, P. and Mosteller F. (1989) Methods for studying coincidences. J. American Statistical Association, **84**, 853-861.

**Examples**

```
require(graphics)

## the standard version
qbirthday()
## same 4-digit PIN number
qbirthday(classes=10^4)
## 0.9 probability of three coincident birthdays
qbirthday(coincident=3, prob=0.9)
## Chance of 4 coincident birthdays in 150 people
pbirthday(150, coincident=4)
## 100 coincident birthdays in 1000 people: *very* rare:
pbirthday(1000, coincident=100)

## Accuracy compared to exact calculation
x1<- sapply(10:100, pbirthday)
x2<- 1-sapply(10:100, function(n)prod((365:(365-n+1))/rep(365,n)))
par(mfrow=c(2,2))
plot(x1, x2, xlab="approximate", ylab="exact")
abline(0,1)
plot(x1, x1-x2, xlab="approximate", ylab="error")
abline(h=0)
plot(x1, x2, log="xy", xlab="approximate", ylab="exact")
abline(0,1)
plot(1-x1, 1-x2, log="xy", xlab="approximate", ylab="exact")
abline(0,1)
```

**Description**

Compute the Box–Pierce or Ljung–Box test statistic for examining the null hypothesis of independence in a given time series. These are sometimes known as ‘portmanteau’ tests.

**Usage**

```
Box.test(x, lag = 1, type = c("Box-Pierce", "Ljung-Box"), fitdf = 0)
```

**Arguments**

`x` a numeric vector or univariate time series.  
`lag` the statistic will be based on `lag` autocorrelation coefficients.  
`type` test to be performed: partial matching is used.  
`fitdf` number of degrees of freedom to be subtracted if `x` is a series of residuals.

**Details**

These tests are sometimes applied to the residuals from an ARMA( $p$ ,  $q$ ) fit, in which case the references suggest a better approximation to the null-hypothesis distribution is obtained by setting `fitdf = p+q`, provided of course that `lag > fitdf`.

**Value**

A list with class "htest" containing the following components:

`statistic` the value of the test statistic.  
`parameter` the degrees of freedom of the approximate chi-squared distribution of the test statistic (taking `fitdf` into account).  
`p.value` the p-value of the test.  
`method` a character string indicating which type of test was performed.  
`data.name` a character string giving the name of the data.

**Note**

Missing values are not handled.

**Author(s)**

A. Trapletti

**References**

Box, G. E. P. and Pierce, D. A. (1970), Distribution of residual correlations in autoregressive-integrated moving average time series models. *Journal of the American Statistical Association*, **65**, 1509–1526.

Ljung, G. M. and Box, G. E. P. (1978), On a measure of lack of fit in time series models. *Biometrika* **65**, 297–303.

Harvey, A. C. (1993) *Time Series Models*. 2nd Edition, Harvester Wheatsheaf, NY, pp. 44, 45.

**Examples**

```
x <- rnorm(100)
Box.test(x, lag = 1)
Box.test(x, lag = 1, type="Ljung")
```

---

C *Sets Contrasts for a Factor*


---

**Description**

Sets the "contrasts" attribute for the factor.

**Usage**

```
C(object, contr, how.many, ...)
```

**Arguments**

object	a factor or ordered factor
contr	which contrasts to use. Can be a matrix with one row for each level of the factor or a suitable function like <code>contr.poly</code> or a character string giving the name of the function
how.many	the number of contrasts to set, by default one less than <code>nlevels(object)</code> .
...	additional arguments for the function <code>contr</code> .

**Details**

For compatibility with S, `contr` can be `treatment`, `helmert`, `sum` or `poly` (without quotes) as shorthand for `contr.treatment` and so on.

**Value**

The factor `object` with the "contrasts" attribute set.

**References**

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models*. Chapter 2 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

`contrasts`, `contr.sum`, etc.

**Examples**

```
## reset contrasts to defaults
options(contrasts=c("contr.treatment", "contr.poly"))
tens <- with(warpbreaks, C(tension, poly, 1))
attributes(tens)
## tension SHOULD be an ordered factor, but as it is not we can use
aov(breaks ~ wool + tens + tension, data=warpbreaks)

## show the use of ... The default contrast is contr.treatment here
summary(lm(breaks ~ wool + C(tension, base=2), data=warpbreaks))

# following on from help(esoph)
```

```

model3 <- glm(cbind(ncases, ncontrols) ~ agegp + C(tobgp, , 1) +
             C(alcgp, , 1), data = esoph, family = binomial())
summary(model3)

```

---

cancor

*Canonical Correlations*


---

## Description

Compute the canonical correlations between two data matrices.

## Usage

```
cancor(x, y, xcenter = TRUE, ycenter = TRUE)
```

## Arguments

x	numeric matrix ( $n \times p_1$ ), containing the x coordinates.
y	numeric matrix ( $n \times p_2$ ), containing the y coordinates.
xcenter	logical or numeric vector of length $p_1$ , describing any centering to be done on the x values before the analysis. If TRUE (default), subtract the column means. If FALSE, do not adjust the columns. Otherwise, a vector of values to be subtracted from the columns.
ycenter	analogous to xcenter, but for the y values.

## Details

The canonical correlation analysis seeks linear combinations of the y variables which are well explained by linear combinations of the x variables. The relationship is symmetric as ‘well explained’ is measured by correlations.

## Value

A list containing the following components:

cor	correlations.
xcoef	estimated coefficients for the x variables.
ycoef	estimated coefficients for the y variables.
xcenter	the values used to adjust the x variables.
ycenter	the values used to adjust the x variables.

## References

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- Hotelling H. (1936). Relations between two sets of variables. *Biometrika*, **28**, 321–327.
- Seber, G. A. F. (1984). *Multivariate Observations*. New York: Wiley, p. 506f.

**See Also**

[qr](#), [svd](#).

**Examples**

```
pop <- LifeCycleSavings[, 2:3]
oec <- LifeCycleSavings[, -(2:3)]
cancor(pop, oec)

x <- matrix(rnorm(150), 50, 3)
y <- matrix(rnorm(250), 50, 5)
(cxy <- cancor(x, y))
all(abs(cor(x %*% cxy$xcoef,
            y %*% cxy$ycoef)[,1:3] - diag(cxy $ cor)) < 1e-15)
all(abs(cor(x %*% cxy$xcoef) - diag(3)) < 1e-15)
all(abs(cor(y %*% cxy$ycoef) - diag(5)) < 1e-15)
```

---

case/variable.names

*Case and Variable Names of Fitted Models*

---

**Description**

Simple utilities returning (non-missing) case names, and (non-eliminated) variable names.

**Usage**

```
case.names(object, ...)
## S3 method for class 'lm':
case.names(object, full = FALSE, ...)

variable.names(object, ...)
## S3 method for class 'lm':
variable.names(object, full = FALSE, ...)
```

**Arguments**

<code>object</code>	an R object, typically a fitted model.
<code>full</code>	logical; if TRUE, all names (including zero weights, ...) are returned.
<code>...</code>	further arguments passed to or from other methods.

**Value**

A character vector.

**See Also**

[lm](#); further, [all.names](#), [all.vars](#) for functions with a similar name but only slightly related purpose.



**Examples**

```
x <- 1:20
y <- x + (x/4 - 2)^3 + rnorm(20, sd=3)
names(y) <- paste("0",x,sep=".")
ww <- rep(1,20); ww[13] <- 0
summary(lmxy <- lm(y ~ x + I(x^2)+I(x^3) + I((x-10)^2),
                 weights = ww), cor = TRUE)
variable.names(lmxy)
variable.names(lmxy, full= TRUE)# includes the last
case.names(lmxy)
case.names(lmxy, full = TRUE)# includes the 0-weight case
```

Cauchy

*The Cauchy Distribution***Description**

Density, distribution function, quantile function and random generation for the Cauchy distribution with location parameter `location` and scale parameter `scale`.

**Usage**

```
dcauchy(x, location = 0, scale = 1, log = FALSE)
pcauchy(q, location = 0, scale = 1, lower.tail = TRUE, log.p = FALSE)
qcauchy(p, location = 0, scale = 1, lower.tail = TRUE, log.p = FALSE)
rcauchy(n, location = 0, scale = 1)
```

**Arguments**

`x`, `q`            vector of quantiles.  
`p`                 vector of probabilities.  
`n`                 number of observations. If `length(n) > 1`, the length is taken to be the number required.  
`location`, `scale`    location and scale parameters.  
`log`, `log.p`        logical; if TRUE, probabilities `p` are given as `log(p)`.  
`lower.tail`        logical; if TRUE (default), probabilities are  $P[X \leq x]$ , otherwise,  $P[X > x]$ .

**Details**

If `location` or `scale` are not specified, they assume the default values of 0 and 1 respectively.

The Cauchy distribution with location  $l$  and scale  $s$  has density

$$f(x) = \frac{1}{\pi s} \left( 1 + \left( \frac{x-l}{s} \right)^2 \right)^{-1}$$

for all  $x$ .

**Value**

dcauchy, pcauchy, and qcauchy are respectively the density, distribution function and quantile function of the Cauchy distribution. rcauchy generates random deviates from the Cauchy.

**Source**

dcauchy, pcauchy and qcauchy are all calculated from numerically stable versions of the definitions.

rcauchy uses inversion.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 1, chapter 16. Wiley, New York.

**See Also**

dt for the t distribution which generalizes dcauchy(\*, l = 0, s = 1).

**Examples**

```
dcauchy(-1:4)
```

---

```
chisq.test
```

*Pearson's Chi-squared Test for Count Data*

---

**Description**

chisq.test performs chi-squared contingency table tests and goodness-of-fit tests.

**Usage**

```
chisq.test(x, y = NULL, correct = TRUE,
           p = rep(1/length(x), length(x)), rescale.p = FALSE,
           simulate.p.value = FALSE, B = 2000)
```

**Arguments**

x	a vector or matrix.
y	a vector; ignored if x is a matrix.
correct	a logical indicating whether to apply continuity correction when computing the test statistic for 2x2 tables: one half is subtracted from all $ O - E $ differences. No correction is done if simulate.p.value = TRUE.
p	a vector of probabilities of the same length of x. An error is given if any entry of p is negative.
rescale.p	a logical scalar; if TRUE then p is rescaled (if necessary) to sum to 1. If rescale.p is FALSE, and p does not sum to 1, an error is given.
simulate.p.value	a logical indicating whether to compute p-values by Monte Carlo simulation.
B	an integer specifying the number of replicates used in the Monte Carlo test.

## Details

If  $x$  is a matrix with one row or column, or if  $x$  is a vector and  $y$  is not given, then a *goodness-of-fit test* is performed ( $x$  is treated as a one-dimensional contingency table). The entries of  $x$  must be non-negative integers. In this case, the hypothesis tested is whether the population probabilities equal those in  $p$ , or are all equal if  $p$  is not given.

If  $x$  is a matrix with at least two rows and columns, it is taken as a two-dimensional contingency table. Again, the entries of  $x$  must be non-negative integers. Otherwise,  $x$  and  $y$  must be vectors or factors of the same length; incomplete cases are removed, the objects are coerced into factor objects, and the contingency table is computed from these. Then, Pearson's chi-squared test of the null hypothesis that the joint distribution of the cell counts in a 2-dimensional contingency table is the product of the row and column marginals is performed.

If `simulate.p.value` is `FALSE`, the p-value is computed from the asymptotic chi-squared distribution of the test statistic; continuity correction is only used in the 2-by-2 case (if `correct` is `TRUE`, the default). Otherwise the p-value is computed for a Monte Carlo test (Hope, 1968) with `B` replicates.

In the contingency table case simulation is done by random sampling from the set of all contingency tables with given marginals, and works only if the marginals are strictly positive. (A C translation of the algorithm of Patefield (1981) is used.) Continuity correction is never used, and the statistic is quoted without it. Note that this is not the usual sampling situation for the chi-squared test but rather that for Fisher's exact test.

In the goodness-of-fit case simulation is done by random sampling from the discrete distribution specified by  $p$ , each sample being of size  $n = \text{sum}(x)$ . This simulation is done in `R` and may be slow.

## Value

A list with class "htest" containing the following components:

<code>statistic</code>	the value the chi-squared test statistic.
<code>parameter</code>	the degrees of freedom of the approximate chi-squared distribution of the test statistic, <code>NA</code> if the p-value is computed by Monte Carlo simulation.
<code>p.value</code>	the p-value for the test.
<code>method</code>	a character string indicating the type of test performed, and whether Monte Carlo simulation or continuity correction was used.
<code>data.name</code>	a character string giving the name(s) of the data.
<code>observed</code>	the observed counts.
<code>expected</code>	the expected counts under the null hypothesis.
<code>residuals</code>	the Pearson residuals, $(\text{observed} - \text{expected}) / \sqrt{\text{expected}}$ .

## References

- Hope, A. C. A. (1968) A simplified Monte Carlo significance test procedure. *J. Roy, Statist. Soc. B* **30**, 582–598.
- Patefield, W. M. (1981) Algorithm AS159. An efficient method of generating  $r \times c$  tables with given row and column totals. *Applied Statistics* **30**, 91–97.

**Examples**

```
## Not really a good example
chisq.test(InsectSprays$count > 7, InsectSprays$spray)
# Prints test summary
chisq.test(InsectSprays$count > 7, InsectSprays$spray)$observed
# Counts observed
chisq.test(InsectSprays$count > 7, InsectSprays$spray)$expected
# Counts expected under the null

## Effect of simulating p-values
x <- matrix(c(12, 5, 7, 7), ncol = 2)
chisq.test(x)$p.value # 0.4233
chisq.test(x, simulate.p.value = TRUE, B = 10000)$p.value
# around 0.29!

## Testing for population probabilities
## Case A. Tabulated data
x <- c(A = 20, B = 15, C = 25)
chisq.test(x)
chisq.test(as.table(x)) # the same
x <- c(89, 37, 30, 28, 2)
p <- c(40, 20, 20, 15, 5)
try(
  chisq.test(x, p = p) # gives an error
)
chisq.test(x, p = p, rescale.p = TRUE)
# works
p <- c(0.40, 0.20, 0.20, 0.19, 0.01)
# Expected count in category 5
# is 1.86 < 5 ==> chi square approx.
chisq.test(x, p = p) # maybe doubtful, but is ok!
chisq.test(x, p = p, simulate.p.value = TRUE)

## Case B. Raw data
x <- trunc(5 * runif(100))
chisq.test(table(x)) # NOT 'chisq.test(x)'
```

Chisquare

*The (non-central) Chi-Squared Distribution***Description**

Density, distribution function, quantile function and random generation for the chi-squared ( $\chi^2$ ) distribution with `df` degrees of freedom and optional non-centrality parameter `ncp`.

**Usage**

```
dchisq(x, df, ncp=0, log = FALSE)
pchisq(q, df, ncp=0, lower.tail = TRUE, log.p = FALSE)
qchisq(p, df, ncp=0, lower.tail = TRUE, log.p = FALSE)
rchisq(n, df, ncp=0)
```

**Arguments**

<code>x, q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
<code>df</code>	degrees of freedom (non-negative, but can be non-integer).
<code>ncp</code>	non-centrality parameter (non-negative).
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .

**Details**

The chi-squared distribution with  $df = n \geq 0$  degrees of freedom has density

$$f_n(x) = \frac{1}{2^{n/2} \Gamma(n/2)} x^{n/2-1} e^{-x/2}$$

for  $x > 0$ . The mean and variance are  $n$  and  $2n$ .

The non-central chi-squared distribution with  $df = n$  degrees of freedom and non-centrality parameter  $ncp = \lambda$  has density

$$f(x) = e^{-\lambda/2} \sum_{r=0}^{\infty} \frac{(\lambda/2)^r}{r!} f_{n+2r}(x)$$

for  $x \geq 0$ . For integer  $n$ , this is the distribution of the sum of squares of  $n$  normals each with variance one,  $\lambda$  being the sum of squares of the normal means; further,  $E(X) = n + \lambda$ ,  $Var(X) = 2(n + 2 * \lambda)$ , and  $E((X - E(X))^3) = 8(n + 3 * \lambda)$ .

Note that the degrees of freedom  $df = n$ , can be non-integer, and also  $n = 0$  which is relevant for non-centrality  $\lambda > 0$ , see Johnson et al. (1995, chapter 29).

Note that `ncp` values larger than about  $1e5$  may give inaccurate results with many warnings for `pchisq` and `qchisq`.

**Value**

`dchisq` gives the density, `pchisq` gives the distribution function, `qchisq` gives the quantile function, and `rchisq` generates random deviates.

Invalid arguments will result in return value `NaN`, with a warning.

**Note**

The code for non-zero `ncp` is principally intended to be used for moderate values of `ncp`: it will not be highly accurate, especially in the tails, for large values.

**Source**

The central cases are computed via the gamma distribution.

The non-central `dchisq` and `rchisq` are computed as a Poisson mixture central of chi-squares (Johnson et al, 1995, p.436).

The non-central `pchisq` is for `ncp < 80` computed from the Poisson mixture of central chi-squares and for larger `ncp` via a C translation of

Ding, C. G. (1992) Algorithm AS275: Computing the non-central chi-squared distribution function. *Appl.Statist.*, **41** 478–482.

which computes the lower tail only (so the upper tail suffers from cancellation and a warning will be given when this is likely to be significant).

The non-central `qchisq` is based on inversion of `pchisq`.

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, chapters 18 (volume 1) and 29 (volume 2). Wiley, New York.

## See Also

A central chi-squared distribution with  $n$  degrees of freedom is the same as a Gamma distribution with shape  $\alpha = n/2$  and scale  $\sigma = 2$ . Hence, see [dgamma](#) for the Gamma distribution.

## Examples

```
require(graphics)

dchisq(1, df=1:3)
pchisq(1, df= 3)
pchisq(1, df= 3, ncp = 0:4)# includes the above

x <- 1:10
## Chi-squared(df = 2) is a special exponential distribution
all.equal(dchisq(x, df=2), dexp(x, 1/2))
all.equal(pchisq(x, df=2), pexp(x, 1/2))

## non-central RNG -- df=0 with ncp > 0: Z0 has point mass at 0!
Z0 <- rchisq(100, df = 0, ncp = 2.)
graphics::stem(Z0)

## Not run: ## visual testing
## do P-P plots for 1000 points at various degrees of freedom
L <- 1.2; n <- 1000; pp <- ppoints(n)
op <- par(mfrow = c(3,3), mar= c(3,3,1,1)+.1, mgp= c(1.5,.6,0),
          oma = c(0,0,3,0))
for(df in 2^(4*rnorm(9))) {
  plot(pp, sort(pchisq(rr <- rchisq(n,df=df, ncp=L), df=df, ncp=L)),
        ylab="pchisq(rchisq(.),.)", pch=".")
  mtext(paste("df = ",formatC(df, digits = 4)), line= -2, adj=0.05)
  abline(0,1,col=2)
}
mtext(expression("P-P plots : Noncentral " *
                 chi^2 * "(n=1000, df=X, ncp= 1.2)"),
        cex = 1.5, font = 2, outer=TRUE)
par(op)
## End(Not run)

## "analytical" test
lam <- seq(0,100, by=.25)
p00 <- pchisq(0,          df=0, ncp=lam)
```

```
p.0 <- pchisq(1e-300, df=0, ncp=lam)
stopifnot(all.equal(p.0, exp(-lam/2)),
          all.equal(p.0, exp(-lam/2)))
```

---

cmdscale                      *Classical (Metric) Multidimensional Scaling*

---

### Description

Classical multidimensional scaling of a data matrix. Also known as *principal coordinates analysis* (Gower, 1966).

### Usage

```
cmdscale(d, k = 2, eig = FALSE, add = FALSE, x.ret = FALSE)
```

### Arguments

d	a distance structure such as that returned by <code>dist</code> or a full symmetric matrix containing the dissimilarities.
k	the dimension of the space which the data are to be represented in; must be in $\{1, 2, \dots, n - 1\}$ .
eig	indicates whether eigenvalues should be returned.
add	logical indicating if an additive constant $c^*$ should be computed, and added to the non-diagonal dissimilarities such that all $n - 1$ eigenvalues are non-negative.
x.ret	indicates whether the doubly centred symmetric distance matrix should be returned.

### Details

Multidimensional scaling takes a set of dissimilarities and returns a set of points such that the distances between the points are approximately equal to the dissimilarities.

The functions `isoMDS` and `sammon` in package **MASS** provide alternative ordination techniques.

When `add = TRUE`, an additive constant  $c^*$  is computed, and the dissimilarities  $d_{ij} + c^*$  are used instead of the original  $d_{ij}$ 's.

Whereas S (Becker *et al.*, 1988) computes this constant using an approximation suggested by Torgerson, R uses the analytical solution of Cailliez (1983), see also Cox and Cox (1994).

### Value

If `eig = FALSE` and `x.ret = FALSE` (default), a matrix with `k` columns whose rows give the coordinates of the points chosen to represent the dissimilarities.

Otherwise, a list containing the following components.

points	a matrix with <code>k</code> columns whose rows give the coordinates of the points chosen to represent the dissimilarities.
eig	the $n - 1$ eigenvalues computed during the scaling process if <code>eig</code> is true.
x	the doubly centered distance matrix if <code>x.ret</code> is true.
GOF	a numeric vector of length 2, equal to say $(g_1, g_2)$ , where $g_i = (\sum_{j=1}^k \lambda_j) / (\sum_{j=1}^n T_i(\lambda_j))$ , where $\lambda_j$ are the eigenvalues (sorted in decreasing order), $T_1(v) =  v $ , and $T_2(v) = \max(v, 0)$ .

## References

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- Cailliez, F. (1983) The analytical solution of the additive constant problem. *Psychometrika* **48**, 343–349.
- Cox, T. F. and Cox, M. A. A. (1994) *Multidimensional Scaling*. Chapman and Hall.
- Gower, J. C. (1966) Some distance properties of latent root and vector methods used in multivariate analysis. *Biometrika* **53**, 325–328.
- Mardia, K. V., Kent, J. T. and Bibby, J. M. (1979). Chapter 14 of *Multivariate Analysis*, London: Academic Press.
- Seber, G. A. F. (1984). *Multivariate Observations*. New York: Wiley.
- Torgerson, W. S. (1958). *Theory and Methods of Scaling*. New York: Wiley.

## See Also

[dist](#). Also [isoMDS](#) and [sammon](#) in package **MASS**.

## Examples

```
require(graphics)

loc <- cmdscale(eurodist)
x <- loc[,1]
y <- -loc[,2]
plot(x, y, type="n", xlab="", ylab="", main="cmdscale(eurodist)")
text(x, y, rownames(loc), cex=0.8)

cmdsE <- cmdscale(eurodist, k=20, add = TRUE, eig = TRUE, x.ret = TRUE)
utils::str(cmdsE)
```

---

coef

*Extract Model Coefficients*

---

## Description

`coef` is a generic function which extracts model coefficients from objects returned by modeling functions. `coefficients` is an *alias* for it.

## Usage

```
coef(object, ...)
coefficients(object, ...)
```

## Arguments

`object` an object for which the extraction of model coefficients is meaningful.

`...` other arguments.



## Details

All object classes which are returned by model fitting functions should provide a `coef` method or use the default one. (Note that the method is for `coef` and not `coefficients`.)

Class "aov" has a `coef` method that does not report aliased coefficients (see [alias](#)).

## Value

Coefficients extracted from the model object `object`.

## References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

## See Also

[fitted.values](#) and [residuals](#) for related methods; [glm](#), [lm](#) for model fitting.

## Examples

```
x <- 1:5; coef(lm(c(1:3, 7, 6) ~ x))
```

---

complete.cases      *Find Complete Cases*

---

## Description

Return a logical vector indicating which cases are complete, i.e., have no missing values.

## Usage

```
complete.cases(...)
```

## Arguments

...                    a sequence of vectors, matrices and data frames.

## Value

A logical vector specifying which observations/rows have no missing values across the entire sequence.

## See Also

[is.na](#), [na.omit](#), [na.fail](#).

**Examples**

```
x <- airquality[, -1] # x is a regression design matrix
y <- airquality[, 1] # y is the corresponding response

stopifnot(complete.cases(y) != is.na(y))
ok <- complete.cases(x, y)
sum(!ok) # how many are not "ok" ?
x <- x[ok,]
y <- y[ok]
```

---

 confint

*Confidence Intervals for Model Parameters*


---

**Description**

Computes confidence intervals for one or more parameters in a fitted model. There is a default and a method for objects inheriting from class "lm".

**Usage**

```
confint(object, parm, level = 0.95, ...)
```

**Arguments**

object	a fitted model object.
parm	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
level	the confidence level required.
...	additional argument(s) for methods.

**Details**

confint is a generic function. The default method assumes asymptotic normality, and needs suitable `coef` and `vcov` methods to be available. The default method can be called directly for comparison with other methods.

For objects of class "lm" the direct formulae based on  $t$  values are used.

There are stub methods for classes "glm" and "nls" which invoke those in package MASS which are based on profile likelihoods.

**Value**

A matrix (or vector) with columns giving lower and upper confidence limits for each parameter. These will be labelled as  $(1-level)/2$  and  $1 - (1-level)/2$  in % (by default 2.5% and 97.5%).

**See Also**

`confint.glm` and `confint.nls` in package MASS.

**Examples**

```

fit <- lm(100/mpg ~ disp + hp + wt + am, data=mtcars)
confint(fit)
confint(fit, "wt")

## from example(glm) (needs MASS to be present on the system)
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9); treatment <- gl(3,3)
glm.D93 <- glm(counts ~ outcome + treatment, family=poisson())
confint(glm.D93)
confint.default(glm.D93) # based on asymptotic normality

```

constrOptim

*Linearly Constrained Optimization***Description**

Minimise a function subject to linear inequality constraints using an adaptive barrier algorithm.

**Usage**

```

constrOptim(theta, f, grad, ui, ci, mu = 1e-04, control = list(),
            method = if(is.null(grad)) "Nelder-Mead" else "BFGS",
            outer.iterations = 100, outer.eps = 1e-05, ...)

```

**Arguments**

theta	Starting value: must be in the feasible region.
f	Function to minimise (see below).
grad	Gradient of f, or NULL (see below).
ui	Constraints (see below).
ci	Constraints (see below).
mu	(Small) tuning parameter.
control	Passed to <a href="#">optim</a> .
method	Passed to <a href="#">optim</a> .
outer.iterations	Iterations of the barrier algorithm.
outer.eps	Criterion for relative convergence of the barrier algorithm.
...	Other named arguments to be passed to f and grad: needs to be passed through <a href="#">optim</a> so should not match its argument names.

**Details**

The feasible region is defined by  $ui \%*\% theta - ci \geq 0$ . The starting value must be in the interior of the feasible region, but the minimum may be on the boundary.

A logarithmic barrier is added to enforce the constraints and then [optim](#) is called. The barrier function is chosen so that the objective function should decrease at each outer iteration. Minima in the interior of the feasible region are typically found quite quickly, but a substantial number of outer iterations may be needed for a minimum on the boundary.

The tuning parameter `mu` multiplies the barrier term. Its precise value is often relatively unimportant. As `mu` increases the augmented objective function becomes closer to the original objective function but also less smooth near the boundary of the feasible region.

Any `optim` method that permits infinite values for the objective function may be used (currently all but "L-BFGS-B").

The objective function `f` takes as first argument the vector of parameters over which minimisation is to take place. It should return a scalar result. Optional arguments `...` will be passed to `optim` and then (if not used by `optim`) to `f`. As with `optim`, the default is to minimise, but maximisation can be performed by setting `control$fnscale` to a negative value.

The gradient function `grad` must be supplied except with `method="Nelder-Mead"`. It should take arguments matching those of `f` and return a vector containing the gradient.

### Value

As for `optim`, but with two extra components: `barrier.value` giving the value of the barrier function at the optimum and `outer.iterations` gives the number of outer iterations (calls to `optim`)

### References

K. Lange *Numerical Analysis for Statisticians*. Springer 2001, p185ff

### See Also

`optim`, especially `method="L-BFGS-B"` which does box-constrained optimisation.

### Examples

```
## from optim
fr <- function(x) { ## Rosenbrock Banana function
  x1 <- x[1]
  x2 <- x[2]
  100 * (x2 - x1 * x1)^2 + (1 - x1)^2
}
grr <- function(x) { ## Gradient of 'fr'
  x1 <- x[1]
  x2 <- x[2]
  c(-400 * x1 * (x2 - x1 * x1) - 2 * (1 - x1),
    200 * (x2 - x1 * x1))
}

optim(c(-1.2,1), fr, grr)
#Box-constraint, optimum on the boundary
constrOptim(c(-1.2,0.9), fr, grr, ui=rbind(c(-1,0),c(0,-1)), ci=c(-1,-1))
# x<=0.9, y-x>0.1
constrOptim(c(.5,0), fr, grr, ui=rbind(c(-1,0),c(1,-1)), ci=c(-0.9,0.1))

## Solves linear and quadratic programming problems
## but needs a feasible starting value
#
# from example(solve.QP) in 'quadprog'
# no derivative
fQP <- function(b) {-sum(c(0,5,0)*b)+0.5*sum(b*b)}
Amat <- matrix(c(-4,-3,0,2,1,0,0,-2,1),3,3)
```

```

bvec      <- c(-8,2,0)
constrOptim(c(2,-1,-1), fQP, NULL, ui=t(Amat),ci=bvec)
# derivative
gQP <- function(b) {-c(0,5,0)+b}
constrOptim(c(2,-1,-1), fQP, gQP, ui=t(Amat), ci=bvec)

## Now with maximisation instead of minimisation
hQP <- function(b) {sum(c(0,5,0)*b)-0.5*sum(b*b)}
constrOptim(c(2,-1,-1), hQP, NULL, ui=t(Amat), ci=bvec,
            control=list(fnscale=-1))

```

---

 contrast

*(Possibly Sparse) Contrast Matrices*


---

## Description

Return a matrix of contrasts.

## Usage

```

contr.helmert(n, contrasts = TRUE, sparse = FALSE)
contr.poly(n, scores = 1:n, contrasts = TRUE, sparse = FALSE)
contr.sum(n, contrasts = TRUE, sparse = FALSE)
contr.treatment(n, base = 1, contrasts = TRUE, sparse = FALSE)
contr.SAS(n, contrasts = TRUE, sparse = FALSE)

```

## Arguments

n	a vector of levels for a factor, or the number of levels.
contrasts	a logical indicating whether contrasts should be computed.
sparse	logical indicating if the result should be sparse (of class <code>dgCMatrix</code> ), using package <b>Matrix</b> .
scores	the set of values over which orthogonal polynomials are to be computed.
base	an integer specifying which group is considered the baseline group. Ignored if <code>contrasts</code> is <code>FALSE</code> .

## Details

These functions are used for creating contrast matrices for use in fitting analysis of variance and regression models. The columns of the resulting matrices contain contrasts which can be used for coding a factor with `n` levels. The returned value contains the computed contrasts. If the argument `contrasts` is `FALSE` a square indicator matrix (the dummy coding) is returned **except** for `contr.poly` (which includes the 0-degree, i.e. constant, polynomial when `contrasts = FALSE`).

`contr.helmert` returns Helmert contrasts, which contrast the second level with the first, the third with the average of the first two, and so on. `contr.poly` returns contrasts based on orthogonal polynomials. `contr.sum` uses ‘sum to zero contrasts’.

`contr.treatment` contrasts each level with the baseline level (specified by `base`): the baseline level is omitted. Note that this does not produce ‘contrasts’ as defined in the standard theory for linear models as they are not orthogonal to the intercept.

`contr.SAS` is a wrapper for `contr.treatment` that sets the base level to be the last level of the factor. The coefficients produced when using these contrasts should be equivalent to those produced by many (but not all) SAS procedures.

For consistency, `sparse` is an argument to all these contrast functions, however `sparse = TRUE` for `contr.poly` is typically pointless and is rarely useful for `contr.helmert`.

### Value

A matrix with `n` rows and `k` columns, with `k=n-1` if `contrasts` is `TRUE` and `k=n` if `contrasts` is `FALSE`.

### References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models*. Chapter 2 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

### See Also

[contrasts](#), [C](#), and [aov](#), [glm](#), [lm](#).

### Examples

```
(cH <- contr.helmert(4))
apply(cH, 2, sum) # column sums are 0
crossprod(cH) # diagonal -- columns are orthogonal
contr.helmert(4, contrasts = FALSE) # just the 4 x 4 identity matrix

(cT <- contr.treatment(5))
all(crossprod(cT) == diag(4)) # TRUE: even orthonormal

(cT. <- contr.SAS(5))
all(crossprod(cT.) == diag(4)) # TRUE

(cP <- contr.poly(3)) # Linear and Quadratic
zapsmall(crossprod(cP), digits=15) # orthonormal up to fuzz
```

---

contrasts

*Get and Set Contrast Matrices*

---

### Description

Set and view the contrasts associated with a factor.

### Usage

```
contrasts(x, contrasts = TRUE, sparse = FALSE)
contrasts(x, how.many) <- value
```

**Arguments**

<code>x</code>	a factor or a logical variable.
<code>contrasts</code>	logical. See ‘Details’.
<code>sparse</code>	logical indicating if the result should be sparse (of class <code>dgCMatrix</code> ), using package <b>Matrix</b> .
<code>how.many</code>	How many contrasts should be made. Defaults to one less than the number of levels of <code>x</code> . This need not be the same as the number of columns of <code>value</code> .
<code>value</code>	either a numeric matrix (or a sparse or dense matrix of a class extending <code>dMatrix</code> from package <b>Matrix</b> ) whose columns give coefficients for contrasts in the levels of <code>x</code> , or the (quoted) name of a function which computes such matrices.

**Details**

If contrasts are not set for a factor the default functions from `options("contrasts")` are used.

A logical vector `x` is converted into a two-level factor with levels `c(FALSE, TRUE)` (regardless of which levels occur in the variable).

The argument `contrasts` is ignored if `x` has a matrix `contrasts` attribute set. Otherwise if `contrasts = TRUE` it is passed to a contrasts function such as `contr.treatment` and if `contrasts = FALSE` an identity matrix is returned. Suitable functions have a first argument which is the character vector of levels, a named argument `contrasts` (always called with `contrasts = TRUE`) and optionally from R 2.10.0 a logical argument `sparse`.

If `value` supplies more than `how.many` contrasts, the first `how.many` are used. If too few are supplied, a suitable contrast matrix is created by extending `value` after ensuring its columns are contrasts (orthogonal to the constant term) and not collinear.

**References**

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models*. Chapter 2 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

`C`, `contr.helmert`, `contr.poly`, `contr.sum`, `contr.treatment`; `glm`, `aov`, `lm`.

**Examples**

```
utils::example(factor)
fff <- ff[, drop=TRUE] # reduce to 5 levels.
contrasts(fff) # treatment contrasts by default
contrasts(C(fff, sum))
contrasts(fff, contrasts = FALSE) # the 5x5 identity matrix

contrasts(fff) <- contr.sum(5); contrasts(fff) # set sum contrasts
contrasts(fff, 2) <- contr.sum(5); contrasts(fff) # set 2 contrasts
# supply 2 contrasts, compute 2 more to make full set of 4.
contrasts(fff) <- contr.sum(5)[,1:2]; contrasts(fff)

## using sparse contrasts: % useful, once model.matrix() works with these :
ffs <- fff
contrasts(ffs) <- contr.sum(5, sparse=TRUE)[,1:2]; contrasts(ffs)
stopifnot(all.equal(ffs, fff))
contrasts(ffs) <- contr.sum(5, sparse=TRUE); contrasts(ffs)
```

convolve

*Convolution of Sequences via FFT***Description**

Use the Fast Fourier Transform to compute the several kinds of convolutions of two sequences.

**Usage**

```
convolve(x, y, conj = TRUE, type = c("circular", "open", "filter"))
```

**Arguments**

<code>x, y</code>	numeric sequences <i>of the same length</i> to be convolved.
<code>conj</code>	logical; if TRUE, take the complex <i>conjugate</i> before back-transforming (default, and used for usual convolution).
<code>type</code>	character; one of "circular", "open", "filter" (beginning of word is ok). For <i>circular</i> , the two sequences are treated as <i>circular</i> , i.e., periodic. For <i>open</i> and <i>filter</i> , the sequences are padded with 0s (from left and right) first; "filter" returns the middle sub-vector of "open", namely, the result of running a weighted mean of <code>x</code> with weights <code>y</code> .

**Details**

The Fast Fourier Transform, `fft`, is used for efficiency.

The input sequences `x` and `y` must have the same length if `circular` is true.

Note that the usual definition of convolution of two sequences `x` and `y` is given by `convolve(x, rev(y), type = "o")`.

**Value**

If `r <- convolve(x, y, type = "open")` and `n <- length(x)`, `m <- length(y)`, then

$$r_k = \sum_i x_{k-m+i} y_i$$

where the sum is over all valid indices  $i$ , for  $k = 1, \dots, n + m - 1$ .

If `type == "circular"`,  $n = m$  is required, and the above is true for  $i, k = 1, \dots, n$  when  $x_j := x_{n+j}$  for  $j < 1$ .

**References**

Brillinger, D. R. (1981) *Time Series: Data Analysis and Theory*, Second Edition. San Francisco: Holden-Day.

**See Also**

`fft`, `nextn`, and particularly `filter` (from the `stats` package) which may be more appropriate.



**Examples**

```

require(graphics)

x <- c(0,0,0,100,0,0,0)
y <- c(0,0,1, 2 ,1,0,0)/4
zapsmall(convolve(x,y)) # *NOT* what you first thought.
zapsmall(convolve(x, y[3:5], type="f")) # rather
x <- rnorm(50)
y <- rnorm(50)
# Circular convolution *has* this symmetry:
all.equal(convolve(x,y, conj = FALSE), rev(convolve(rev(y),x)))

n <- length(x <- -20:24)
y <- (x-10)^2/1000 + rnorm(x)/8

Han <- function(y) # Hanning
  convolve(y, c(1,2,1)/4, type = "filter")

plot(x,y, main="Using convolve(.) for Hanning filters")
lines(x[-c(1 , n) ], Han(y), col="red")
lines(x[-c(1:2, (n-1):n)], Han(Han(y)), lwd=2, col="dark blue")

```

---

cophenetic

*Cophenetic Distances for a Hierarchical Clustering*


---

**Description**

Computes the cophenetic distances for a hierarchical clustering.

**Usage**

```

cophenetic(x)
## Default S3 method:
cophenetic(x)
## S3 method for class 'dendrogram':
cophenetic(x)

```

**Arguments**

**x** an R object representing a hierarchical clustering. For the default method, an object of class `hclust` or with a method for `as.hclust()` such as `agnes` in package `cluster`.

**Details**

The cophenetic distance between two observations that have been clustered is defined to be the intergroup dissimilarity at which the two observations are first combined into a single cluster. Note that this distance has many ties and restrictions.

It can be argued that a dendrogram is an appropriate summary of some data if the correlation between the original distances and the cophenetic distances is high. Otherwise, it should simply be viewed as the description of the output of the clustering algorithm.

`cophenetic` is a generic function. Support for classes which represent hierarchical clusterings (total indexed hierarchies) can be added by providing an `as.hclust()` or, more directly, a `cophenetic()` method for such a class.

The method for objects of class "`dendrogram`" requires that all leaves of the dendrogram object have non-null labels.

### Value

An object of class `dist`.

### Author(s)

Robert Gentleman

### References

Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy: The Principles and Practice of Numerical Classification*, p. 278 ff; Freeman, San Francisco.

### See Also

`dist`, `hclust`

### Examples

```
require(graphics)

d1 <- dist(USArrests)
hc <- hclust(d1, "ave")
d2 <- cophenetic(hc)
cor(d1,d2) # 0.7659

## Example from Sneath & Sokal, Fig. 5-29, p.279
d0 <- c(1,3.8,4.4,5.1, 4,4.2,5, 2.6,5.3, 5.4)
attributes(d0) <- list(Size = 5, diag=TRUE)
class(d0) <- "dist"
names(d0) <- letters[1:5]
d0
utils::str(upgma <- hclust(d0, method = "average"))
plot(upgma, hang = -1)
#
(d.coph <- cophenetic(upgma))
cor(d0, d.coph) # 0.9911
```

### Description

`var`, `cov` and `cor` compute the variance of `x` and the covariance or correlation of `x` and `y` if these are vectors. If `x` and `y` are matrices then the covariances (or correlations) between the columns of `x` and the columns of `y` are computed.

`cov2cor` scales a covariance matrix into the corresponding correlation matrix *efficiently*.

**Usage**

```
var(x, y = NULL, na.rm = FALSE, use)

cov(x, y = NULL, use = "everything",
    method = c("pearson", "kendall", "spearman"))

cor(x, y = NULL, use = "everything",
    method = c("pearson", "kendall", "spearman"))

cov2cor(V)
```

**Arguments**

<code>x</code>	a numeric vector, matrix or data frame.
<code>y</code>	NULL (default) or a vector, matrix or data frame with compatible dimensions to <code>x</code> . The default is equivalent to <code>y = x</code> (but more efficient).
<code>na.rm</code>	logical. Should missing values be removed?
<code>use</code>	an optional character string giving a method for computing covariances in the presence of missing values. This must be (an abbreviation of) one of the strings "everything", "all.obs", "complete.obs", "na.or.complete", or "pairwise.complete.obs".
<code>method</code>	a character string indicating which correlation coefficient (or covariance) is to be computed. One of "pearson" (default), "kendall", or "spearman", can be abbreviated.
<code>V</code>	symmetric numeric matrix, usually positive definite such as a covariance matrix.

**Details**

For `cov` and `cor` one must *either* give a matrix or data frame for `x` *or* give both `x` and `y`.

The inputs must be numeric (as determined by `is.numeric`: logical values are also allowed for historical compatibility): the "kendall" and "spearman" methods make sense for ordered inputs but `xtfrm` can be used to find a suitable prior transformation to numbers.

`var` is just another interface to `cov`, where `na.rm` is used to determine the default for `use` when that is unspecified. If `na.rm` is TRUE then the complete observations (rows) are used (`use = "na.or.complete"`) to compute the variance. Otherwise, by default `use = "everything"`.

If `use` is "everything", NAs will propagate conceptually, i.e., a resulting value will be NA whenever one of its contributing observations is NA.

If `use` is "all.obs", then the presence of missing observations will produce an error. If `use` is "complete.obs" then missing values are handled by casewise deletion (and if there are no complete cases, that gives an error).

"na.or.complete" is the same unless there are no complete cases, that gives NA. Finally, if `use` has the value "pairwise.complete.obs" then the correlation or covariance between each pair of variables is computed using all complete pairs of observations on those variables. This can result in covariance or correlation matrices which are not positive semi-definite, as well as NA entries if there are no complete pairs for that pair of variables. For `cov` and `var`, "pairwise.complete.obs" only works with the "pearson" method. Note that (the equivalent of) `var(double(0), use=*)` gives NA for `use = "everything"` and "na.or.complete", and gives an error in the other cases.

The denominator  $n - 1$  is used which gives an unbiased estimator of the (co)variance for i.i.d. observations. These functions return `NA` when there is only one observation (whereas `S-PLUS` has been returning `NaN`), and fail if `x` has length zero.

For `cor()`, if `method` is `"kendall"` or `"spearman"`, Kendall's  $\tau$  or Spearman's  $\rho$  statistic is used to estimate a rank-based measure of association. These are more robust and have been recommended if the data do not necessarily come from a bivariate normal distribution.

For `cov()`, a non-Pearson method is unusual but available for the sake of completeness. Note that `"spearman"` basically computes `cor(R(x), R(y))` (or `cov(., .)`) where `R(u) := rank(u, na.last="keep")`. In the case of missing values, the ranks are calculated depending on the value of `use`, either based on complete observations, or based on pairwise completeness with reranking for each pair.

Scaling a covariance matrix into a correlation one can be achieved in many ways, mathematically most appealing by multiplication with a diagonal matrix from left and right, or more efficiently by using `sweep(., FUN = "/")` twice. The `cov2cor` function is even a bit more efficient, and provided mostly for didactical reasons.

### Value

For `r <- cor(*, use = "all.obs")`, it is now guaranteed that `all(r <= 1)`.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

`cor.test` for confidence intervals (and tests).

`cov.wt` for *weighted* covariance computation.

`sd` for standard deviation (vectors).

### Examples

```
var(1:10) # 9.166667

var(1:5, 1:5) # 2.5

## Two simple vectors
cor(1:10, 2:11) # == 1

## Correlation Matrix of Multivariate sample:
(C1 <- cor(longley))
## Graphical Correlation Matrix:
symnum(C1) # highly correlated

## Spearman's rho and Kendall's tau
symnum(c1S <- cor(longley, method = "spearman"))
symnum(c1K <- cor(longley, method = "kendall"))
## How much do they differ?
i <- lower.tri(C1)
cor(cbind(P = C1[i], S = c1S[i], K = c1K[i]))

## cov2cor() scales a covariance matrix by its diagonal
```

```
##           to become the correlation matrix.
cov2cor # see the function definition {and learn ..}
stopifnot(all.equal(C1, cov2cor(cov(longley))),
           all.equal(cor(longley, method="kendall"),
                     cov2cor(cov(longley, method="kendall"))))

##--- Missing value treatment:
C1 <- cov(swiss)
range(eigen(C1, only.values=TRUE)$values) # 6.19      1921
swM <- swiss
swM[1,2] <- swM[7,3] <- swM[25,5] <- NA # create 3 "missing"
try(cov(swM)) # Error: missing obs...
C2 <- cov(swM, use = "complete")
range(eigen(C2, only.values=TRUE)$values) # 6.46      1930
C3 <- cov(swM, use = "pairwise")
range(eigen(C3, only.values=TRUE)$values) # 6.19      1938

symnum(cor(swM, method = "kendall", use = "complete"))
## Kendall's tau doesn't change much:
symnum(cor(swiss, method = "kendall"))
```

---

cor.test

*Test for Association/Correlation Between Paired Samples*


---

### Description

Test for association between paired samples, using one of Pearson's product moment correlation coefficient, Kendall's  $\tau$  or Spearman's  $\rho$ .

### Usage

```
cor.test(x, ...)

## Default S3 method:
cor.test(x, y,
         alternative = c("two.sided", "less", "greater"),
         method = c("pearson", "kendall", "spearman"),
         exact = NULL, conf.level = 0.95, continuity = FALSE, ...)

## S3 method for class 'formula':
cor.test(formula, data, subset, na.action, ...)
```

### Arguments

<code>x, y</code>	numeric vectors of data values. <code>x</code> and <code>y</code> must have the same length.
<code>alternative</code>	indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. "greater" corresponds to positive association, "less" to negative association.
<code>method</code>	a character string indicating which correlation coefficient is to be used for the test. One of "pearson", "kendall", or "spearman", can be abbreviated.
<code>exact</code>	a logical indicating whether an exact p-value should be computed. Used for Kendall's $\tau$ and Spearman's $\rho$ . See 'Details' for the meaning of NULL (the default).

<code>conf.level</code>	confidence level for the returned confidence interval. Currently only used for the Pearson product moment correlation coefficient if there are at least 4 complete pairs of observations.
<code>continuity</code>	logical: if true, a continuity correction is used for Kendall's $\tau$ and Spearman's $\rho$ when not computed exactly.
<code>formula</code>	a formula of the form $\sim u + v$ , where each of $u$ and $v$ are numeric variables giving the data values for one sample. The samples must be of the same length.
<code>data</code>	an optional matrix or data frame (or similar: see <code>model.frame</code> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>subset</code>	an optional vector specifying a subset of observations to be used.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. Defaults to <code>getOption("na.action")</code> .
<code>...</code>	further arguments to be passed to or from methods.

### Details

The three methods each estimate the association between paired samples and compute a test of the value being zero. They use different measures of association, all in the range  $[-1, 1]$  with 0 indicating no association. These are sometimes referred to as tests of no *correlation*, but that term is often confined to the default method.

If `method` is "pearson", the test statistic is based on Pearson's product moment correlation coefficient `cor(x, y)` and follows a t distribution with `length(x) - 2` degrees of freedom if the samples follow independent normal distributions. If there are at least 4 complete pairs of observation, an asymptotic confidence interval is given based on Fisher's Z transform.

If `method` is "kendall" or "spearman", Kendall's  $\tau$  or Spearman's  $\rho$  statistic is used to estimate a rank-based measure of association. These tests may be used if the data do not necessarily come from a bivariate normal distribution.

For Kendall's test, by default (if `exact` is NULL), an exact p-value is computed if there are less than 50 paired samples containing finite values and there are no ties. Otherwise, the test statistic is the estimate scaled to zero mean and unit variance, and is approximately normally distributed.

For Spearman's test, p-values are computed using algorithm AS 89 for  $n < 1290$  and `exact = TRUE`, otherwise via the asymptotic  $t$  approximation. Note that these are 'exact' for  $n < 10$ , and use an Edgeworth series approximation for larger sample sizes (the cutoff has been changed from the original paper).

### Value

A list with class "htest" containing the following components:

<code>statistic</code>	the value of the test statistic.
<code>parameter</code>	the degrees of freedom of the test statistic in the case that it follows a t distribution.
<code>p.value</code>	the p-value of the test.
<code>estimate</code>	the estimated measure of association, with name "cor", "tau", or "rho" corresponding to the method employed.
<code>null.value</code>	the value of the association measure under the null hypothesis, always 0.
<code>alternative</code>	a character string describing the alternative hypothesis.

method	a character string indicating how the association was measured.
data.name	a character string giving the names of the data.
conf.int	a confidence interval for the measure of association. Currently only given for Pearson's product moment correlation coefficient in case of at least 4 complete pairs of observations.

## References

D. J. Best & D. E. Roberts (1975), Algorithm AS 89: The Upper Tail Probabilities of Spearman's  $\rho$ . *Applied Statistics*, **24**, 377–379.

Myles Hollander & Douglas A. Wolfe (1973), *Nonparametric Statistical Methods*. New York: John Wiley & Sons. Pages 185–194 (Kendall and Spearman tests).

## See Also

[Kendall](#) in package **Kendall**.

[pKendall](#) and [pSpearman](#) in package **SuppDists**, [spearman.test](#) in package `pspearman`, which supply different (and often more accurate) approximations.

## Examples

```
## Hollander & Wolfe (1973), p. 187f.
## Assessment of tuna quality. We compare the Hunter L measure of
## lightness to the averages of consumer panel scores (recoded as
## integer values from 1 to 6 and averaged over 80 such values) in
## 9 lots of canned tuna.

x <- c(44.4, 45.9, 41.9, 53.3, 44.7, 44.1, 50.7, 45.2, 60.1)
y <- c( 2.6,  3.1,  2.5,  5.0,  3.6,  4.0,  5.2,  2.8,  3.8)

## The alternative hypothesis of interest is that the
## Hunter L value is positively associated with the panel score.

cor.test(x, y, method = "kendall", alternative = "greater")
## => p=0.05972

cor.test(x, y, method = "kendall", alternative = "greater",
         exact = FALSE) # using large sample approximation
## => p=0.04765

## Compare this to
cor.test(x, y, method = "spearm", alternative = "g")
cor.test(x, y,          alternative = "g")

## Formula interface.
require(graphics)
pairs(USJudgeRatings)
cor.test(~ CONT + INTG, data = USJudgeRatings)
```

cov.wt

*Weighted Covariance Matrices***Description**

Returns a list containing estimates of the weighted covariance matrix and the mean of the data, and optionally of the (weighted) correlation matrix.

**Usage**

```
cov.wt(x, wt = rep(1/nrow(x), nrow(x)), cor = FALSE, center = TRUE,
       method = c("unbiased", "ML"))
```

**Arguments**

<code>x</code>	a matrix or data frame. As usual, rows are observations and columns are variables.
<code>wt</code>	a non-negative and non-zero vector of weights for each observation. Its length must equal the number of rows of <code>x</code> .
<code>cor</code>	a logical indicating whether the estimated correlation weighted matrix will be returned as well.
<code>center</code>	either a logical or a numeric vector specifying the centers to be used when computing covariances. If <code>TRUE</code> , the (weighted) mean of each variable is used, if <code>FALSE</code> , zero is used. If <code>center</code> is numeric, its length must equal the number of columns of <code>x</code> .
<code>method</code>	string specifying how the result is scaled, see ‘Details’ below.

**Details**

By default, `method = "unbiased"`, The covariance matrix is divided by one minus the sum of squares of the weights, so if the weights are the default ( $1/n$ ) the conventional unbiased estimate of the covariance matrix with divisor  $(n - 1)$  is obtained. This differs from the behaviour in S-PLUS which corresponds to `method = "ML"` and does not divide.

**Value**

A list containing the following named components:

<code>cov</code>	the estimated (weighted) covariance matrix
<code>center</code>	an estimate for the center (mean) of the data.
<code>n.obs</code>	the number of observations (rows) in <code>x</code> .
<code>wt</code>	the weights used in the estimation. Only returned if given as an argument.
<code>cor</code>	the estimated correlation matrix. Only returned if <code>cor</code> is <code>TRUE</code> .

**See Also**

[cov](#) and [var](#).



**Examples**

```
(xy <- cbind(x = 1:10, y = c(1:3, 8:5, 8:10)))
w1 <- c(0,0,0,1,1,1,1,1,0,0)
cov.wt(xy, wt = w1) # i.e. method = "unbiased"
cov.wt(xy, wt = w1, method = "ML", cor = TRUE)
```

---

cpgram

*Plot Cumulative Periodogram*


---

**Description**

Plots a cumulative periodogram.

**Usage**

```
cpgram(ts, taper = 0.1,
       main = paste("Series: ", deparse(substitute(ts))),
       ci.col = "blue")
```

**Arguments**

ts	a univariate time series
taper	proportion tapered in forming the periodogram
main	main title
ci.col	colour for confidence band.

**Value**

None.

**Side Effects**

Plots the cumulative periodogram in a square plot.

**Note**

From package **MASS**.

**Author(s)**

B.D. Ripley

**Examples**

```
require(graphics)

par(pty = "s", mfrow = c(1,2))
cpgram(lh)
lh.ar <- ar(lh, order.max = 9)
cpgram(lh.ar$resid, main = "AR(3) fit to lh")

cpgram(ldeaths)
```

---

`cutree`*Cut a Tree into Groups of Data*

---

### Description

Cuts a tree, e.g., as resulting from `hclust`, into several groups either by specifying the desired number(s) of groups or the cut height(s).

### Usage

```
cutree(tree, k = NULL, h = NULL)
```

### Arguments

<code>tree</code>	a tree as produced by <code>hclust</code> . <code>cutree()</code> only expects a list with components <code>merge</code> , <code>height</code> , and <code>labels</code> , of appropriate content each.
<code>k</code>	an integer scalar or vector with the desired number of groups
<code>h</code>	numeric scalar or vector with heights where the tree should be cut. At least one of <code>k</code> or <code>h</code> must be specified, <code>k</code> overrides <code>h</code> if both are given.

### Value

`cutree` returns a vector with group memberships if `k` or `h` are scalar, otherwise a matrix with group memberships is returned where each column corresponds to the elements of `k` or `h`, respectively (which are also used as column names).

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

`hclust`, `dendrogram` for cutting trees themselves.

### Examples

```
hc <- hclust(dist(USArrests))

cutree(hc, k=1:5) #k = 1 is trivial
cutree(hc, h=250)

## Compare the 2 and 4 grouping:
g24 <- cutree(hc, k = c(2,4))
table(grp2=g24[, "2"], grp4=g24[, "4"])
```

decompose

*Classical Seasonal Decomposition by Moving Averages***Description**

Decompose a time series into seasonal, trend and irregular components using moving averages. Deals with additive or multiplicative seasonal component.

**Usage**

```
decompose(x, type = c("additive", "multiplicative"), filter = NULL)
```

**Arguments**

<code>x</code>	A time series.
<code>type</code>	The type of seasonal component. Can be abbreviated.
<code>filter</code>	A vector of filter coefficients in reverse time order (as for AR or MA coefficients), used for filtering out the seasonal component. If <code>NULL</code> , a moving average with symmetric window is performed.

**Details**

The additive model used is:

$$Y_t = T_t + S_t + e_t$$

The multiplicative model used is:

$$Y_t = T_t S_t e_t$$

The function first determines the trend component using a moving average (if `filter` is `NULL`, a symmetric window with equal weights is used), and removes it from the time series. Then, the seasonal figure is computed by averaging, for each time unit, over all periods. The seasonal figure is then centered. Finally, the error component is determined by removing trend and seasonal figure (recycled as needed) from the original time series.

**Value**

An object of class "decomposed.ts" with following components:

<code>seasonal</code>	The seasonal component (i.e., the repeated seasonal figure)
<code>figure</code>	The estimated seasonal figure only
<code>trend</code>	The trend component
<code>random</code>	The remainder part
<code>type</code>	The value of <code>type</code>

**Note**

The function `stl` provides a much more sophisticated decomposition.

**Author(s)**

David Meyer <David.Meyer@wu-wien.ac.at>

## References

M. Kendall and A. Stuart (1983) *The Advanced Theory of Statistics, Vol.3, Griffin*, 410–414.

## See Also

[stl](#)

## Examples

```
require(graphics)

m <- decompose(co2)
m$figure
plot(m)

## example taken from Kendall/Stuart
x <- c(-50, 175, 149, 214, 247, 237, 225, 329, 729, 809,
      530, 489, 540, 457, 195, 176, 337, 239, 128, 102, 232, 429, 3,
      98, 43, -141, -77, -13, 125, 361, -45, 184)
x <- ts(x, start = c(1951, 1), end = c(1958, 4), frequency = 4)
m <- decompose(x)
## seasonal figure: 6.25, 8.62, -8.84, -6.03
round(decompose(x)$figure / 10, 2)
```

---

delete.response      *Modify Terms Objects*

---

## Description

`delete.response` returns a `terms` object for the same model but with no response variable.  
`drop.terms` removes variables from the right-hand side of the model. There is also a `"[.terms"` method to perform the same function (with `keep.response=TRUE`).  
`reformulate` creates a formula from a character vector.

## Usage

```
delete.response(termsobj)

reformulate(termlabels, response = NULL)

drop.terms(termsobj, dropx = NULL, keep.response = FALSE)
```

## Arguments

<code>termsobj</code>	A <code>terms</code> object
<code>termlabels</code>	character vector giving the right-hand side of a model formula. Cannot be zero-length.
<code>response</code>	character string, symbol or call giving the left-hand side of a model formula, or <code>NULL</code> .
<code>dropx</code>	vector of positions of variables to drop from the right-hand side of the model.
<code>keep.response</code>	Keep the response in the resulting object?

**Value**

`delete.response` and `drop.terms` return a terms object.  
`reformulate` returns a formula.

**See Also**

[terms](#)

**Examples**

```
ff <- y ~ z + x + w
tt <- terms(ff)
tt
delete.response(tt)
drop.terms(tt, 2:3, keep.response = TRUE)
tt[-1]
tt[2:3]
reformulate(attr(tt, "term.labels"))

## keep LHS :
reformulate("x*w", ff[[2]])
fS <- surv(ft, case) ~ a + b
reformulate(c("a", "b*f"), fS[[2]])

stopifnot(identical(      ~ var, reformulate("var")),
           identical(~ a + b + c, reformulate(letters[1:3])),
           identical( y ~ a + b, reformulate(letters[1:2], "y"))
          )
```

---

dendrapply

*Apply a Function to All Nodes of a Dendrogram*


---

**Description**

Apply function FUN to each node of a [dendrogram](#) recursively. When `y <- dendrapply(x, fn)`, then `y` is a dendrogram of the same graph structure as `x` and for each node, `y.node[j] <- FUN(x.node[j], ...)` (where `y.node[j]` is an (invalid!) notation for the `j`-th node of `y`).

**Usage**

```
dendrapply(X, FUN, ...)
```

**Arguments**

`X` an object of class "[dendrogram](#)".  
`FUN` an R function to be applied to each dendrogram node, typically working on its [attributes](#) alone, returning an altered version of the same node.  
`...` potential further arguments passed to FUN.

**Value**

Usually a dendrogram of the same (graph) structure as X. For that, the function must be conceptually of the form `FUN <- function(X) { attributes(X) <- .....; X }`, i.e. returning the node with some attributes added or changed.

**Note**

this is still somewhat experimental, and suggestions for enhancements (or nice examples of usage) are very welcome.

**Author(s)**

Martin Maechler

**See Also**

[as.dendrogram](#), [lapply](#) for applying a function to each component of a list, [rapply](#) for doing so to each non-list component of a nested list.

**Examples**

```
require(graphics)

## a smallish simple dendrogram
dhc <- as.dendrogram(hc <- hclust(dist(USArrests), "ave"))
(dhc21 <- dhc[[2]][[1]])

## too simple:
dendrapply(dhc21, function(n) utils::str(attributes(n)))

## toy example to set colored leaf labels :
local({
  colLab <-< function(n) {
    if(is.leaf(n)) {
      a <- attributes(n)
      i <-< i+1
      attr(n, "nodePar") <-
        c(a$nodePar, list(lab.col = mycols[i], lab.font= i%3))
    }
    n
  }
  mycols <- grDevices::rainbow(attr(dhc21, "members"))
  i <- 0
})
dL <- dendrapply(dhc21, colLab)
op <- par(mfrow=2:1)
plot(dhc21)
plot(dL) ## --> colored labels!
par(op)
```

## Description

Class "dendrogram" provides general functions for handling tree-like structures. It is intended as a replacement for similar functions in hierarchical clustering and classification/regression trees, such that all of these can use the same engine for plotting or cutting trees.

The code is still in testing stage and the API may change in the future.

## Usage

```
as.dendrogram(object, ...)
## S3 method for class 'hclust':
as.dendrogram(object, hang = -1, ...)

## S3 method for class 'dendrogram':
plot(x, type = c("rectangle", "triangle"),
      center = FALSE,
      edge.root = is.leaf(x) || !is.null(attr(x, "edgetext")),
      nodePar = NULL, edgePar = list(),
      leaflab = c("perpendicular", "textlike", "none"),
      dLeaf = NULL, xlab = "", ylab = "", xaxt = "n", yaxt = "s",
      horiz = FALSE, frame.plot = FALSE, xlim, ylim, ...)

## S3 method for class 'dendrogram':
cut(x, h, ...)

## S3 method for class 'dendrogram':
print(x, digits, ...)

## S3 method for class 'dendrogram':
rev(x)

## S3 method for class 'dendrogram':
str(object, max.level = NA, digits.d = 3,
     give.attr = FALSE, wid = getOption("width"),
     nest.lev = 0, indent.str = "", stem = "--", ...)

is.leaf(object)
```

## Arguments

object	any R object that can be made into one of class "dendrogram".
x	object of class "dendrogram".
hang	numeric scalar indicating how the <i>height</i> of leaves should be computed from the heights of their parents; see <a href="#">plot.hclust</a> .
type	type of plot.
center	logical; if TRUE, nodes are plotted centered with respect to the leaves in the branch. Otherwise (default), plot them in the middle of all direct child nodes.

<code>edge.root</code>	logical; if true, draw an edge to the root node.
<code>nodePar</code>	a list of plotting parameters to use for the nodes (see <a href="#">points</a> ) or NULL by default which does not draw symbols at the nodes. The list may contain components named <code>pch</code> , <code>cex</code> , <code>col</code> , and/or <code>bg</code> each of which can have length two for specifying separate attributes for <i>inner</i> nodes and <i>leaves</i> .
<code>edgePar</code>	a list of plotting parameters to use for the edge <a href="#">segments</a> and labels (if there's an <code>edgetext</code> ). The list may contain components named <code>col</code> , <code>lty</code> and <code>lwd</code> (for the segments), <code>p.col</code> , <code>p.lwd</code> , and <code>p.lty</code> (for the <a href="#">polygon</a> around the text) and <code>t.col</code> for the text color. As with <code>nodePar</code> , each can have length two for differentiating leaves and inner nodes.
<code>leaflab</code>	a string specifying how leaves are labeled. The default "perpendicular" write text vertically (by default). "textlike" writes text horizontally (in a rectangle), and "none" suppresses leaf labels.
<code>dLeaf</code>	a number specifying the distance in user coordinates between the tip of a leaf and its label. If NULL as per default, 3/4 of a letter width or height is used.
<code>horiz</code>	logical indicating if the dendrogram should be drawn <i>horizontally</i> or not.
<code>frame.plot</code>	logical indicating if a box around the plot should be drawn, see <a href="#">plot.default</a> .
<code>h</code>	height at which the tree is cut.
<code>xlim, ylim</code>	optional x- and y-limits of the plot, passed to <a href="#">plot.default</a> . The defaults for these show the full dendrogram.
<code>..., xlab, ylab, xaxt, yaxt</code>	graphical parameters, or arguments for other methods.
<code>digits</code>	integer specifying the precision for printing, see <a href="#">print.default</a> .
<code>max.level, digits.d, give.attr, wid, nest.lev, indent.str</code>	arguments to <code>str</code> , see <a href="#">str.default()</a> . Note that <code>give.attr = FALSE</code> still shows height and members attributes for each node.
<code>stem</code>	a string used for <code>str()</code> specifying the <i>stem</i> to use for each dendrogram branch.

## Details

**Warning:** This documentation is preliminary.

The dendrogram is directly represented as a nested list where each component corresponds to a branch of the tree. Hence, the first branch of tree `z` is `z[[1]]`, the second branch of the corresponding subtree is `z[[1]][[2]]` etc.. Each node of the tree carries some information needed for efficient plotting or cutting as attributes, of which only `members`, `height` and `leaf` for leaves are compulsory:

`members` total number of leaves in the branch

`height` numeric non-negative height at which the node is plotted.

`midpoint` numeric horizontal distance of the node from the left border (the leftmost leaf) of the branch (unit 1 between all leaves). This is used for `plot(*, center=FALSE)`.

`label` character; the label of the node

`x.member` for `cut()$upper`, the number of *former* members; more generally a substitute for the `members` component used for 'horizontal' (when `horiz = FALSE`, else 'vertical') alignment.

`edgetext` character; the label for the edge leading to the node



`nodePar` a named list (of length-1 components) specifying node-specific attributes for `points` plotting, see the `nodePar` argument above.

`edgePar` a named list (of length-1 components) specifying attributes for `segments` plotting of the edge leading to the node, and drawing of the `edgetext` if available, see the `edgePar` argument above.

`leaf` logical, if TRUE, the node is a leaf of the tree.

`cut.dendrogram()` returns a list with components `$upper` and `$lower`, the first is a truncated version of the original tree, also of class `dendrogram`, the latter a list with the branches obtained from cutting the tree, each a `dendrogram`.

There are `[[`, `print`, and `str` methods for "dendrogram" objects where the first one (extraction) ensures that selecting sub-branches keeps the class.

Objects of class "hclust" can be converted to class "dendrogram" using method `as.dendrogram`.

`rev.dendrogram` simply returns the dendrogram `x` with reversed nodes, see also `reorder.dendrogram`.

`is.leaf(object)` is logical indicating if `object` is a leaf (the most simple dendrogram). `plotNode()` and `plotNodeLimit()` are helper functions.

### Warning

Some operations on dendrograms (including plotting) make use of recursion. For very deep trees It may be necessary to increase `options("expressions")`: if you do you are likely to need to set the C stack size larger than the OS default if possible (which it is not on Windows).

### Note

When using `type = "triangle"`, `center = TRUE` often looks better.

### See Also

`order.dendrogram` also on the `labels` method for dendrograms.

### Examples

```
require(graphics); require(utils)

hc <- hclust(dist(USArrests), "ave")
(dend1 <- as.dendrogram(hc)) # "print()" method
str(dend1)                  # "str()" method
str(dend1, max = 2) # only the first two sub-levels

op <- par(mfrow= c(2,2), mar = c(5,2,1,4))
plot(dend1)
## "triangle" type and show inner nodes:
plot(dend1, nodePar=list(pch = c(1,NA), cex=0.8, lab.cex = 0.8),
      type = "t", center=TRUE)
plot(dend1, edgePar=list(col = 1:2, lty = 2:3),
      dLeaf=1, edge.root = TRUE)
plot(dend1, nodePar=list(pch = 2:1, cex=.4*2:1, col = 2:3),
      horiz=TRUE)

dend2 <- cut(dend1, h=70)
```

```

plot(dend2$upper)
## leaves are wrong horizontally:
plot(dend2$upper, nodePar=list(pch = c(1,7), col = 2:1))
## dend2$lower is *NOT* a dendrogram, but a list of .. :
plot(dend2$lower[[3]], nodePar=list(col=4), horiz = TRUE, type = "tr")
## "inner" and "leaf" edges in different type & color :
plot(dend2$lower[[2]], nodePar=list(col=1), # non empty list
      edgePar = list(lty=1:2, col=2:1), edge.root=TRUE)
par(op)
str(d3 <- dend2$lower[[2]][[2]][[1]])

## "Zoom" in to the first dendrogram :
plot(dend1, xlim = c(1,20), ylim = c(1,50))

nP <- list(col=3:2, cex=c(2.0, 0.75), pch= 21:22,
          bg= c("light blue", "pink"),
          lab.cex = 0.75, lab.col = "tomato")
plot(d3, nodePar= nP, edgePar = list(col="gray", lwd=2), horiz = TRUE)

addE <- function(n) {
  if(!is.leaf(n)) {
    attr(n, "edgePar") <- list(p.col="plum")
    attr(n, "edgetext") <- paste(attr(n,"members"),"members")
  }
  n
}
d3e <- dendrapply(d3, addE)
plot(d3e, nodePar= nP)
plot(d3e, nodePar= nP, leaflab = "textlike")

```

---

density

*Kernel Density Estimation*


---

## Description

The (S3) generic function `density` computes kernel density estimates. Its default method does so with the given kernel and bandwidth for univariate observations.

## Usage

```

density(x, ...)
## Default S3 method:
density(x, bw = "nrd0", adjust = 1,
        kernel = c("gaussian", "epanechnikov", "rectangular",
                  "triangular", "biweight",
                  "cosine", "optcosine"),
        weights = NULL, window = kernel, width,
        give.Rkern = FALSE,
        n = 512, from, to, cut = 3, na.rm = FALSE, ...)

```

**Arguments**

<code>x</code>	the data from which the estimate is to be computed.
<code>bw</code>	the smoothing bandwidth to be used. The kernels are scaled such that this is the standard deviation of the smoothing kernel. (Note this differs from the reference books cited below, and from S-PLUS.)  <code>bw</code> can also be a character string giving a rule to choose the bandwidth. See <a href="#">bw.nrd</a> .  The specified (or computed) value of <code>bw</code> is multiplied by <code>adjust</code> .
<code>adjust</code>	the bandwidth used is actually <code>adjust*bw</code> . This makes it easy to specify values like ‘half the default’ bandwidth.
<code>kernel, window</code>	a character string giving the smoothing kernel to be used. This must be one of "gaussian", "rectangular", "triangular", "epanechnikov", "biweight", "cosine" or "optcosine", with default "gaussian", and may be abbreviated to a unique prefix (single letter).  "cosine" is smoother than "optcosine", which is the usual ‘cosine’ kernel in the literature and almost MSE-efficient. However, "cosine" is the version used by S.
<code>weights</code>	numeric vector of non-negative observation weights, hence of same length as <code>x</code> . The default NULL is equivalent to <code>weights = rep(1/nx, nx)</code> where <code>nx</code> is the length of (the finite entries of) <code>x[]</code> .
<code>width</code>	this exists for compatibility with S; if given, and <code>bw</code> is not, will set <code>bw</code> to <code>width</code> if this is a character string, or to a kernel-dependent multiple of <code>width</code> if this is numeric.
<code>give.Rkern</code>	logical; if true, <i>no</i> density is estimated, and the ‘canonical bandwidth’ of the chosen <code>kernel</code> is returned instead.
<code>n</code>	the number of equally spaced points at which the density is to be estimated. When <code>n &gt; 512</code> , it is rounded up to a power of 2 during the calculations (as <a href="#">fft</a> is used) and the final result is interpolated by <a href="#">approx</a> . So it almost always makes sense to specify <code>n</code> as a power of two.
<code>from, to</code>	the left and right-most points of the grid at which the density is to be estimated; the defaults are <code>cut * bw</code> outside of <code>range(x)</code> .
<code>cut</code>	by default, the values of <code>from</code> and <code>to</code> are <code>cut</code> bandwidths beyond the extremes of the data. This allows the estimated density to drop to approximately zero at the extremes.
<code>na.rm</code>	logical; if TRUE, missing values are removed from <code>x</code> . If FALSE any missing values cause an error.
<code>...</code>	further arguments for (non-default) methods.

**Details**

The algorithm used in `density.default` disperses the mass of the empirical distribution function over a regular grid of at least 512 points and then uses the fast Fourier transform to convolve this approximation with a discretized version of the kernel and then uses linear approximation to evaluate the density at the specified points.

The statistical properties of a kernel are determined by  $\sigma_K^2 = \int t^2 K(t) dt$  which is always = 1 for our kernels (and hence the bandwidth `bw` is the standard deviation of the kernel) and  $R(K) = \int K^2(t) dt$ .

MSE-equivalent bandwidths (for different kernels) are proportional to  $\sigma_K R(K)$  which is scale invariant and for our kernels equal to  $R(K)$ . This value is returned when `give.Rkern = TRUE`. See the examples for using exact equivalent bandwidths.

Infinite values in `x` are assumed to correspond to a point mass at  $+/-\text{Inf}$  and the density estimate is of the sub-density on  $(-\text{Inf}, +\text{Inf})$ .

### Value

If `give.Rkern` is true, the number  $R(K)$ , otherwise an object with class "density" whose underlying structure is a list containing the following components.

<code>x</code>	the <code>n</code> coordinates of the points where the density is estimated.
<code>y</code>	the estimated density values. These will be non-negative, but can be zero.
<code>bw</code>	the bandwidth used.
<code>n</code>	the sample size after elimination of missing values.
<code>call</code>	the call which produced the result.
<code>data.name</code>	the deparsed name of the <code>x</code> argument.
<code>has.na</code>	logical, for compatibility (always <code>FALSE</code> ).

The `print` method reports `summary` values on the `x` and `y` components.

### References

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole (for S version).
- Scott, D. W. (1992) *Multivariate Density Estimation. Theory, Practice and Visualization*. New York: Wiley.
- Sheather, S. J. and Jones M. C. (1991) A reliable data-based bandwidth selection method for kernel density estimation. *J. Roy. Statist. Soc. B*, 683–690.
- Silverman, B. W. (1986) *Density Estimation*. London: Chapman and Hall.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. New York: Springer.

### See Also

[bw.nrd](#), [plot.density](#), [hist](#).

### Examples

```
require(graphics)

plot(density(c(-20,rep(0,98),20)), xlim = c(-4,4))# IQR = 0

# The Old Faithful geyser data
d <- density(faithful$eruptions, bw = "sj")
d
plot(d)

plot(d, type = "n")
polygon(d, col = "wheat")

## Missing values:
x <- xx <- faithful$eruptions
```

```

x[i.out <- sample(length(x), 10)] <- NA
doR <- density(x, bw = 0.15, na.rm = TRUE)
lines(doR, col = "blue")
points(xx[i.out], rep(0.01, 10))

## Weighted observations:
fe <- sort(faithful$eruptions) # has quite a few non-unique values
## use 'counts / n' as weights:
dw <- density(unique(fe), weights = table(fe)/length(fe), bw = d$bw)
utils::str(dw) ## smaller n: only 126, but identical estimate:
stopifnot(all.equal(d[1:3], dw[1:3]))

## simulation from a density() fit:
# a kernel density fit is an equally-weighted mixture.
fit <- density(xx)
N <- 1e6
x.new <- rnorm(N, sample(xx, size = N, replace = TRUE), fit$bw)
plot(fit)
lines(density(x.new), col="blue")

(kernels <- eval(formals(density.default)$kernel))

## show the kernels in the R parametrization
plot(density(0, bw = 1), xlab = "",
      main="R's density() kernels with bw = 1")
for(i in 2:length(kernels))
  lines(density(0, bw = 1, kernel = kernels[i]), col = i)
legend(1.5, .4, legend = kernels, col = seq(kernels),
      lty = 1, cex = .8, y.intersp = 1)

## show the kernels in the S parametrization
plot(density(0, from=-1.2, to=1.2, width=2, kernel="gaussian"), type="l",
      ylim = c(0, 1), xlab="", main="R's density() kernels with width = 1")
for(i in 2:length(kernels))
  lines(density(0, width = 2, kernel = kernels[i]), col = i)
legend(0.6, 1.0, legend = kernels, col = seq(kernels), lty = 1)

##----- Semi-advanced theoretic from here on -----

(RKs <- cbind(sapply(kernels,
                    function(k) density(kernel = k, give.Rkern = TRUE))))
100*round(RKs["epanechnikov",]/RKs, 4) ## Efficiencies

bw <- bw.SJ(precip) ## sensible automatic choice
plot(density(precip, bw = bw),
      main = "same sd bandwidths, 7 different kernels")
for(i in 2:length(kernels))
  lines(density(precip, bw = bw, kernel = kernels[i]), col = i)

## Bandwidth Adjustment for "Exactly Equivalent Kernels"
h.f <- sapply(kernels, function(k) density(kernel = k, give.Rkern = TRUE))
(h.f <- (h.f["gaussian"] / h.f)^ .2)
## -> 1, 1.01, .995, 1.007, ... close to 1 => adjustment barely visible..

plot(density(precip, bw = bw),

```

```

    main = "equivalent bandwidths, 7 different kernels")
  for(i in 2:length(kernels))
    lines(density(precip, bw = bw, adjust = h.f[i], kernel = kernels[i]),
          col = i)
  legend(55, 0.035, legend = kernels, col = seq(kernels), lty = 1)

```

---

 deriv

---

*Symbolic and Algorithmic Derivatives of Simple Expressions*


---

## Description

Compute derivatives of simple expressions, symbolically.

## Usage

```

  D (expr, name)
  deriv(expr, ...)
  deriv3(expr, ...)

  ## Default S3 method:
  deriv(expr, namevec, function.arg = NULL, tag = ".expr",
        hessian = FALSE, ...)
  ## S3 method for class 'formula':
  deriv(expr, namevec, function.arg = NULL, tag = ".expr",
        hessian = FALSE, ...)

  ## Default S3 method:
  deriv3(expr, namevec, function.arg = NULL, tag = ".expr",
         hessian = TRUE, ...)
  ## S3 method for class 'formula':
  deriv3(expr, namevec, function.arg = NULL, tag = ".expr",
         hessian = TRUE, ...)

```

## Arguments

<code>expr</code>	A <a href="#">expression</a> or <a href="#">call</a> or (except D) a formula with no lhs.
<code>name, namevec</code>	character vector, giving the variable names (only one for D()) with respect to which derivatives will be computed.
<code>function.arg</code>	If specified and non-NULL, a character vector of arguments for a function return, or a function (with empty body) or TRUE, the latter indicating that a function with argument names <code>namevec</code> should be used.
<code>tag</code>	character; the prefix to be used for the locally created variables in result.
<code>hessian</code>	a logical value indicating whether the second derivatives should be calculated and incorporated in the return value.
<code>...</code>	arguments to be passed to or from methods.

## Details

D is modelled after its S namesake for taking simple symbolic derivatives.

deriv is a *generic* function with a default and a `formula` method. It returns a `call` for computing the `expr` and its (partial) derivatives, simultaneously. It uses so-called *algorithmic derivatives*. If `function.arg` is a function, its arguments can have default values, see the `fx` example below.

Currently, `deriv.formula` just calls `deriv.default` after extracting the expression to the right of `~`.

`deriv3` and its methods are equivalent to `deriv` and its methods except that `hessian` defaults to `TRUE` for `deriv3`.

The internal code knows about the arithmetic operators `+`, `-`, `*`, `/` and `^`, and the single-variable functions `exp`, `log`, `sin`, `cos`, `tan`, `sinh`, `cosh`, `sqrt`, `pnorm`, `dnorm`, `asin`, `acos`, `atan`, `gamma`, `lgamma`, `digamma` and `trigamma`, as well as `psigamma` for one or two arguments (but derivative only with respect to the first). (Note that only the standard normal distribution is considered.)

## Value

D returns a `call` and therefore can easily be iterated for higher derivatives.

`deriv` and `deriv3` normally return an `expression` object whose evaluation returns the function values with a `"gradient"` attribute containing the gradient matrix. If `hessian` is `TRUE` the evaluation also returns a `"hessian"` attribute containing the Hessian array.

If `function.arg` is not `NULL`, `deriv` and `deriv3` return a function with those arguments rather than an `expression`.

## References

Griewank, A. and Corliss, G. F. (1991) *Automatic Differentiation of Algorithms: Theory, Implementation, and Application*. SIAM proceedings, Philadelphia.

Bates, D. M. and Chambers, J. M. (1992) *Nonlinear models*. Chapter 10 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

## See Also

`nlm` and `optim` for numeric minimization which could make use of derivatives,

## Examples

```
## formula argument :
dx2x <- deriv(~ x^2, "x") ; dx2x
## Not run: expression({
  .value <- x^2
  .grad <- array(0, c(length(.value), 1), list(NULL, c("x")))
  .grad[, "x"] <- 2 * x
  attr(.value, "gradient") <- .grad
  .value
})
## End(Not run)
mode(dx2x)
x <- -1:2
eval(dx2x)

## Something 'tougher':
```

```

trig.exp <- expression(sin(cos(x + y^2)))
( D.sc <- D(trig.exp, "x") )
all.equal(D(trig.exp[[1]], "x"), D.sc)

( dxy <- deriv(trig.exp, c("x", "y")) )
y <- 1
eval(dxy)
eval(D.sc)

## function returned:
deriv((y ~ sin(cos(x) * y)), c("x", "y"), func = TRUE)

## function with defaulted arguments:
(fx <- deriv(y ~ b0 + b1 * 2^(-x/th), c("b0", "b1", "th"),
            function(b0, b1, th, x = 1:7){} ) )
fx(2,3,4)

## Higher derivatives
deriv3(y ~ b0 + b1 * 2^(-x/th), c("b0", "b1", "th"),
      c("b0", "b1", "th", "x") )

## Higher derivatives:
DD <- function(expr,name, order = 1) {
  if(order < 1) stop("'order' must be >= 1")
  if(order == 1) D(expr,name)
  else DD(D(expr, name), name, order - 1)
}
DD(expression(sin(x^2)), "x", 3)
## showing the limits of the internal "simplify()" :
## Not run:
-sin(x^2) * (2 * x) * 2 + ((cos(x^2) * (2 * x) * (2 * x) + sin(x^2) *
  2) * (2 * x) + sin(x^2) * (2 * x) * 2)

## End(Not run)

```

---

deviance

---

*Model Deviance*


---

### Description

Returns the deviance of a fitted model object.

### Usage

```
deviance(object, ...)
```

### Arguments

object            an object for which the deviance is desired.  
...                additional optional argument.

### Details

This is a generic function which can be used to extract deviances for fitted models. Consult the individual modeling functions for details on how to use this function.



**Value**

The value of the deviance extracted from the object `object`.

**References**

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

**See Also**

`df.residual`, `extractAIC`, `glm`, `lm`.

---

<code>df.residual</code>	<i>Residual Degrees-of-Freedom</i>
--------------------------	------------------------------------

---

**Description**

Returns the residual degrees-of-freedom extracted from a fitted model object.

**Usage**

```
df.residual(object, ...)
```

**Arguments**

<code>object</code>	an object for which the degrees-of-freedom are desired.
<code>...</code>	additional optional arguments.

**Details**

This is a generic function which can be used to extract residual degrees-of-freedom for fitted models. Consult the individual modeling functions for details on how to use this function.

The default method just extracts the `df.residual` component.

**Value**

The value of the residual degrees-of-freedom extracted from the object `x`.

**See Also**

`deviance`, `glm`, `lm`.

**Description**

Computes the inverse function of the lagged differences function `diff`.

**Usage**

```
diffinv(x, ...)  
  
## Default S3 method:  
diffinv(x, lag = 1, differences = 1, xi, ...)  
## S3 method for class 'ts':  
diffinv(x, lag = 1, differences = 1, xi, ...)
```

**Arguments**

<code>x</code>	a numeric vector, matrix, or time series.
<code>lag</code>	a scalar lag parameter.
<code>differences</code>	an integer representing the order of the difference.
<code>xi</code>	a numeric vector, matrix, or time series containing the initial values for the integrals. If missing, zeros are used.
<code>...</code>	arguments passed to or from other methods.

**Details**

`diffinv` is a generic function with methods for class "ts" and default for vectors and matrices.

Missing values are not handled.

**Value**

A numeric vector, matrix, or time series (the latter for the "ts" method) representing the discrete integral of `x`.

**Author(s)**

A. Trapletti

**See Also**

`diff`

**Examples**

```
s <- 1:10  
d <- diff(s)  
diffinv(d, xi = 1)
```

---

 dist

*Distance Matrix Computation*


---

### Description

This function computes and returns the distance matrix computed by using the specified distance measure to compute the distances between the rows of a data matrix.

### Usage

```
dist(x, method = "euclidean", diag = FALSE, upper = FALSE, p = 2)

as.dist(m, diag = FALSE, upper = FALSE)
## Default S3 method:
as.dist(m, diag = FALSE, upper = FALSE)

## S3 method for class 'dist':
print(x, diag = NULL, upper = NULL,
      digits = getOption("digits"), justify = "none",
      right = TRUE, ...)

## S3 method for class 'dist':
as.matrix(x, ...)
```

### Arguments

x	a numeric matrix, data frame or "dist" object.
method	the distance measure to be used. This must be one of "euclidean", "maximum", "manhattan", "canberra", "binary" or "minkowski". Any unambiguous substring can be given.
diag	logical value indicating whether the diagonal of the distance matrix should be printed by <code>print.dist</code> .
upper	logical value indicating whether the upper triangle of the distance matrix should be printed by <code>print.dist</code> .
p	The power of the Minkowski distance.
m	An object with distance information to be converted to a "dist" object. For the default method, a "dist" object, or a matrix (of distances) or an object which can be coerced to such a matrix using <code>as.matrix()</code> . (Only the lower triangle of the matrix is used, the rest is ignored).
digits, justify	passed to <code>format</code> inside of <code>print()</code> .
right, ...	further arguments, passed to other methods.

### Details

Available distance measures are (written for two vectors  $x$  and  $y$ ):

**euclidean:** Usual square distance between the two vectors (2 norm).

**maximum:** Maximum distance between two components of  $x$  and  $y$  (supremum norm)

**manhattan:** Absolute distance between the two vectors (1 norm).

**canberra:**  $\sum_i |x_i - y_i| / |x_i + y_i|$ . Terms with zero numerator and denominator are omitted from the sum and treated as if the values were missing.

This is intended for non-negative values (e.g. counts): taking the absolute value of the denominator is a 1998 R modification to avoid negative distances.

**binary:** (aka *asymmetric binary*): The vectors are regarded as binary bits, so non-zero elements are 'on' and zero elements are 'off'. The distance is the *proportion* of bits in which only one is on amongst those in which at least one is on.

**minkowski:** The  $p$  norm, the  $p$ th root of the sum of the  $p$ th powers of the differences of the components.

Missing values are allowed, and are excluded from all computations involving the rows within which they occur. Further, when Inf values are involved, all pairs of values are excluded when their contribution to the distance gave NaN or NA.

If some columns are excluded in calculating a Euclidean, Manhattan, Canberra or Minkowski distance, the sum is scaled up proportionally to the number of columns used. If all pairs are excluded when calculating a particular distance, the value is NA.

The "dist" method of `as.matrix()` and `as.dist()` can be used for conversion between objects of class "dist" and conventional distance matrices.

`as.dist()` is a generic function. Its default method handles objects inheriting from class "dist", or coercible to matrices using `as.matrix()`. Support for classes representing distances (also known as dissimilarities) can be added by providing an `as.matrix()` or, more directly, an `as.dist` method for such a class.

## Value

`dist` returns an object of class "dist".

The lower triangle of the distance matrix stored by columns in a vector, say `do`. If  $n$  is the number of observations, i.e.,  $n \leftarrow \text{attr}(do, "Size")$ , then for  $i < j \leq n$ , the dissimilarity between (row)  $i$  and  $j$  is `do[n*(i-1) - i*(i-1)/2 + j-i]`. The length of the vector is  $n*(n-1)/2$ , i.e., of order  $n^2$ .

The object has the following attributes (besides "class" equal to "dist"):

Size	integer, the number of observations in the dataset.
Labels	optionally, contains the labels, if any, of the observations of the dataset.
Diag, Upper	logicals corresponding to the arguments <code>diag</code> and <code>upper</code> above, specifying how the object should be printed.
call	optionally, the <code>call</code> used to create the object.
method	optionally, the distance method used; resulting from <code>dist()</code> , the <code>(match.arg())</code> ed method argument.

## References

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- Mardia, K. V., Kent, J. T. and Bibby, J. M. (1979) *Multivariate Analysis*. Academic Press.
- Borg, I. and Groenen, P. (1997) *Modern Multidimensional Scaling. Theory and Applications*. Springer.

**See Also**

[daisy](#) in the **cluster** package with more possibilities in the case of *mixed* (continuous / categorical) variables. [hclust](#).

**Examples**

```
require(graphics)

x <- matrix(rnorm(100), nrow=5)
dist(x)
dist(x, diag = TRUE)
dist(x, upper = TRUE)
m <- as.matrix(dist(x))
d <- as.dist(m)
stopifnot(d == dist(x))

## Use correlations between variables "as distance"
dd <- as.dist((1 - cor(USJudgeRatings))/2)
round(1000 * dd) # (prints more nicely)
plot(hclust(dd)) # to see a dendrogram of clustered variables

## example of binary and canberra distances.
x <- c(0, 0, 1, 1, 1, 1)
y <- c(1, 0, 1, 1, 0, 1)
dist(rbind(x,y), method= "binary")
## answer 0.4 = 2/5
dist(rbind(x,y), method= "canberra")
## answer 2 * (6/5)

## To find the names
labels(eurodist)

## Examples involving "Inf" :
## 1)
x[6] <- Inf
(m2 <- rbind(x,y))
dist(m2, method="binary")# warning, answer 0.5 = 2/4
## These all give "Inf":
stopifnot(Inf == dist(m2, method= "euclidean"),
          Inf == dist(m2, method= "maximum"),
          Inf == dist(m2, method= "manhattan"))
## "Inf" is same as very large number:
x1 <- x; x1[6] <- 1e100
stopifnot(dist(cbind(x ,y), method="canberra") ==
          print(dist(cbind(x1,y), method="canberra"))))

## 2)
y[6] <- Inf #-> 6-th pair is excluded
dist(rbind(x,y), method="binary") # warning; 0.5
dist(rbind(x,y), method="canberra") # 3
dist(rbind(x,y), method="maximum") # 1
dist(rbind(x,y), method="manhattan")# 2.4
```

---

 dummy.coef

*Extract Coefficients in Original Coding*


---

### Description

This extracts coefficients in terms of the original levels of the coefficients rather than the coded variables.

### Usage

```
dummy.coef(object, ...)

## S3 method for class 'lm':
dummy.coef(object, use.na = FALSE, ...)

## S3 method for class 'aovlist':
dummy.coef(object, use.na = FALSE, ...)
```

### Arguments

object	a linear model fit.
use.na	logical flag for coefficients in a singular model. If use.na is true, undetermined coefficients will be missing; if false they will get one possible value.
...	arguments passed to or from other methods.

### Details

A fitted linear model has coefficients for the contrasts of the factor terms, usually one less in number than the number of levels. This function re-expresses the coefficients in the original coding; as the coefficients will have been fitted in the reduced basis, any implied constraints (e.g., zero sum for `contr.helmert` or `contr.sum` will be respected. There will be little point in using `dummy.coef` for `contr.treatment` contrasts, as the missing coefficients are by definition zero.

The method used has some limitations, and will give incomplete results for terms such as `poly(x, 2)`. However, it is adequate for its main purpose, `aov` models.

### Value

A list giving for each term the values of the coefficients. For a multistratum `aov` model, such a list for each stratum.

### Warning

This function is intended for human inspection of the output: it should not be used for calculations. Use coded variables for all calculations.

The results differ from S for singular values, where S can be incorrect.

### See Also

[aov, model.tables](#)

**Examples**

```
options(contrasts=c("contr.helmert", "contr.poly"))
## From Venables and Ripley (2002) p.165.
utils::data(npk, package="MASS")
npk.aov <- aov(yield ~ block + N*P*K, npk)
dummy.coef(npk.aov)

npk.aovE <- aov(yield ~ N*P*K + Error(block), npk)
dummy.coef(npk.aovE)
```

ecdf

*Empirical Cumulative Distribution Function***Description**

Compute or plot an empirical cumulative distribution function.

**Usage**

```
ecdf(x)

## S3 method for class 'ecdf':
plot(x, ..., ylab="Fn(x)", verticals = FALSE,
      col.01line = "gray70", pch = 19)

## S3 method for class 'ecdf':
print(x, digits= getOption("digits") - 2, ...)

## S3 method for class 'ecdf':
summary(object, ...)
```

**Arguments**

<code>x</code> , <code>object</code>	numeric vector of the observations for <code>ecdf</code> ; for the methods, an object inheriting from class "ecdf".
<code>...</code>	arguments to be passed to subsequent methods, e.g., <code>plot.stepfun</code> for the <code>plot</code> method.
<code>ylab</code>	label for the y-axis.
<code>verticals</code>	see <code>plot.stepfun</code> .
<code>col.01line</code>	numeric or character specifying the color of the horizontal lines at $y = 0$ and $1$ , see <code>colors</code> .
<code>pch</code>	plotting character.
<code>digits</code>	number of significant digits to use, see <code>print</code> .

## Details

The e.c.d.f. (empirical cumulative distribution function)  $F_n$  is a step function with jumps  $i/n$  at observation values, where  $i$  is the number of tied observations at that value. Missing values are ignored.

For observations  $x = (x_1, x_2, \dots, x_n)$ ,  $F_n$  is the fraction of observations less or equal to  $t$ , i.e.,

$$F_n(t) = \#\{x_i \leq t\} / n = \frac{1}{n} \sum_{i=1}^n \mathbf{1}_{[x_i \leq t]}.$$

The function `plot.ecdf` which implements the `plot` method for `ecdf` objects, is implemented via a call to `plot.stepfun`; see its documentation.

## Value

For `ecdf`, a function of class "ecdf", inheriting from the "stepfun" class.

For the summary method, a summary of the knots of object with a "header" attribute.

## Author(s)

Martin Maechler, <maechler@stat.math.ethz.ch>.  
Corrections by R-core.

## See Also

[stepfun](#), the more general class of step functions, [approxfun](#) and [splinefun](#).

## Examples

```
##-- Simple didactical ecdf example :
x <- rnorm(12)
Fn <- ecdf(x)
Fn      # a *function*
Fn(x)   # returns the percentiles for x
tt <- seq(-2,2, by = 0.1)
12 * Fn(tt) # Fn is a 'simple' function {with values k/12}
summary(Fn)
##--> see below for graphics
knots(Fn) # the unique data values {12 of them if there were no ties}

y <- round(rnorm(12),1); y[3] <- y[1]
Fn12 <- ecdf(y)
Fn12
knots(Fn12) # unique values (always less than 12!)
summary(Fn12)
summary.stepfun(Fn12)

## Advanced: What's inside the function closure?
print(ls.Fn12 <- ls(environment(Fn12)))
##[1] "f" "method" "n" "x" "y" "yleft" "yright"
utils::ls.str(environment(Fn12))

###----- Plotting -----
require(graphics)
```



```

op <- par(mfrow=c(3,1), mgp=c(1.5, 0.8,0), mar= .1+c(3,3,2,1))

F10 <- ecdf(rnorm(10))
summary(F10)

plot(F10)
plot(F10, verticals= TRUE, do.points = FALSE)

plot(Fn12 , lwd = 2) ; mtext("lwd = 2", adj=1)
xx <- unique(sort(c(seq(-3, 2, length=201), knots(Fn12))))
lines(xx, Fn12(xx), col='blue')
abline(v=knots(Fn12), lty=2, col='gray70')

plot(xx, Fn12(xx), type='o', cex=.1) #- plot.default {ugly}
plot(Fn12, col.hor='red', add= TRUE) #- plot method
abline(v=knots(Fn12), lty=2, col='gray70')
## luxury plot
plot(Fn12, verticals=TRUE, col.points='blue',
      col.hor='red', col.vert='bisque')

##-- this works too (automatic call to ecdf(.)):
plot.ecdf(rnorm(24))
title("via simple plot.ecdf(x)", adj=1)

par(op)

```

---

 eff.aovlist

---

*Compute Efficiencies of Multistratum Analysis of Variance*


---

## Description

Computes the efficiencies of fixed-effect terms in an analysis of variance model with multiple strata.

## Usage

```
eff.aovlist(aovlist)
```

## Arguments

aovlist      The result of a call to aov with an Error term.

## Details

Fixed-effect terms in an analysis of variance model with multiple strata may be estimable in more than one stratum, in which case there is less than complete information in each. The efficiency for a term is the fraction of the maximum possible precision (inverse variance) obtainable by estimating in just that stratum. Under the assumption of balance, this is the same for all contrasts involving that term.

This function is used to pick strata in which to estimate terms in `model.tables.aovlist` and `se.contrast.aovlist`.

In many cases terms will only occur in one stratum, when all the efficiencies will be one: this is detected and no further calculations are done.

The calculation used requires orthogonal contrasts for each term, and will throw an error if non-orthogonal contrasts (e.g. treatment contrasts or an unbalanced design) are detected.

### Value

A matrix giving for each non-pure-error stratum (row) the efficiencies for each fixed-effect term in the model.

### References

Heiberger, R. M. (1989) *Computation for the Analysis of Designed Experiments*. Wiley.

### See Also

[aov.model.tables.aovlist](#), [se.contrast.aovlist](#)

### Examples

```
## An example from Yates (1932),
## a 2^3 design in 2 blocks replicated 4 times

Block <- gl(8, 4)
A <- factor(c(0,1,0,1,0,1,0,1,0,1,0,1,0,1,0,1,
             0,1,0,1,0,1,0,1,0,1,0,1))
B <- factor(c(0,0,1,1,0,0,1,1,0,1,0,1,1,0,1,0,0,0,1,1,
             0,0,1,1,0,0,1,1,0,0,1,1))
C <- factor(c(0,1,1,0,1,0,0,1,0,0,1,1,0,0,1,1,0,1,0,1,
             1,0,1,0,0,0,1,1,1,1,0,0))
Yield <- c(101, 373, 398, 291, 312, 106, 265, 450, 106, 306, 324, 449,
          272, 89, 407, 338, 87, 324, 279, 471, 323, 128, 423, 334,
          131, 103, 445, 437, 324, 361, 302, 272)
aovdat <- data.frame(Block, A, B, C, Yield)

old <- getOption("contrasts")
options(contrasts=c("contr.helmert", "contr.poly"))
(fit <- aov(Yield ~ A*B*C + Error(Block), data = aovdat))
eff.aovlist(fit)
options(contrasts = old)
```

---

effects

*Effects from Fitted Model*

---

### Description

Returns (orthogonal) effects from a fitted model, usually a linear model. This is a generic function, but currently only has a methods for objects inheriting from classes "lm" and "glm".

### Usage

```
effects(object, ...)

## S3 method for class 'lm':
effects(object, set.sign = FALSE, ...)
```

**Arguments**

<code>object</code>	an R object; typically, the result of a model fitting function such as <code>lm</code> .
<code>set.sign</code>	logical. If <code>TRUE</code> , the sign of the effects corresponding to coefficients in the model will be set to agree with the signs of the corresponding coefficients, otherwise the sign is arbitrary.
<code>...</code>	arguments passed to or from other methods.

**Details**

For a linear model fitted by `lm` or `aoa`, the effects are the uncorrelated single-degree-of-freedom values obtained by projecting the data onto the successive orthogonal subspaces generated by the QR decomposition during the fitting process. The first  $r$  (the rank of the model) are associated with coefficients and the remainder span the space of residuals (but are not associated with particular residuals).

Empty models do not have effects.

**Value**

A (named) numeric vector of the same length as `residuals`, or a matrix if there were multiple responses in the fitted model, in either case of class `"coef"`.

The first  $r$  rows are labelled by the corresponding coefficients, and the remaining rows are unlabelled. Note that in rank-deficient models the corresponding coefficients will be in a different order if pivoting occurred.

**References**

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

**See Also**

`coef`

**Examples**

```
y <- c(1:3, 7, 5)
x <- c(1:3, 6:7)
( ee <- effects(lm(y ~ x)) )
c( round(ee - effects(lm(y+10 ~ I(x-3.8))), 3) )
# just the first is different
```

---

embed

*Embedding a Time Series*

---

**Description**

Embeds the time series `x` into a low-dimensional Euclidean space.

**Usage**

```
embed(x, dimension = 1)
```

**Arguments**

`x` a numeric vector, matrix, or time series.  
`dimension` a scalar representing the embedding dimension.

**Details**

Each row of the resulting matrix consists of sequences  $x[t]$ ,  $x[t-1]$ , ...,  $x[t-dimension+1]$ , where  $t$  is the original index of  $x$ . If  $x$  is a matrix, i.e.,  $x$  contains more than one variable, then  $x[t]$  consists of the  $t$ th observation on each variable.

**Value**

A matrix containing the embedded time series  $x$ .

**Author(s)**

A. Trapletti, B.D. Ripley

**Examples**

```
x <- 1:10
embed(x, 3)
```

---

`expand.model.frame` *Add new variables to a model frame*

---

**Description**

Evaluates new variables as if they had been part of the formula of the specified model. This ensures that the same `na.action` and `subset` arguments are applied and allows, for example,  $x$  to be recovered for a model using `sin(x)` as a predictor.

**Usage**

```
expand.model.frame(model, extras,
                  envir = environment(formula(model)),
                  na.expand = FALSE)
```

**Arguments**

`model` a fitted model  
`extras` one-sided formula or vector of character strings describing new variables to be added  
`envir` an environment to evaluate things in  
`na.expand` logical; see below

**Details**

If `na.expand=FALSE` then NA values in the extra variables will be passed to the `na.action` function used in `model`. This may result in a shorter data frame (with `na.omit`) or an error (with `na.fail`). If `na.expand=TRUE` the returned data frame will have precisely the same rows as `model.frame(model)`, but the columns corresponding to the extra variables may contain NA.

**Value**

A data frame.

**See Also**

[model.frame](#), [predict](#)

**Examples**

```
model <- lm(log(Volume) ~ log(Girth) + log(Height), data=trees)
expand.model.frame(model, ~ Girth) # prints data.frame like
```

```
dd <- data.frame(x=1:5, y=rnorm(5), z=c(1,2,NA,4,5))
model <- glm(y ~ x, data=dd, subset=1:4, na.action=na.omit)
expand.model.frame(model, "z", na.expand=FALSE) # = default
expand.model.frame(model, "z", na.expand=TRUE)
```

---

Exponential

*The Exponential Distribution*

---

**Description**

Density, distribution function, quantile function and random generation for the exponential distribution with rate `rate` (i.e., mean  $1/\text{rate}$ ).

**Usage**

```
dexp(x, rate = 1, log = FALSE)
pexp(q, rate = 1, lower.tail = TRUE, log.p = FALSE)
qexp(p, rate = 1, lower.tail = TRUE, log.p = FALSE)
rexp(n, rate = 1)
```

**Arguments**

<code>x</code> , <code>q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
<code>rate</code>	vector of rates.
<code>log</code> , <code>log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$ .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .

**Details**

If `rate` is not specified, it assumes the default value of 1.

The exponential distribution with rate  $\lambda$  has density

$$f(x) = \lambda e^{-\lambda x}$$

for  $x \geq 0$ .

**Value**

dexp gives the density, pexp gives the distribution function, qexp gives the quantile function, and rexp generates random deviates.

**Note**

The cumulative hazard  $H(t) = -\log(1 - F(t))$  is `-pexp(t, r, lower = FALSE, log = TRUE)`.

**Source**

dexp, pexp and qexp are all calculated from numerically stable versions of the definitions.

rexp uses

Ahrens, J. H. and Dieter, U. (1972). Computer methods for sampling from the exponential and normal distributions. *Communications of the ACM*, **15**, 873–882.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 1, chapter 19. Wiley, New York.

**See Also**

[exp](#) for the exponential function, [dgamma](#) for the gamma distribution and [dweibull](#) for the Weibull distribution, both of which generalize the exponential.

**Examples**

```
dexp(1) - exp(-1) #-> 0
```

---

extractAIC

*Extract AIC from a Fitted Model*

---

**Description**

Computes the (generalized) Akaike An Information Criterion for a fitted parametric model.

**Usage**

```
extractAIC(fit, scale, k = 2, ...)
```

**Arguments**

fit	fitted model, usually the result of a fitter like <code>lm</code> .
scale	optional numeric specifying the scale parameter of the model, see <code>scale</code> in <code>step</code> . Currently only used in the "lm" method, where <code>scale</code> specifies the estimate of the error variance, and <code>scale = 0</code> indicates that it is to be estimated by maximum likelihood.
k	numeric specifying the ‘weight’ of the <i>equivalent degrees of freedom</i> ( $\equiv$ edf) part in the AIC formula.
...	further arguments (currently unused in base R).

**Details**

This is a generic function, with methods in base R for "aov", "coxph", "glm", "lm", "negbin" and "survreg" classes.

The criterion used is

$$AIC = -2 \log L + k \times \text{edf},$$

where  $L$  is the likelihood and edf the equivalent degrees of freedom (i.e., the number of free parameters for usual parametric models) of `fit`.

For linear models with unknown scale (i.e., for `lm` and `aov`),  $-2 \log L$  is computed from the *deviance* and uses a different additive constant to `logLik` and hence `AIC`. If  $RSS$  denotes the (weighted) residual sum of squares then `extractAIC` uses for  $-2 \log L$  the formulae  $RSS/s - n$  (corresponding to Mallows'  $C_p$ ) in the case of known scale  $s$  and  $n \log(RSS/n)$  for unknown scale. `AIC` only handles unknown scale and uses the formula  $n \log(RSS/n) - n + n \log 2\pi - \sum \log w$  where  $w$  are the weights.

For `glm` fits the family's `aic()` function is used to compute the AIC: see the note under `logLik` about the assumptions this makes.

$k = 2$  corresponds to the traditional AIC, using  $k = \log(n)$  provides the BIC (Bayesian IC) instead.

**Value**

A numeric vector of length 2, giving

edf	the ‘equivalent <b>d</b> egrees of <b>f</b> reedom’ for the fitted model <code>fit</code> .
AIC	the (generalized) Akaike Information Criterion for <code>fit</code> .

**Note**

This function is used in `add1`, `drop1` and `step` and similar functions in package **MASS** from which it was adopted.

**Author(s)**

B. D. Ripley

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. New York: Springer (4th ed).

**See Also**

[AIC](#), [deviance](#), [add1](#), [step](#)

**Examples**

```
utils::example(glm)
extractAIC(glm.D93) #>> 5 15.129
```

---

factanal

*Factor Analysis*

---

**Description**

Perform maximum-likelihood factor analysis on a covariance matrix or data matrix.

**Usage**

```
factanal(x, factors, data = NULL, covmat = NULL, n.obs = NA,
         subset, na.action, start = NULL,
         scores = c("none", "regression", "Bartlett"),
         rotation = "varimax", control = NULL, ...)
```

**Arguments**

<code>x</code>	A formula or a numeric matrix or an object that can be coerced to a numeric matrix.
<code>factors</code>	The number of factors to be fitted.
<code>data</code>	An optional data frame (or similar: see <a href="#">model.frame</a> ), used only if <code>x</code> is a formula. By default the variables are taken from <code>environment(formula)</code> .
<code>covmat</code>	A covariance matrix, or a covariance list as returned by <a href="#">cov.wt</a> . Of course, correlation matrices are covariance matrices.
<code>n.obs</code>	The number of observations, used if <code>covmat</code> is a covariance matrix.
<code>subset</code>	A specification of the cases to be used, if <code>x</code> is used as a matrix or formula.
<code>na.action</code>	The <code>na.action</code> to be used if <code>x</code> is used as a formula.
<code>start</code>	NULL or a matrix of starting values, each column giving an initial set of uniquenesses.
<code>scores</code>	Type of scores to produce, if any. The default is <code>none</code> , <code>"regression"</code> gives Thompson's scores, <code>"Bartlett"</code> gives Bartlett's weighted least-squares scores. Partial matching allows these names to be abbreviated.
<code>rotation</code>	character. <code>"none"</code> or the name of a function to be used to rotate the factors: it will be called with first argument the loadings matrix, and should return a list with component <code>loadings</code> giving the rotated loadings, or just the rotated loadings.
<code>control</code>	A list of control values, <ul style="list-style-type: none"> <li><b>nstart</b> The number of starting values to be tried if <code>start = NULL</code>. Default 1.</li> <li><b>trace</b> logical. Output tracing information? Default <code>FALSE</code>.</li> </ul>



- lower** The lower bound for uniquenesses during optimization. Should be  $> 0$ . Default 0.005.
- opt** A list of control values to be passed to `optim`'s `control` argument.
- rotate** a list of additional arguments for the rotation function.
- ... Components of `control` can also be supplied as named arguments to `factanal`.

## Details

The factor analysis model is

$$x = \Lambda f + e$$

for a  $p$ -element row-vector  $x$ , a  $p \times k$  matrix of *loadings*, a  $k$ -element vector of *scores* and a  $p$ -element vector of errors. None of the components other than  $x$  is observed, but the major restriction is that the scores be uncorrelated and of unit variance, and that the errors be independent with variances  $\Phi$ , the *uniquenesses*. Thus factor analysis is in essence a model for the covariance matrix of  $x$ ,

$$\Sigma = \Lambda' \Lambda + \Psi$$

There is still some indeterminacy in the model for it is unchanged if  $\Lambda$  is replaced by  $G\Lambda$  for any orthogonal matrix  $G$ . Such matrices  $G$  are known as *rotations* (although the term is applied also to non-orthogonal invertible matrices).

If `covmat` is supplied it is used. Otherwise `x` is used if it is a matrix, or a formula `x` is used with `data` to construct a model matrix, and that is used to construct a covariance matrix. (It makes no sense for the formula to have a response, and all the variables must be numeric.) Once a covariance matrix is found or calculated from `x`, it is converted to a correlation matrix for analysis. The correlation matrix is returned as component `correlation` of the result.

The fit is done by optimizing the log likelihood assuming multivariate normality over the uniquenesses. (The maximizing loadings for given uniquenesses can be found analytically: Lawley & Maxwell (1971, p. 27).) All the starting values supplied in `start` are tried in turn and the best fit obtained is used. If `start = NULL` then the first fit is started at the value suggested by Jöreskog (1963) and given by Lawley & Maxwell (1971, p. 31), and then `control$nstart - 1` other values are tried, randomly selected as equal values of the uniquenesses.

The uniquenesses are technically constrained to lie in  $[0, 1]$ , but near-zero values are problematical, and the optimization is done with a lower bound of `control$lower`, default 0.005 (Lawley & Maxwell, 1971, p. 32).

Scores can only be produced if a data matrix is supplied and used. The first method is the regression method of Thomson (1951), the second the weighted least squares method of Bartlett (1937, 8). Both are estimates of the unobserved scores  $f$ . Thomson's method regresses (in the population) the unknown  $f$  on  $x$  to yield

$$\hat{f} = \Lambda' \Sigma^{-1} x$$

and then substitutes the sample estimates of the quantities on the right-hand side. Bartlett's method minimizes the sum of squares of standardized errors over the choice of  $f$ , given (the fitted)  $\Lambda$ .

If `x` is a formula then the standard NA-handling is applied to the scores (if requested): see [napredict](#).

The `print` method (documented under [loadings](#)) follows the factor analysis convention of drawing attention to the patterns of the results, so the default precision is three decimal places, and small loadings are suppressed.

**Value**

An object of class "factanal" with components

loadings	A matrix of loadings, one column for each factor. The factors are ordered in decreasing order of sums of squares of loadings, and given the sign that will make the sum of the loadings positive. This is of class "loadings": see <a href="#">loadings</a> for its print method.
uniquenesses	The uniquenesses computed.
correlation	The correlation matrix used.
criteria	The results of the optimization: the value of the negative log-likelihood and information on the iterations used.
factors	The argument factors.
dof	The number of degrees of freedom of the factor analysis model.
method	The method: always "mle".
scores	If requested, a matrix of scores. <code>napredict</code> is applied to handle the treatment of values omitted by the <code>na.action</code> .
n.obs	The number of observations if available, or NA.
call	The matched call.
na.action	If relevant.
STATISTIC, PVAL	The significance-test statistic and P value, if it can be computed.

**Note**

There are so many variations on factor analysis that it is hard to compare output from different programs. Further, the optimization in maximum likelihood factor analysis is hard, and many other examples we compared had less good fits than produced by this function. In particular, solutions which are Heywood cases (with one or more uniquenesses essentially zero) are much often common than most texts and some other programs would lead one to believe.

**References**

- Bartlett, M. S. (1937) The statistical conception of mental factors. *British Journal of Psychology*, **28**, 97–104.
- Bartlett, M. S. (1938) Methods of estimating mental factors. *Nature*, **141**, 609–610.
- Jöreskog, K. G. (1963) *Statistical Estimation in Factor Analysis*. Almqvist and Wicksell.
- Lawley, D. N. and Maxwell, A. E. (1971) *Factor Analysis as a Statistical Method*. Second edition. Butterworths.
- Thomson, G. H. (1951) *The Factorial Analysis of Human Ability*. London University Press.

**See Also**

[loadings](#) (which explains some details of the print method), [varimax](#), [princomp](#), [ability.cov](#), [Harman23.cor](#), [Harman74.cor](#).

**Examples**

```
# A little demonstration, v2 is just v1 with noise,
# and same for v4 vs. v3 and v6 vs. v5
# Last four cases are there to add noise
# and introduce a positive manifold (g factor)
v1 <- c(1,1,1,1,1,1,1,1,1,1,1,3,3,3,3,3,4,5,6)
v2 <- c(1,2,1,1,1,1,1,2,1,2,1,3,4,3,3,3,4,6,5)
v3 <- c(3,3,3,3,3,1,1,1,1,1,1,1,1,1,1,1,1,5,4,6)
v4 <- c(3,3,4,3,3,1,1,2,1,1,1,1,2,1,1,1,5,6,4)
v5 <- c(1,1,1,1,1,3,3,3,3,3,1,1,1,1,1,1,6,4,5)
v6 <- c(1,1,1,2,1,3,3,3,4,3,1,1,1,2,1,6,5,4)
m1 <- cbind(v1,v2,v3,v4,v5,v6)
cor(m1)
factanal(m1, factors=3) # varimax is the default
factanal(m1, factors=3, rotation="promax")
# The following shows the g factor as PC1
prcomp(m1)

## formula interface
factanal(~v1+v2+v3+v4+v5+v6, factors = 3,
        scores = "Bartlett")$scores

## a realistic example from Bartholomew (1987, pp. 61-65)
utils::example(ability.cov)
```

factor.scope

*Compute Allowed Changes in Adding to or Dropping from a Formula***Description**

`add.scope` and `drop.scope` compute those terms that can be individually added to or dropped from a model while respecting the hierarchy of terms.

**Usage**

```
add.scope(terms1, terms2)

drop.scope(terms1, terms2)

factor.scope(factor, scope)
```

**Arguments**

<code>terms1</code>	the terms or formula for the base model.
<code>terms2</code>	the terms or formula for the upper ( <code>add.scope</code> ) or lower ( <code>drop.scope</code> ) scope. If missing for <code>drop.scope</code> it is taken to be the null formula, so all terms (except any intercept) are candidates to be dropped.
<code>factor</code>	the "factor" attribute of the terms of the base object.
<code>scope</code>	a list with one or both components <code>drop</code> and <code>add</code> giving the "factor" attribute of the lower and upper scopes respectively.

**Details**

`factor.scope` is not intended to be called directly by users.

**Value**

For `add.scope` and `drop.scope` a character vector of terms labels. For `factor.scope`, a list with components `drop` and `add`, character vectors of terms labels.

**See Also**

[add1](#), [drop1](#), [aov](#), [lm](#)

**Examples**

```
add.scope( ~ a + b + c + a:b, ~ (a + b + c)^3)
# [1] "a:c" "b:c"
drop.scope( ~ a + b + c + a:b)
# [1] "c" "a:b"
```

---

family

*Family Objects for Models*

---

**Description**

Family objects provide a convenient way to specify the details of the models used by functions such as `glm`. See the documentation for `glm` for the details on how such model fitting takes place.

**Usage**

```
family(object, ...)

binomial(link = "logit")
gaussian(link = "identity")
Gamma(link = "inverse")
inverse.gaussian(link = "1/mu^2")
poisson(link = "log")
quasi(link = "identity", variance = "constant")
quasibinomial(link = "logit")
quasipoisson(link = "log")
```

**Arguments**

**link** a specification for the model link function. This can be a name/expression, a literal character string, a length-one character vector or an object of class "`link-glm`" (such as generated by `make.link`) provided it is not specified *via* one of the standard names given next.

The gaussian family accepts the links (as names) `identity`, `log` and `inverse`; the binomial family the links `logit`, `probit`, `cauchit`, (corresponding to logistic, normal and Cauchy CDFs respectively) `log` and `cloglog` (complementary log-log); the Gamma family the links `inverse`, `identity` and `log`; the poisson family the links `log`, `identity`, and

	sqrt and the inverse.gaussian family the links 1/mu^2, inverse, identity and log.
	The quasi family accepts the links logit, probit, cloglog, identity, inverse, log, 1/mu^2 and sqrt, and the function <a href="#">power</a> can be used to create a power link function.
variance	for all families other than quasi, the variance function is determined by the family. The quasi family will accept the literal character string (or unquoted as a name/expression) specifications "constant", "mu(1-mu)", "mu", "mu^2" and "mu^3", a length-one character vector taking one of those values, or a list containing components varfun, validmu, dev.resids, initialize and name.
object	the function family accesses the family objects which are stored within objects created by modelling functions (e.g., glm).
...	further arguments passed to methods.

### Details

family is a generic function with methods for classes "glm" and "lm" (the latter returning gaussian()).

The quasibinomial and quasipoisson families differ from the binomial and poisson families only in that the dispersion parameter is not fixed at one, so they can model over-dispersion. For the binomial case see McCullagh and Nelder (1989, pp. 124–8). Although they show that there is (under some restrictions) a model with variance proportional to mean as in the quasi-binomial model, note that glm does not compute maximum-likelihood estimates in that model. The behaviour of S is closer to the quasi- variants.

### Value

An object of class "family" (which has a concise print method). This is a list with elements

family	character: the family name.
link	character: the link name.
linkfun	function: the link.
linkinv	function: the inverse of the link function.
variance	function: the variance as a function of the mean.
dev.resids	function giving the deviance residuals as a function of (y, mu, wt).
aic	function giving the AIC value if appropriate (but NA for the quasi- families). See <a href="#">logLik</a> for the assumptions made about the dispersion parameter.
mu.eta	function: derivative function(eta) $d\mu/d\eta$ .
initialize	expression. This needs to set up whatever data objects are needed for the family as well as n (needed for AIC in the binomial family) and mustart (see <a href="#">glm</a> ).
valid.mu	logical function. Returns TRUE if a mean vector mu is within the domain of variance.
valid.eta	logical function. Returns TRUE if a linear predictor eta is within the domain of linkinv.
simulate	(optional) function simulate(object, nsim) to be called by the "lm" method of <a href="#">simulate</a> . It will normally return a matrix with nsim columns and one row for each fitted value, but it can also return a list of length nsim. Clearly this will be missing for 'quasi-' families.

**Note**

The `link` and `variance` arguments have rather awkward semantics for back-compatibility. The recommended way to supply them is as quoted character strings, but they can also be supplied unquoted (as names or expressions). In addition, they can also be supplied as a length-one character vector giving the name of one of the options, or as a list (for `link`, of class "link-glm"). The restrictions apply only to links given as names: when given as a character string all the links known to `make.link` are accepted.

This is potentially ambiguous: supplying `link=logit` could mean the unquoted name of a link or the value of object `logit`. It is interpreted if possible as the name of an allowed link, then as an object. (You can force the interpretation to always be the value of an object via `logit[1]`.)

**Author(s)**

The design was inspired by S functions of the same names described in Hastie & Pregibon (1992) (except `quasibinomial` and `quasipoisson`).

**References**

- McCullagh P. and Nelder, J. A. (1989) *Generalized Linear Models*. London: Chapman and Hall.
- Dobson, A. J. (1983) *An Introduction to Statistical Modelling*. London: Chapman and Hall.
- Cox, D. R. and Snell, E. J. (1981). *Applied Statistics; Principles and Examples*. London: Chapman and Hall.
- Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models*. Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

`glm`, `power`, `make.link`.

**Examples**

```
require(utils) # for str

nf <- gaussian() # Normal family
nf
str(nf) # internal STRucture

gf <- Gamma()
gf
str(gf)
gf$linkinv
gf$variance(-3:4) #- == (.)^2

## quasipoisson. compare with example(glm)
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
d.AD <- data.frame(treatment, outcome, counts)
glm.qD93 <- glm(counts ~ outcome + treatment, family=quasipoisson())
glm.qD93
anova(glm.qD93, test="F")
summary(glm.qD93)
```

```

## for Poisson results use
anova(glm.qD93, dispersion = 1, test="Chisq")
summary(glm.qD93, dispersion = 1)

## Example of user-specified link, a logit model for p^days
## See Shaffer, T. 2004. Auk 121(2): 526-540.
logexp <- function(days = 1)
{
  linkfun <- function(mu) qlogis(mu^(1/days))
  linkinv <- function(eta) plogis(eta)^days
  mu.eta <- function(eta) days * plogis(eta)^(days-1) *
    .Call("logit_mu_eta", eta, PACKAGE = "stats")
  valideta <- function(eta) TRUE
  link <- paste("logexp(", days, ")", sep="")
  structure(list(linkfun = linkfun, linkinv = linkinv,
    mu.eta = mu.eta, valideta = valideta, name = link),
    class = "link-glm")
}
binomial(logexp(3))
## in practice this would be used with a vector of 'days', in
## which case use an offset of 0 in the corresponding formula
## to get the null deviance right.

## Binomial with identity link: often not a good idea.
## Not run: binomial(link=make.link("identity"))

## tests of quasi
x <- rnorm(100)
y <- rpois(100, exp(1+x))
glm(y ~x, family=quasi(variance="mu", link="log"))
# which is the same as
glm(y ~x, family=poisson)
glm(y ~x, family=quasi(variance="mu^2", link="log"))
## Not run: glm(y ~x, family=quasi(variance="mu^3", link="log")) # fails
y <- rbinom(100, 1, plogis(x))
# needs to set a starting value for the next fit
glm(y ~x, family=quasi(variance="mu(1-mu)", link="logit"), start=c(0,1))

```

---

FDist

*The F Distribution*


---

### Description

Density, distribution function, quantile function and random generation for the F distribution with df1 and df2 degrees of freedom (and optional non-centrality parameter ncp).

### Usage

```

df(x, df1, df2, ncp, log = FALSE)
pf(q, df1, df2, ncp, lower.tail = TRUE, log.p = FALSE)
qf(p, df1, df2, ncp, lower.tail = TRUE, log.p = FALSE)
rf(n, df1, df2, ncp)

```

**Arguments**

<code>x, q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
<code>df1, df2</code>	degrees of freedom. <code>Inf</code> is allowed.
<code>ncp</code>	non-centrality parameter. If omitted the central F is assumed.
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .

**Details**

The F distribution with `df1 =  $n_1$`  and `df2 =  $n_2$`  degrees of freedom has density

$$f(x) = \frac{\Gamma(n_1/2 + n_2/2)}{\Gamma(n_1/2)\Gamma(n_2/2)} \left(\frac{n_1}{n_2}\right)^{n_1/2} x^{n_1/2-1} \left(1 + \frac{n_1x}{n_2}\right)^{-(n_1+n_2)/2}$$

for  $x > 0$ .

It is the distribution of the ratio of the mean squares of  $n_1$  and  $n_2$  independent standard normals, and hence of the ratio of two independent chi-squared variates each divided by its degrees of freedom. Since the ratio of a normal and the root mean-square of  $m$  independent normals has a Student's  $t_m$  distribution, the square of a  $t_m$  variate has a F distribution on 1 and  $m$  degrees of freedom.

The non-central F distribution is again the ratio of mean squares of independent normals of unit variance, but those in the numerator are allowed to have non-zero means and `ncp` is the sum of squares of the means. See [Chisquare](#) for further details on non-central distributions.

**Value**

`df` gives the density, `pf` gives the distribution function `qf` gives the quantile function, and `rf` generates random deviates.

Invalid arguments will result in return value `NaN`, with a warning.

**Note**

The code for non-zero `ncp` is principally intended to be used for moderate values of `ncp`: it will not be highly accurate, especially in the tails, for large values.

**Source**

For `df`, and `ncp == 0`, computed via a binomial probability, code contributed by Catherine Loader (see [dbinom](#)); for `ncp != 0`, computed via a [dbeta](#), code contributed by Peter Ruckdeschel.

For `pf`, via [pbeta](#) (or for large `df2`, via [pchisq](#)).

For `qf`, via [qchisq](#) for large `df2`, else via [qbeta](#).

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 2, chapters 27 and 30. Wiley, New York.



**See Also**

[dchisq](#) for chi-squared and [dt](#) for Student's t distributions.

**Examples**

```
## the density of the square of a t_m is 2*dt(x, m)/(2*x)
# check this is the same as the density of F_{1,m}
x <- seq(0.001, 5, len=100)
all.equal(df(x^2, 1, 5), dt(x, 5)/x)

## Identity: qf(2*p - 1, 1, df) == qt(p, df)^2 for p >= 1/2
p <- seq(1/2, .99, length=50); df <- 10
rel.err <- function(x,y) ifelse(x==y,0, abs(x-y)/mean(abs(c(x,y))))
quantile(rel.err(qf(2*p - 1, df1=1, df2=df), qt(p, df)^2), .90) # ~ = 7e-9
```

fft

*Fast Discrete Fourier Transform***Description**

Performs the Fast Fourier Transform of an array.

**Usage**

```
fft(z, inverse = FALSE)
mvfft(z, inverse = FALSE)
```

**Arguments**

<code>z</code>	a real or complex array containing the values to be transformed.
<code>inverse</code>	if TRUE, the unnormalized inverse transform is computed (the inverse has a + in the exponent of $e$ , but here, we do <i>not</i> divide by $1/\text{length}(x)$ ).

**Value**

When `z` is a vector, the value computed and returned by `fft` is the unnormalized univariate Fourier transform of the sequence of values in `z`.

When `z` contains an array, `fft` computes and returns the multivariate (spatial) transform. If `inverse` is TRUE, the (unnormalized) inverse Fourier transform is returned, i.e., if `y <- fft(z)`, then `z` is `fft(y, inverse = TRUE) / length(y)`.

By contrast, `mvfft` takes a real or complex matrix as argument, and returns a similar shaped matrix, but with each column replaced by its discrete Fourier transform. This is useful for analyzing vector-valued series.

The FFT is fastest when the length of the series being transformed is highly composite (i.e., has many factors). If this is not the case, the transform may take a long time to compute and will use a large amount of memory.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Singleton, R. C. (1979) Mixed Radix Fast Fourier Transforms, in *Programs for Digital Signal Processing*, IEEE Digital Signal Processing Committee eds. IEEE Press.

**See Also**

[convolve](#), [nextn](#).

**Examples**

```
x <- 1:4
fft(x)
fft(fft(x), inverse = TRUE)/length(x)
```

---

 filter

---

*Linear Filtering on a Time Series*


---

**Description**

Applies linear filtering to a univariate time series or to each series separately of a multivariate time series.

**Usage**

```
filter(x, filter, method = c("convolution", "recursive"),
       sides = 2, circular = FALSE, init)
```

**Arguments**

x	a univariate or multivariate time series.
filter	a vector of filter coefficients in reverse time order (as for AR or MA coefficients).
method	Either "convolution" or "recursive" (and can be abbreviated). If "convolution" a moving average is used: if "recursive" an autoregression is used.
sides	for convolution filters only. If sides=1 the filter coefficients are for past values only; if sides=2 they are centred around lag 0. In this case the length of the filter should be odd, but if it is even, more of the filter is forward in time than backward.
circular	for convolution filters only. If TRUE, wrap the filter around the ends of the series, otherwise assume external values are missing (NA).
init	for recursive filters only. Specifies the initial values of the time series just prior to the start value, in reverse time order. The default is a set of zeros.

**Details**

Missing values are allowed in `x` but not in `filter` (where they would lead to missing values everywhere in the output).

Note that there is an implied coefficient 1 at lag 0 in the recursive filter, which gives

$$y_i = x_i + f_1 y_{i-1} + \cdots + f_p y_{i-p}$$

No check is made to see if recursive filter is invertible: the output may diverge if it is not.

The convolution filter is

$$y_i = f_1 x_{i+o} + \cdots + f_p x_{i+o-(p-1)}$$

where `o` is the offset: see `sides` for how it is determined.

**Value**

A time series object.

**Note**

`convolve(, type="filter")` uses the FFT for computations and so *may* be faster for long filters on univariate series, but it does not return a time series (and so the time alignment is unclear), nor does it handle missing values. `filter` is faster for a filter of length 100 on a series of length 1000, for example.

**See Also**

[convolve](#), [arima.sim](#)

**Examples**

```
x <- 1:100
filter(x, rep(1, 3))
filter(x, rep(1, 3), sides = 1)
filter(x, rep(1, 3), sides = 1, circular = TRUE)

filter(presidents, rep(1,3))
```

---

fisher.test

*Fisher's Exact Test for Count Data*

---

**Description**

Performs Fisher's exact test for testing the null of independence of rows and columns in a contingency table with fixed marginals.

**Usage**

```
fisher.test(x, y = NULL, workspace = 200000, hybrid = FALSE,
            control = list(), or = 1, alternative = "two.sided",
            conf.int = TRUE, conf.level = 0.95,
            simulate.p.value = FALSE, B = 2000)
```

**Arguments**

<code>x</code>	either a two-dimensional contingency table in matrix form, or a factor object.
<code>y</code>	a factor object; ignored if <code>x</code> is a matrix.
<code>workspace</code>	an integer specifying the size of the workspace used in the network algorithm. In units of 4 bytes. Only used for non-simulated p-values larger than $2 \times 2$ tables.
<code>hybrid</code>	a logical. Only used for larger than $2 \times 2$ tables, in which cases it indicated whether the exact probabilities (default) or a hybrid approximation thereof should be computed. See ‘Details’.
<code>control</code>	a list with named components for low level algorithm control. At present the only one used is "mult", a positive integer $\geq 2$ with default 30 used only for larger than $2 \times 2$ tables. This says how many times as much space should be allocated to paths as to keys: see file ‘fexact.c’ in the sources of this package.
<code>or</code>	the hypothesized odds ratio. Only used in the $2 \times 2$ case.
<code>alternative</code>	indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. Only used in the $2 \times 2$ case.
<code>conf.int</code>	logical indicating if a confidence interval should be computed (and returned).
<code>conf.level</code>	confidence level for the returned confidence interval. Only used in the $2 \times 2$ case if <code>conf.int = TRUE</code> .
<code>simulate.p.value</code>	a logical indicating whether to compute p-values by Monte Carlo simulation, in larger than $2 \times 2$ tables.
<code>B</code>	an integer specifying the number of replicates used in the Monte Carlo test.

**Details**

If `x` is a matrix, it is taken as a two-dimensional contingency table, and hence its entries should be nonnegative integers. Otherwise, both `x` and `y` must be vectors of the same length. Incomplete cases are removed, the vectors are coerced into factor objects, and the contingency table is computed from these.

For  $2 \times 2$  cases, p-values are obtained directly using the (central or non-central) hypergeometric distribution. Otherwise, computations are based on a C version of the FORTRAN subroutine FEXACT which implements the network developed by Mehta and Patel (1986) and improved by Clarkson, Fan and Joe (1993). The FORTRAN code can be obtained from <http://www.netlib.org/toms/643>. Note this fails (with an error message) when the entries of the table are too large. (It transposes the table if necessary so it has no more rows than columns. One constraint is that the product of the row marginals be less than  $2^{31} - 1$ .)

For  $2 \times 2$  tables, the null of conditional independence is equivalent to the hypothesis that the odds ratio equals one. ‘Exact’ inference can be based on observing that in general, given all marginal totals fixed, the first element of the contingency table has a non-central hypergeometric distribution with non-centrality parameter given by the odds ratio (Fisher, 1935). The alternative for a one-sided test is based on the odds ratio, so `alternative = "greater"` is a test of the odds ratio being bigger than `or`.

Two-sided tests are based on the probabilities of the tables, and take as ‘more extreme’ all tables with probabilities less than or equal to that of the observed table, the p-value being the sum of such probabilities.

For larger than  $2 \times 2$  tables and `hybrid = TRUE`, asymptotic chi-squared probabilities are only used if the ‘Cochran conditions’ are satisfied, that is if no cell has count zero, and more than 80% of the cells have counts at least 5.

Simulation is done conditional on the row and column marginals, and works only if the marginals are strictly positive. (A C translation of the algorithm of Patefield (1981) is used.)

### Value

A list with class "htest" containing the following components:

p.value	the p-value of the test.
conf.int	a confidence interval for the odds ratio. Only present in the $2 \times 2$ case if argument <code>conf.int = TRUE</code> .
estimate	an estimate of the odds ratio. Note that the <i>conditional</i> Maximum Likelihood Estimate (MLE) rather than the unconditional MLE (the sample odds ratio) is used. Only present in the $2 \times 2$ case.
null.value	the odds ratio under the null, <code>OR</code> . Only present in the $2 \times 2$ case.
alternative	a character string describing the alternative hypothesis.
method	the character string "Fisher's Exact Test for Count Data".
data.name	a character string giving the names of the data.

### References

- Agresti, A. (1990) *Categorical data analysis*. New York: Wiley. Pages 59–66.
- Agresti, A. (2002) *Categorical data analysis*. Second edition. New York: Wiley. Pages 91–101.
- Fisher, R. A. (1935) The logic of inductive inference. *Journal of the Royal Statistical Society Series A* **98**, 39–54.
- Fisher, R. A. (1962) Confidence limits for a cross-product ratio. *Australian Journal of Statistics* **4**, 41.
- Fisher, R. A. (1970) *Statistical Methods for Research Workers*. Oliver & Boyd.
- Mehta, C. R. and Patel, N. R. (1986) Algorithm 643. FEXACT: A Fortran subroutine for Fisher's exact test on unordered  $r \times c$  contingency tables. *ACM Transactions on Mathematical Software*, **12**, 154–161.
- Clarkson, D. B., Fan, Y. and Joe, H. (1993) A Remark on Algorithm 643: FEXACT: An Algorithm for Performing Fisher's Exact Test in  $r \times c$  Contingency Tables. *ACM Transactions on Mathematical Software*, **19**, 484–488.
- Patefield, W. M. (1981) Algorithm AS159. An efficient method of generating  $r \times c$  tables with given row and column totals. *Applied Statistics* **30**, 91–97.

### See Also

[chisq.test](#)

### Examples

```
## Agresti (1990, p. 61f; 2002, p. 91) Fisher's Tea Drinker
## A British woman claimed to be able to distinguish whether milk or
## tea was added to the cup first. To test, she was given 8 cups of
## tea, in four of which milk was added first. The null hypothesis
## is that there is no association between the true order of pouring
## and the woman's guess, the alternative that there is a positive
## association (that the odds ratio is greater than 1).
TeaTasting <-
```

```

matrix(c(3, 1, 1, 3),
       nrow = 2,
       dimnames = list(Guess = c("Milk", "Tea"),
                       Truth = c("Milk", "Tea")))
fisher.test(TeaTasting, alternative = "greater")
## => p=0.2429, association could not be established

## Fisher (1962, 1970), Criminal convictions of like-sex twins
Convictions <-
matrix(c(2, 10, 15, 3),
       nrow = 2,
       dimnames =
         list(c("Dizygotic", "Monozygotic"),
              c("Convicted", "Not convicted")))
Convictions
fisher.test(Convictions, alternative = "less")
fisher.test(Convictions, conf.int = FALSE)
fisher.test(Convictions, conf.level = 0.95)$conf.int
fisher.test(Convictions, conf.level = 0.99)$conf.int

## A r x c table Agresti (2002, p. 57) Job Satisfaction
Job <- matrix(c(1,2,1,0, 3,3,6,1, 10,10,14,9, 6,7,12,11), 4, 4,
             dimnames = list(income=c("< 15k", "15-25k", "25-40k", "> 40k"),
                             satisfaction=c("VeryD", "LittleD", "ModerateS", "VeryS")))
fisher.test(Job)
fisher.test(Job, simulate.p.value=TRUE, B=1e5)

```

fitted

*Extract Model Fitted Values***Description**

`fitted` is a generic function which extracts fitted values from objects returned by modeling functions. `fitted.values` is an alias for it.

All object classes which are returned by model fitting functions should provide a `fitted` method. (Note that the generic is `fitted` and not `fitted.values`.)

Methods can make use of `napredict` methods to compensate for the omission of missing values. The default and `nls` methods do.

**Usage**

```

fitted(object, ...)
fitted.values(object, ...)

```

**Arguments**

`object` an object for which the extraction of model fitted values is meaningful.  
`...` other arguments.

**Value**

Fitted values extracted from the object `x`.

## References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

## See Also

[coefficients](#), [glm](#), [lm](#), [residuals](#).

---

fivenum

*Tukey Five-Number Summaries*

---

## Description

Returns Tukey's five number summary (minimum, lower-hinge, median, upper-hinge, maximum) for the input data.

## Usage

```
fivenum(x, na.rm = TRUE)
```

## Arguments

<code>x</code>	numeric, maybe including <a href="#">NAs</a> and $\pm$ <a href="#">Infs</a> .
<code>na.rm</code>	logical; if TRUE, all <a href="#">NA</a> and <a href="#">NaNs</a> are dropped, before the statistics are computed.

## Value

A numeric vector of length 5 containing the summary information. See [boxplot.stats](#) for more details.

## See Also

[IQR](#), [boxplot.stats](#), [median](#), [quantile](#), [range](#).

## Examples

```
fivenum(c(rnorm(100), -1:1/0))
```

---

fligner.test

*Fligner-Killeen Test of Homogeneity of Variances*


---

### Description

Performs a Fligner-Killeen (median) test of the null that the variances in each of the groups (samples) are the same.

### Usage

```
fligner.test(x, ...)

## Default S3 method:
fligner.test(x, g, ...)

## S3 method for class 'formula':
fligner.test(formula, data, subset, na.action, ...)
```

### Arguments

<code>x</code>	a numeric vector of data values, or a list of numeric data vectors.
<code>g</code>	a vector or factor object giving the group for the corresponding elements of <code>x</code> . Ignored if <code>x</code> is a list.
<code>formula</code>	a formula of the form <code>lhs ~ rhs</code> where <code>lhs</code> gives the data values and <code>rhs</code> the corresponding groups.
<code>data</code>	an optional matrix or data frame (or similar: see <a href="#">model.frame</a> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>subset</code>	an optional vector specifying a subset of observations to be used.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. Defaults to <code>getOption("na.action")</code> .
<code>...</code>	further arguments to be passed to or from methods.

### Details

If `x` is a list, its elements are taken as the samples to be compared for homogeneity of variances, and hence have to be numeric data vectors. In this case, `g` is ignored, and one can simply use `fligner.test(x)` to perform the test. If the samples are not yet contained in a list, use `fligner.test(list(x, ...))`.

Otherwise, `x` must be a numeric data vector, and `g` must be a vector or factor object of the same length as `x` giving the group for the corresponding elements of `x`.

The Fligner-Killeen (median) test has been determined in a simulation study as one of the many tests for homogeneity of variances which is most robust against departures from normality, see Conover, Johnson & Johnson (1981). It is a  $k$ -sample simple linear rank which uses the ranks of the absolute values of the centered samples and weights  $a(i) = \text{qnorm}((1+i/(n+1))/2)$ . The version implemented here uses median centering in each of the samples (F-K:med  $X^2$  in the reference).



**Value**

A list of class "htest" containing the following components:

statistic	the Fligner-Killeen:med $X^2$ test statistic.
parameter	the degrees of freedom of the approximate chi-squared distribution of the test statistic.
p.value	the p-value of the test.
method	the character string "Fligner-Killeen test of homogeneity of variances".
data.name	a character string giving the names of the data.

**References**

William J. Conover, Mark E. Johnson and Myrle M. Johnson (1981). A comparative study of tests for homogeneity of variances, with applications to the outer continental shelf bidding data. *Technometrics* **23**, 351–361.

**See Also**

[ansari.test](#) and [mood.test](#) for rank-based two-sample test for a difference in scale parameters; [var.test](#) and [bartlett.test](#) for parametric tests for the homogeneity of variances.

**Examples**

```
require(graphics)

plot(count ~ spray, data = InsectSprays)
fligner.test(InsectSprays$count, InsectSprays$spray)
fligner.test(count ~ spray, data = InsectSprays)
## Compare this to bartlett.test()
```

---

formula

*Model Formulae*

---

**Description**

The generic function `formula` and its specific methods provide a way of extracting formulae which have been included in other objects.

`as.formula` is almost identical, additionally preserving attributes when `object` already inherits from "formula". The default value of the `env` argument is used only when the formula would otherwise lack an environment.

**Usage**

```
formula(x, ...)
as.formula(object, env = parent.frame())
```

**Arguments**

<code>x</code> , <code>object</code>	R object.
<code>...</code>	further arguments passed to or from other methods.
<code>env</code>	the environment to associate with the result.

## Details

The models fit by, e.g., the `lm` and `glm` functions are specified in a compact symbolic form. The `~` operator is basic in the formation of such models. An expression of the form `y ~ model` is interpreted as a specification that the response `y` is modelled by a linear predictor specified symbolically by `model`. Such a model consists of a series of terms separated by `+` operators. The terms themselves consist of variable and factor names separated by `:` operators. Such a term is interpreted as the interaction of all the variables and factors appearing in the term.

In addition to `+` and `:`, a number of other operators are useful in model formulae. The `*` operator denotes factor crossing: `a*b` interpreted as `a+b+a:b`. The `^` operator indicates crossing to the specified degree. For example `(a+b+c)^2` is identical to `(a+b+c)*(a+b+c)` which in turn expands to a formula containing the main effects for `a`, `b` and `c` together with their second-order interactions. The `%in%` operator indicates that the terms on its left are nested within those on the right. For example `a + b %in% a` expands to the formula `a + a:b`. The `-` operator removes the specified terms, so that `(a+b+c)^2 - a:b` is identical to `a + b + c + b:c + a:c`. It can also be used to remove the intercept term: `y ~ x - 1` is a line through the origin. A model with no intercept can be also specified as `y ~ x + 0` or `y ~ 0 + x`.

While formulae usually involve just variable and factor names, they can also involve arithmetic expressions. The formula `log(y) ~ a + log(x)` is quite legal. When such arithmetic expressions involve operators which are also used symbolically in model formulae, there can be confusion between arithmetic and symbolic operator use.

To avoid this confusion, the function `I()` can be used to bracket those portions of a model formula where the operators are used in their arithmetic sense. For example, in the formula `y ~ a + I(b+c)`, the term `b+c` is to be interpreted as the sum of `b` and `c`.

Variable names can be quoted by backticks ``like this`` in formulae, although there is no guarantee that all code using formulae will accept such non-syntactic names.

Most model-fitting functions accept formulae with right-hand-side including the function `offset` to indicate terms with a fixed coefficient of one. Some functions accept other 'specials' such as `strata` or `cluster` (see the `specials` argument of `terms.formula`).

There are two special interpretations of `.` in a formula. The usual one is in the context of a data argument of model fitting functions and means 'all columns not otherwise in the formula': see `terms.formula`. In the context of `update.formula`, **only**, it means 'what was previously in this part of the formula'.

When `formula` is called on a fitted model object, either a specific method is used (such as that for class `"nls"`) or the default method. The default first looks for a `"formula"` component of the object (and evaluates it), then a `"terms"` component, then a `formula` parameter of the call (and evaluates its value) and finally a `"formula"` attribute.

There is a method for data frames. If there is only one column this forms the RHS with an empty LHS. For more columns, the first column is the LHS of the formula and the remaining columns separated by `+` form the RHS.

## Value

All the functions above produce an object of class `"formula"` which contains a symbolic model formula.

## Environments

A formula object has an associated environment, and this environment (rather than the parent environment) is used by `model.frame` to evaluate variables that are not found in the supplied `data` argument.

Formulas created with the `~` operator use the environment in which they were created. Formulas created with `as.formula` will use the `env` argument for their environment. Pre-existing formulas extracted with `as.formula` will only have their environment changed if `env` is given explicitly.

## References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models*. Chapter 2 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

## See Also

[I](#), [offset](#).

For formula manipulation: [terms](#), and [all.vars](#); for typical use: [lm](#), [glm](#), and [coplot](#).

## Examples

```
class(fo <- y ~ x1*x2) # "formula"
fo
typeof(fo) # R internal : "language"
terms(fo)

environment(fo)
environment(as.formula("y ~ x"))
environment(as.formula("y ~ x", env=new.env()))

## Create a formula for a model with a large number of variables:
xnam <- paste("x", 1:25, sep="")
(fmla <- as.formula(paste("y ~ ", paste(xnam, collapse= "+"))))
```

---

formula.nls

*Extract Model Formula from nls Object*

---

## Description

Returns the model used to fit object.

## Usage

```
## S3 method for class 'nls':
formula(x, ...)
```

## Arguments

`x` an object inheriting from class "nls", representing a nonlinear least squares fit.

`...` further arguments passed to or from other methods.

## Value

a formula representing the model used to obtain object.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**[nls](#), [formula](#)**Examples**

```
fml <- nls(circumference ~ A/(1+exp((B-age)/C)), Orange,
          start = list(A=160, B=700, C = 350))
formula(fml)
```

---

friedman.test	<i>Friedman Rank Sum Test</i>
---------------	-------------------------------

---

**Description**

Performs a Friedman rank sum test with unreplicated blocked data.

**Usage**

```
friedman.test(y, ...)

## Default S3 method:
friedman.test(y, groups, blocks, ...)

## S3 method for class 'formula':
friedman.test(formula, data, subset, na.action, ...)
```

**Arguments**

<code>y</code>	either a numeric vector of data values, or a data matrix.
<code>groups</code>	a vector giving the group for the corresponding elements of <code>y</code> if this is a vector; ignored if <code>y</code> is a matrix. If not a factor object, it is coerced to one.
<code>blocks</code>	a vector giving the block for the corresponding elements of <code>y</code> if this is a vector; ignored if <code>y</code> is a matrix. If not a factor object, it is coerced to one.
<code>formula</code>	a formula of the form <code>a ~ b   c</code> , where <code>a</code> , <code>b</code> and <code>c</code> give the data values and corresponding groups and blocks, respectively.
<code>data</code>	an optional matrix or data frame (or similar: see <a href="#">model.frame</a> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>subset</code>	an optional vector specifying a subset of observations to be used.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. Defaults to <code>getOption("na.action")</code> .
<code>...</code>	further arguments to be passed to or from methods.

**Details**

`friedman.test` can be used for analyzing unreplicated complete block designs (i.e., there is exactly one observation in `y` for each combination of levels of `groups` and `blocks`) where the normality assumption may be violated.

The null hypothesis is that apart from an effect of `blocks`, the location parameter of `y` is the same in each of the `groups`.

If `y` is a matrix, `groups` and `blocks` are obtained from the column and row indices, respectively. NA's are not allowed in `groups` or `blocks`; if `y` contains NA's, corresponding blocks are removed.

**Value**

A list with class "htest" containing the following components:

<code>statistic</code>	the value of Friedman's chi-squared statistic.
<code>parameter</code>	the degrees of freedom of the approximate chi-squared distribution of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>method</code>	the character string "Friedman rank sum test".
<code>data.name</code>	a character string giving the names of the data.

**References**

Myles Hollander and Douglas A. Wolfe (1973), *Nonparametric Statistical Methods*. New York: John Wiley & Sons. Pages 139–146.

**See Also**

[quade.test](#).

**Examples**

```
## Hollander & Wolfe (1973), p. 140ff.
## Comparison of three methods ("round out", "narrow angle", and
## "wide angle") for rounding first base. For each of 18 players
## and the three method, the average time of two runs from a point on
## the first base line 35ft from home plate to a point 15ft short of
## second base is recorded.
RoundingTimes <-
matrix(c(5.40, 5.50, 5.55,
        5.85, 5.70, 5.75,
        5.20, 5.60, 5.50,
        5.55, 5.50, 5.40,
        5.90, 5.85, 5.70,
        5.45, 5.55, 5.60,
        5.40, 5.40, 5.35,
        5.45, 5.50, 5.35,
        5.25, 5.15, 5.00,
        5.85, 5.80, 5.70,
        5.25, 5.20, 5.10,
        5.65, 5.55, 5.45,
        5.60, 5.35, 5.45,
        5.05, 5.00, 4.95,
        5.50, 5.50, 5.40,
```

```

      5.45, 5.55, 5.50,
      5.55, 5.55, 5.35,
      5.45, 5.50, 5.55,
      5.50, 5.45, 5.25,
      5.65, 5.60, 5.40,
      5.70, 5.65, 5.55,
      6.30, 6.30, 6.25),
  nrow = 22,
  byrow = TRUE,
  dimnames = list(1 : 22,
                  c("Round Out", "Narrow Angle", "Wide Angle")))
friedman.test(RoundingTimes)
## => strong evidence against the null that the methods are equivalent
##   with respect to speed

wb <- aggregate(warpbreaks$breaks,
                by = list(w = warpbreaks$wool,
                          t = warpbreaks$tension),
                FUN = mean)

wb
friedman.test(wb$x, wb$w, wb$t)
friedman.test(x ~ w | t, data = wb)

```

ftable

*Flat Contingency Tables***Description**

Create 'flat' contingency tables.

**Usage**

```

ftable(x, ...)

## Default S3 method:
ftable(..., exclude = c(NA, NaN), row.vars = NULL,
        col.vars = NULL)

```

**Arguments**

<code>x, ...</code>	R objects which can be interpreted as factors (including character strings), or a list (or data frame) whose components can be so interpreted, or a contingency table object of class "table" or "ftable".
<code>exclude</code>	values to use in the exclude argument of <code>factor</code> when interpreting non-factor objects.
<code>row.vars</code>	a vector of integers giving the numbers of the variables, or a character vector giving the names of the variables to be used for the rows of the flat contingency table.
<code>col.vars</code>	a vector of integers giving the numbers of the variables, or a character vector giving the names of the variables to be used for the columns of the flat contingency table.

## Details

`ftable` creates ‘flat’ contingency tables. Similar to the usual contingency tables, these contain the counts of each combination of the levels of the variables (factors) involved. This information is then re-arranged as a matrix whose rows and columns correspond to unique combinations of the levels of the row and column variables (as specified by `row.vars` and `col.vars`, respectively). The combinations are created by looping over the variables in reverse order (so that the levels of the left-most variable vary the slowest). Displaying a contingency table in this flat matrix form (via `print.ftable`, the print method for objects of class "`ftable`") is often preferable to showing it as a higher-dimensional array.

`ftable` is a generic function. Its default method, `ftable.default`, first creates a contingency table in array form from all arguments except `row.vars` and `col.vars`. If the first argument is of class "`table`", it represents a contingency table and is used as is; if it is a flat table of class "`ftable`", the information it contains is converted to the usual array representation using `as.ftable`. Otherwise, the arguments should be R objects which can be interpreted as factors (including character strings), or a list (or data frame) whose components can be so interpreted, which are cross-tabulated using `table`. Then, the arguments `row.vars` and `col.vars` are used to collapse the contingency table into flat form. If neither of these two is given, the last variable is used for the columns. If both are given and their union is a proper subset of all variables involved, the other variables are summed out.

When the arguments are R expressions interpreted as factors, additional arguments will be passed to `table` to control how the variable names are displayed; see the last example below.

Function `ftable.formula` provides a formula method for creating flat contingency tables.

There are methods for `as.table` and `as.data.frame`.

## Value

`ftable` returns an object of class "`ftable`", which is a matrix with counts of each combination of the levels of variables with information on the names and levels of the (row and columns) variables stored as attributes "`row.vars`" and "`col.vars`".

## See Also

`ftable.formula` for the formula interface (which allows a `data = .` argument); `read.ftable` for information on reading, writing and coercing flat contingency tables; `table` for ordinary cross-tabulation; `xtabs` for formula-based cross-tabulation.

## Examples

```
## Start with a contingency table.
ftable(Titanic, row.vars = 1:3)
ftable(Titanic, row.vars = 1:2, col.vars = "Survived")
ftable(Titanic, row.vars = 2:1, col.vars = "Survived")

## Start with a data frame.
x <- ftable(mtcars[c("cyl", "vs", "am", "gear")])
x
ftable(x, row.vars = c(2, 4))

## Start with expressions, use table()'s "dnn" to change labels
ftable(mtcars$cyl, mtcars$vs, mtcars$am, mtcars$gear, row.vars = c(2, 4),
       dnn = c("Cylinders", "V/S", "Transmission", "Gears"))
```

---

ftable.formula      *Formula Notation for Flat Contingency Tables*

---

### Description

Produce or manipulate a flat contingency table using formula notation.

### Usage

```
## S3 method for class 'formula':  
ftable(formula, data = NULL, subset, na.action, ...)
```

### Arguments

<code>formula</code>	a formula object with both left and right hand sides specifying the column and row variables of the flat table.
<code>data</code>	a data frame, list or environment (or similar: see <a href="#">model.frame</a> ) containing the variables to be cross-tabulated, or a contingency table (see below).
<code>subset</code>	an optional vector specifying a subset of observations to be used. Ignored if <code>data</code> is a contingency table.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. Ignored if <code>data</code> is a contingency table.
<code>...</code>	further arguments to the default <code>ftable</code> method may also be passed as arguments, see <a href="#">ftable.default</a> .

### Details

This is a method of the generic function [ftable](#).

The left and right hand side of `formula` specify the column and row variables, respectively, of the flat contingency table to be created. Only the `+` operator is allowed for combining the variables. A `.` may be used once in the formula to indicate inclusion of all the remaining variables.

If `data` is an object of class `"table"` or an array with more than 2 dimensions, it is taken as a contingency table, and hence all entries should be nonnegative. Otherwise, if it is not a flat contingency table (i.e., an object of class `"ftable"`), it should be a data frame or matrix, list or environment containing the variables to be cross-tabulated. In this case, `na.action` is applied to the data to handle missing values, and, after possibly selecting a subset of the data as specified by the `subset` argument, a contingency table is computed from the variables.

The contingency table is then collapsed to a flat table, according to the row and column variables specified by `formula`.

### Value

A flat contingency table which contains the counts of each combination of the levels of the variables, collapsed into a matrix for suitably displaying the counts.

### See Also

[ftable](#), [ftable.default](#); [table](#).



**Examples**

```
Titanic
x <- ftable(Survived ~ ., data = Titanic)
x
ftable(Sex ~ Class + Age, data = x)
```

GammaDist

*The Gamma Distribution***Description**

Density, distribution function, quantile function and random generation for the Gamma distribution with parameters shape and scale.

**Usage**

```
dgamma(x, shape, rate = 1, scale = 1/rate, log = FALSE)
pgamma(q, shape, rate = 1, scale = 1/rate, lower.tail = TRUE,
       log.p = FALSE)
qgamma(p, shape, rate = 1, scale = 1/rate, lower.tail = TRUE,
       log.p = FALSE)
rgamma(n, shape, rate = 1, scale = 1/rate)
```

**Arguments**

`x`, `q` vector of quantiles.  
`p` vector of probabilities.  
`n` number of observations. If `length(n) > 1`, the length is taken to be the number required.  
`rate` an alternative way to specify the scale.  
`shape`, `scale` shape and scale parameters. Must be positive, scale strictly.  
`log`, `log.p` logical; if TRUE, probabilities/densities  $p$  are returned as  $\log(p)$ .  
`lower.tail` logical; if TRUE (default), probabilities are  $P[X \leq x]$ , otherwise,  $P[X > x]$ .

**Details**

If `scale` is omitted, it assumes the default value of 1.

The Gamma distribution with parameters  $\text{shape} = \alpha$  and  $\text{scale} = \sigma$  has density

$$f(x) = \frac{1}{\sigma^\alpha \Gamma(\alpha)} x^{\alpha-1} e^{-x/\sigma}$$

for  $x \geq 0$ ,  $\alpha > 0$  and  $\sigma > 0$ . (Here  $\Gamma(\alpha)$  is the function implemented by R's `gamma()` and defined in its help. Note that  $\alpha = 0$  corresponds to the trivial distribution with all mass at point 0.)

The mean and variance are  $E(X) = \alpha\sigma$  and  $\text{Var}(X) = \alpha\sigma^2$ .

The cumulative hazard  $H(t) = -\log(1 - F(t))$  is `-pgamma(t, ..., lower = FALSE, log = TRUE)`.

Note that for smallish values of `shape` (and moderate `scale`) a large parts of the mass of the Gamma distribution is on values of  $x$  so near zero that they will be represented as zero in computer arithmetic. So `rgamma` can well return values which will be represented as zero. (This will also happen for very large values of `scale` since the actual generation is done for `scale=1`.)

**Value**

`dgamma` gives the density, `pgamma` gives the distribution function, `qgamma` gives the quantile function, and `rgamma` generates random deviates.

Invalid arguments will result in return value `NaN`, with a warning.

**Note**

The S parametrization is via `shape` and `rate`: S has no `scale` parameter.

`pgamma` is closely related to the incomplete gamma function. As defined by Abramowitz and Stegun 6.5.1 (and by ‘Numerical Recipes’) this is

$$P(a, x) = \frac{1}{\Gamma(a)} \int_0^x t^{a-1} e^{-t} dt$$

$P(a, x)$  is `pgamma(x, a)`. Other authors (for example Karl Pearson in his 1922 tables) omit the normalizing factor, defining the incomplete gamma function as `pgamma(x, a) * gamma(a)`. A few use the ‘upper’ incomplete gamma function, the integral from  $x$  to  $\infty$  which can be computed by `pgamma(x, a, lower=FALSE) * gamma(a)`, or its normalized version. See also [http://en.wikipedia.org/wiki/Incomplete\\_gamma\\_function](http://en.wikipedia.org/wiki/Incomplete_gamma_function).

**Source**

`dgamma` is computed via the Poisson density, using code contributed by Catherine Loader (see [dbinom](#)).

`pgamma` uses an unpublished (and not otherwise documented) algorithm ‘mainly by Morten Welinder’.

`qgamma` is based on a C translation of

Best, D. J. and D. E. Roberts (1975). Algorithm AS91. Percentage points of the chi-squared distribution. *Applied Statistics*, **24**, 385–388.

plus a final Newton step to improve the approximation.

`rgamma` for `shape >= 1` uses

Ahrens, J. H. and Dieter, U. (1982). Generating gamma variates by a modified rejection technique. *Communications of the ACM*, **25**, 47–54,

and for  $0 < \text{shape} < 1$  uses

Ahrens, J. H. and Dieter, U. (1974). Computer methods for sampling from gamma, beta, Poisson and binomial distributions. *Computing*, **12**, 223–246.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Shea, B. L. (1988) Algorithm AS 239, Chi-squared and incomplete Gamma integral, *Applied Statistics (JRSS C)* **37**, 466–473.

Abramowitz, M. and Stegun, I. A. (1972) *Handbook of Mathematical Functions*. New York: Dover. Chapter 6: Gamma and Related Functions.

**See Also**

[gamma](#) for the gamma function, [dbeta](#) for the Beta distribution and [dchisq](#) for the chi-squared distribution which is a special case of the Gamma distribution.

**Examples**

```

-log(dgamma(1:4, shape=1))
p <- (1:9)/10
pgamma(qgamma(p, shape=2), shape=2)
1 - 1/exp(qgamma(p, shape=1))

# even for shape = 0.001 about half the mass is on numbers
# that cannot be represented accurately (and most of those as zero)
pgamma(.Machine$double.xmin, 0.001)
pgamma(5e-324, 0.001) # on most machines this is the smallest
                        # representable non-zero number
table(rgamma(1e4, 0.001) == 0)/1e4

```

---

Geometric

*The Geometric Distribution*


---

**Description**

Density, distribution function, quantile function and random generation for the geometric distribution with parameter `prob`.

**Usage**

```

dgeom(x, prob, log = FALSE)
pgeom(q, prob, lower.tail = TRUE, log.p = FALSE)
qgeom(p, prob, lower.tail = TRUE, log.p = FALSE)
rgeom(n, prob)

```

**Arguments**

<code>x</code> , <code>q</code>	vector of quantiles representing the number of failures in a sequence of Bernoulli trials before success occurs.
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
<code>prob</code>	probability of success in each trial. $0 < \text{prob} \leq 1$ .
<code>log</code> , <code>log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .

**Details**

The geometric distribution with `prob = p` has density

$$p(x) = p(1 - p)^x$$

for  $x = 0, 1, 2, \dots$ ,  $0 < p \leq 1$ .

If an element of `x` is not integer, the result of `pgeom` is zero, with a warning.

The quantile is defined as the smallest value  $x$  such that  $F(x) \geq p$ , where  $F$  is the distribution function.

**Value**

dgeom gives the density, pgeom gives the distribution function, qgeom gives the quantile function, and rgeom generates random deviates.

Invalid prob will result in return value NaN, with a warning.

**Source**

dgeom computes via dbinom, using code contributed by Catherine Loader (see dbinom).

pgeom and qgeom are based on the closed-form formulae.

rgeom uses the derivation as an exponential mixture of Poissons, see

Devroye, L. (1986) *Non-Uniform Random Variate Generation*. Springer-Verlag, New York. Page 480.

**See Also**

dnbinom for the negative binomial which generalizes the geometric distribution.

**Examples**

```
qgeom((1:9)/10, prob = .2)
Ni <- rgeom(20, prob = 1/4); table(factor(Ni, 0:max(Ni)))
```

---

getInitial

*Get Initial Parameter Estimates*


---

**Description**

This function evaluates initial parameter estimates for a nonlinear regression model. If data is a parameterized data frame or pframe object, its parameters attribute is returned. Otherwise the object is examined to see if it contains a call to a selfStart object whose initial attribute can be evaluated.

**Usage**

```
getInitial(object, data, ...)
```

**Arguments**

object	a formula or a selfStart model that defines a nonlinear regression model
data	a data frame in which the expressions in the formula or arguments to the selfStart model can be evaluated
...	optional additional arguments

**Value**

A named numeric vector or list of starting estimates for the parameters. The construction of many selfStart models is such that these "starting" estimates are, in fact, the converged parameter estimates.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

[nls](#), [selfStart](#), [selfStart.default](#), [selfStart.formula](#)

**Examples**

```
PurTrt <- Puromycin[ Puromycin$state == "treated", ]
getInitial( rate ~ SSmicmen( conc, Vm, K ), PurTrt )
```

---

 glm

*Fitting Generalized Linear Models*


---

**Description**

glm is used to fit generalized linear models, specified by giving a symbolic description of the linear predictor and a description of the error distribution.

**Usage**

```
glm(formula, family = gaussian, data, weights, subset,
     na.action, start = NULL, etastart, mustart, offset,
     control = list(...), model = TRUE, method = "glm.fit",
     x = FALSE, y = TRUE, contrasts = NULL, ...)
```

```
glm.fit(x, y, weights = rep(1, nobs),
        start = NULL, etastart = NULL, mustart = NULL,
        offset = rep(0, nobs), family = gaussian(),
        control = list(), intercept = TRUE)
```

```
## S3 method for class 'glm':
weights(object, type = c("prior", "working"), ...)
```

**Arguments**

formula	an object of class " <a href="#">formula</a> " (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under ‘Details’.
family	a description of the error distribution and link function to be used in the model. This can be a character string naming a family function, a family function or the result of a call to a family function. (See <a href="#">family</a> for details of family functions.)
data	an optional data frame, list or environment (or object coercible by <a href="#">as.data.frame</a> to a data frame) containing the variables in the model. If not found in data, the variables are taken from environment(formula), typically the environment from which glm is called.
weights	an optional vector of ‘prior weights’ to be used in the fitting process. Should be NULL or a numeric vector.

subset	an optional vector specifying a subset of observations to be used in the fitting process.
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the <code>na.action</code> setting of <code>options</code> , and is <code>na.fail</code> if that is unset. The ‘factory-fresh’ default is <code>na.omit</code> . Another possible value is <code>NULL</code> , no action. Value <code>na.exclude</code> can be useful.
start	starting values for the parameters in the linear predictor.
etastart	starting values for the linear predictor.
mustart	starting values for the vector of means.
offset	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. This should be <code>NULL</code> or a numeric vector of length equal to the number of cases. One or more <code>offset</code> terms can be included in the formula instead or as well, and if more than one is specified their sum is used. See <code>model.offset</code> .
control	a list of parameters for controlling the fitting process. For <code>glm.fit</code> this is passed to <code>glm.control</code> .
model	a logical value indicating whether <i>model frame</i> should be included as a component of the returned value.
method	the method to be used in fitting the model. The default method <code>"glm.fit"</code> uses iteratively reweighted least squares (IWLS), whereas <code>"model.frame"</code> which returns the model frame and does no fitting. User-supplied fitting functions can be supplied either as a function or a character string naming a function, with a function which takes the same arguments as <code>glm.fit</code> .
x, y	For <code>glm</code> : logical values indicating whether the response vector and model matrix used in the fitting process should be returned as components of the returned value. For <code>glm.fit</code> : <code>x</code> is a design matrix of dimension $n * p$ , and <code>y</code> is a vector of observations of length <code>n</code> .
contrasts	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
intercept	logical. Should an intercept be included in the <i>null</i> model?
object	an object inheriting from class <code>"glm"</code> .
type	character, partial matching allowed. Type of weights to extract from the fitted model object.
...	For <code>glm</code> : arguments to be used to form the default <code>control</code> argument if it is not supplied directly. For <code>weights</code> : further arguments passed to or from other methods.

## Details

A typical predictor has the form `response ~ terms` where `response` is the (numeric) response vector and `terms` is a series of terms which specifies a linear predictor for `response`. For `binomial` and `quasibinomial` families the response can also be specified as a `factor` (when the first level denotes failure and all others success) or as a two-column matrix with the columns giving the numbers of successes and failures. A terms specification of the form `first + second` indicates all the terms in `first` together with all the terms in `second` with any duplicates removed.

A specification of the form `first:second` indicates the the set of terms obtained by taking the interactions of all terms in `first` with all terms in `second`. The specification

`first*second` indicates the *cross* of `first` and `second`. This is the same as `first + second + first:second`.

The terms in the formula will be re-ordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on: to avoid this pass a `terms` object as the formula.

Non-NULL `weights` can be used to indicate that different observations have different dispersions (with the values in `weights` being inversely proportional to the dispersions); or equivalently, when the elements of `weights` are positive integers  $w_i$ , that each response  $y_i$  is the mean of  $w_i$  unit-weight observations. For a binomial GLM prior weights are used to give the number of trials when the response is the proportion of successes: they would rarely be used for a Poisson GLM.

`glm.fit` is the workhorse function: it is not normally called directly but can be more efficient where the response vector and design matrix have already been calculated.

If more than one of `etastart`, `start` and `mustart` is specified, the first in the list will be used. It is often advisable to supply starting values for a `quasi` family, and also for families with unusual links such as `gaussian("log")`.

All of `weights`, `subset`, `offset`, `etastart` and `mustart` are evaluated in the same way as variables in `formula`, that is first in data and then in the environment of `formula`.

For the background to warning messages about ‘fitted probabilities numerically 0 or 1 occurred’ for binomial GLMs, see Venables & Ripley (2002, pp. 197–8).

## Value

`glm` returns an object of class inheriting from `"glm"` which inherits from the class `"lm"`. See later in this section. If a non-standard method is used, the object will also inherit from the class (if any) returned by that function.

The function `summary` (i.e., `summary.glm`) can be used to obtain or print a summary of the results and the function `anova` (i.e., `anova.glm`) to produce an analysis of variance table.

The generic accessor functions `coefficients`, `effects`, `fitted.values` and `residuals` can be used to extract various useful features of the value returned by `glm`.

`weights` extracts a vector of weights, one for each case in the fit (after subsetting and `na.action`).

An object of class `"glm"` is a list containing at least the following components:

<code>coefficients</code>	a named vector of coefficients
<code>residuals</code>	the <i>working</i> residuals, that is the residuals in the final iteration of the IWLS fit. Since cases with zero weights are omitted, their working residuals are NA.
<code>fitted.values</code>	the fitted mean values, obtained by transforming the linear predictors by the inverse of the link function.
<code>rank</code>	the numeric rank of the fitted linear model.
<code>family</code>	the <code>family</code> object used.
<code>linear.predictors</code>	the linear fit on link scale.
<code>deviance</code>	up to a constant, minus twice the maximized log-likelihood. Where sensible, the constant is chosen so that a saturated model has deviance zero.
<code>aic</code>	A version of Akaike’s <i>An Information Criterion</i> , minus twice the maximized log-likelihood plus twice the number of parameters, computed by the <code>aic</code> component of the family. For binomial and Poisson families the dispersion is fixed

at one and the number of parameters is the number of coefficients. For gaussian, Gamma and inverse gaussian families the dispersion is estimated from the residual deviance, and the number of parameters is the number of coefficients plus one. For a gaussian family the MLE of the dispersion is used so this is a valid value of AIC, but for Gamma and inverse gaussian families it is not. For families fitted by quasi-likelihood the value is NA.

<code>null.deviance</code>	The deviance for the null model, comparable with <code>deviance</code> . The null model will include the offset, and an intercept if there is one in the model. Note that this will be incorrect if the link function depends on the data other than through the fitted mean: specify a zero offset to force a correct calculation.
<code>iter</code>	the number of iterations of IWLS used.
<code>weights</code>	the <i>working</i> weights, that is the weights in the final iteration of the IWLS fit.
<code>prior.weights</code>	the weights initially supplied, a vector of 1s if none were.
<code>df.residual</code>	the residual degrees of freedom.
<code>df.null</code>	the residual degrees of freedom for the null model.
<code>y</code>	if requested (the default) the <code>y</code> vector used. (It is a vector even for a binomial model.)
<code>x</code>	if requested, the model matrix.
<code>model</code>	if requested (the default), the model frame.
<code>converged</code>	logical. Was the IWLS algorithm judged to have converged?
<code>boundary</code>	logical. Is the fitted value on the boundary of the attainable values?
<code>call</code>	the matched call.
<code>formula</code>	the formula supplied.
<code>terms</code>	the <code>terms</code> object used.
<code>data</code>	the <code>data</code> argument.
<code>offset</code>	the offset vector used.
<code>control</code>	the value of the <code>control</code> argument used.
<code>method</code>	the name of the fitter function used, currently always <code>"glm.fit"</code> .
<code>contrasts</code>	(where relevant) the contrasts used.
<code>xlevels</code>	(where relevant) a record of the levels of the factors used in fitting.
<code>na.action</code>	(where relevant) information returned by <code>model.frame</code> on the special handling of NAs.

In addition, non-empty fits will have components `qr`, `R` and `effects` relating to the final weighted linear fit.

Objects of class `"glm"` are normally of class `c("glm", "lm")`, that is inherit from class `"lm"`, and well-designed methods for class `"lm"` will be applied to the weighted linear model at the final iteration of IWLS. However, care is needed, as extractor functions for class `"glm"` such as `residuals` and `weights` do **not** just pick out the component of the fit with the same name.

If a `binomial` `glm` model was specified by giving a two-column response, the weights returned by `prior.weights` are the total numbers of cases (factored by the supplied case weights) and the component `y` of the result is the proportion of successes.



### Fitting functions

The argument `method` serves two purposes. One is to allow the model frame to be recreated with no fitting. The other is to allow the default fitting function `glm.fit` to be replaced by a function which takes the same arguments and uses a different fitting algorithm. If `glm.fit` is supplied as a character string it is used to search for a function of that name, starting in the **stats** namespace.

The class of the object return by the fitter (if any) will be prepended to the class returned by `glm`.

### Author(s)

The original R implementation of `glm` was written by Simon Davies working for Ross Ihaka at the University of Auckland, but has since been extensively re-written by members of the R Core team.

The design was inspired by the S function of the same name described in Hastie & Pregibon (1992).

### References

- Dobson, A. J. (1990) *An Introduction to Generalized Linear Models*. London: Chapman and Hall.
- Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models*. Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.
- McCullagh P. and Nelder, J. A. (1989) *Generalized Linear Models*. London: Chapman and Hall.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. New York: Springer.

### See Also

`anova.glm`, `summary.glm`, etc. for `glm` methods, and the generic functions `anova`, `summary`, `effects`, `fitted.values`, and `residuals`.

`lm` for non-generalized *linear* models (which SAS calls GLMs, for ‘general’ linear models).

`loglin` and `loglm` (package **MASS**) for fitting log-linear models (which binomial and Poisson GLMs are) to contingency tables.

`bigglm` in package **biglm** for an alternative way to fit GLMs to large datasets (especially those with many cases).

`esoph`, `infert` and `predict.glm` have examples of fitting binomial glms.

### Examples

```
## Dobson (1990) Page 93: Randomized Controlled Trial :
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
print(d.AD <- data.frame(treatment, outcome, counts))
glm.D93 <- glm(counts ~ outcome + treatment, family=poisson())
anova(glm.D93)
summary(glm.D93)

## an example with offsets from Venables & Ripley (2002, p.189)
utils::data(anorexia, package="MASS")

anorex.1 <- glm(Postwt ~ Prewt + Treat + offset(Prewt),
               family = gaussian, data = anorexia)
summary(anorex.1)

# A Gamma example, from McCullagh & Nelder (1989, pp. 300-2)
```

```

clotting <- data.frame(
  u = c(5,10,15,20,30,40,60,80,100),
  lot1 = c(118,58,42,35,27,25,21,19,18),
  lot2 = c(69,35,26,21,18,16,13,12,12))
summary(glm(lot1 ~ log(u), data=clotting, family=Gamma))
summary(glm(lot2 ~ log(u), data=clotting, family=Gamma))

## Not run:
## for an example of the use of a terms object as a formula
demo(glm.vr)

## End(Not run)

```

---

glm.control

*Auxiliary for Controlling GLM Fitting*


---

### Description

Auxiliary function for `glm` fitting. Typically only used internally by `glm.fit`, but may be used to construct a `control` argument to either function.

### Usage

```
glm.control(epsilon = 1e-8, maxit = 25, trace = FALSE)
```

### Arguments

<code>epsilon</code>	positive convergence tolerance $\epsilon$ ; the iterations converge when $ dev - dev_{old}  / ( dev  + 0.1) < \epsilon$ .
<code>maxit</code>	integer giving the maximal number of IWLS iterations.
<code>trace</code>	logical indicating if output should be produced for each iteration.

### Details

The `control` argument of `glm` is by default passed to the `control` argument of `glm.fit`, which uses its elements as arguments to `glm.control`: the latter provides defaults and sanity checking.

If `epsilon` is small (less than  $10^{-10}$ ) it is also used as the tolerance for the detection of collinearity in the least squares solution.

When `trace` is true, calls to `cat` produce the output for each IWLS iteration. Hence, `options(digits = *)` can be used to increase the precision, see the example.

### Value

A list with components named as the arguments.

### References

Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models*. Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

`glm.fit`, the fitting procedure used by `glm`.

**Examples**

```
### A variation on example(glm) :

## Annette Dobson's example ...
counts <- c(18,17,15,20,10,20,25,13,12)
outcome <- gl(3,1,9)
treatment <- gl(3,3)
oo <- options(digits = 12) # to see more when tracing :
glm.D93X <- glm(counts ~ outcome + treatment, family=poisson(),
               trace = TRUE, epsilon = 1e-14)

options(oo)
coef(glm.D93X) # the last two are closer to 0 than in ?glm's glm.D93
```

---

glm.summaries

*Accessing Generalized Linear Model Fits*

---

**Description**

These functions are all [methods](#) for class `glm` or `summary.glm` objects.

**Usage**

```
## S3 method for class 'glm':
family(object, ...)

## S3 method for class 'glm':
residuals(object, type = c("deviance", "pearson", "working",
                          "response", "partial"), ...)
```

**Arguments**

<code>object</code>	an object of class <code>glm</code> , typically the result of a call to <code>glm</code> .
<code>type</code>	the type of residuals which should be returned. The alternatives are: "deviance" (default), "pearson", "working", "response", and "partial".
<code>...</code>	further arguments passed to or from other methods.

**Details**

The references define the types of residuals: Davison & Snell is a good reference for the usages of each.

The partial residuals are a matrix of working residuals, with each column formed by omitting a term from the model.

How `residuals` treats cases with missing values in the original fit is determined by the `na.action` argument of that fit. If `na.action = na.omit` omitted cases will not appear in the residuals, whereas if `na.action = na.exclude` they will appear, with residual value NA. See also [naresid](#).

For fits done with `y = FALSE` the response values are computed from other components.

## References

Davison, A. C. and Snell, E. J. (1991) *Residuals and diagnostics*. In: *Statistical Theory and Modelling*. In Honour of Sir David Cox, FRS, eds. Hinkley, D. V., Reid, N. and Snell, E. J., Chapman & Hall.

Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models*. Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

McCullagh P. and Nelder, J. A. (1989) *Generalized Linear Models*. London: Chapman and Hall.

## See Also

`glm` for computing `glm.obj`, `anova.glm`; the corresponding *generic* functions, `summary.glm`, `coef`, `deviance`, `df.residual`, `effects`, `fitted`, `residuals`.

`influence.measures` for deletion diagnostics, including standardized (`rstandard`) and studentized (`rstudent`) residuals.

---

hclust                      *Hierarchical Clustering*

---

## Description

Hierarchical cluster analysis on a set of dissimilarities and methods for analyzing it.

## Usage

```
hclust(d, method = "complete", members=NULL)

## S3 method for class 'hclust':
plot(x, labels = NULL, hang = 0.1,
     axes = TRUE, frame.plot = FALSE, ann = TRUE,
     main = "Cluster Dendrogram",
     sub = NULL, xlab = NULL, ylab = "Height", ...)

plclust(tree, hang = 0.1, unit = FALSE, level = FALSE, hmin = 0,
        square = TRUE, labels = NULL, plot. = TRUE,
        axes = TRUE, frame.plot = FALSE, ann = TRUE,
        main = "", sub = NULL, xlab = NULL, ylab = "Height")
```

## Arguments

<code>d</code>	a dissimilarity structure as produced by <code>dist</code> .
<code>method</code>	the agglomeration method to be used. This should be (an unambiguous abbreviation of) one of "ward", "single", "complete", "average", "mcquitty", "median" or "centroid".
<code>members</code>	NULL or a vector with length size of <code>d</code> . See the 'Details' section.
<code>x, tree</code>	an object of the type produced by <code>hclust</code> .
<code>hang</code>	The fraction of the plot height by which labels should hang below the rest of the plot. A negative value will cause the labels to hang down from 0.

`labels`            A character vector of labels for the leaves of the tree. By default the row names or row numbers of the original data are used. If `labels=FALSE` no labels at all are plotted.

`axes, frame.plot, ann`  
                      logical flags as in `plot.default`.

`main, sub, xlab, ylab`  
                      character strings for `title`. `sub` and `xlab` have a non-NULL default when there's a `tree$call`.

`...`                Further graphical arguments.

`unit`                logical. If true, the splits are plotted at equally-spaced heights rather than at the height in the object.

`hmin`                numeric. All heights less than `hmin` are regarded as being `hmin`: this can be used to suppress detail at the bottom of the tree.

`level, square, plot.`  
                      as yet unimplemented arguments of `plclust` for S-PLUS compatibility.

### Details

This function performs a hierarchical cluster analysis using a set of dissimilarities for the  $n$  objects being clustered. Initially, each object is assigned to its own cluster and then the algorithm proceeds iteratively, at each stage joining the two most similar clusters, continuing until there is just a single cluster. At each stage distances between clusters are recomputed by the Lance–Williams dissimilarity update formula according to the particular clustering method being used.

A number of different clustering methods are provided. *Ward's* minimum variance method aims at finding compact, spherical clusters. The *complete linkage* method finds similar clusters. The *single linkage* method (which is closely related to the minimal spanning tree) adopts a 'friends of friends' clustering strategy. The other methods can be regarded as aiming for clusters with characteristics somewhere between the single and complete link methods. Note however, that methods "median" and "centroid" are *not* leading to a *monotone distance* measure, or equivalently the resulting dendrograms can have so called *inversions* (which are hard to interpret).

If `members!=NULL`, then `d` is taken to be a dissimilarity matrix between clusters instead of dissimilarities between singletons and `members` gives the number of observations per cluster. This way the hierarchical cluster algorithm can be 'started in the middle of the dendrogram', e.g., in order to reconstruct the part of the tree above a cut (see examples). Dissimilarities between clusters can be efficiently computed (i.e., without `hclust` itself) only for a limited number of distance/linkage combinations, the simplest one being squared Euclidean distance and centroid linkage. In this case the dissimilarities between the clusters are the squared Euclidean distances between cluster means.

In hierarchical cluster displays, a decision is needed at each merge to specify which subtree should go on the left and which on the right. Since, for  $n$  observations there are  $n - 1$  merges, there are  $2^{(n-1)}$  possible orderings for the leaves in a cluster tree, or dendrogram. The algorithm used in `hclust` is to order the subtree so that the tighter cluster is on the left (the last, i.e., most recent, merge of the left subtree is at a lower value than the last merge of the right subtree). Single observations are the tightest clusters possible, and merges involving two observations place them in order by their observation sequence number.

### Value

An object of class **hclust** which describes the tree produced by the clustering process. The object is a list with components:

merge	an $n - 1$ by 2 matrix. Row $i$ of <code>merge</code> describes the merging of clusters at step $i$ of the clustering. If an element $j$ in the row is negative, then observation $-j$ was merged at this stage. If $j$ is positive then the merge was with the cluster formed at the (earlier) stage $j$ of the algorithm. Thus negative entries in <code>merge</code> indicate agglomerations of singletons, and positive entries indicate agglomerations of non-singletons.
height	a set of $n - 1$ non-decreasing real values. The clustering <i>height</i> : that is, the value of the criterion associated with the clustering <code>method</code> for the particular agglomeration.
order	a vector giving the permutation of the original observations suitable for plotting, in the sense that a cluster plot using this ordering and matrix <code>merge</code> will not have crossings of the branches.
labels	labels for each of the objects being clustered.
call	the call which produced the result.
method	the cluster method that has been used.
dist.method	the distance that has been used to create <code>d</code> (only returned if the distance object has a "method" attribute).

There are `print`, `plot` and `identify` (see `identify.hclust`) methods and the `rect.hclust()` function for `hclust` objects. The `plclust()` function is basically the same as the `plot` method, `plot.hclust`, primarily for back compatibility with S-PLUS. Its extra arguments are not yet implemented.

### Author(s)

The `hclust` function is based on Fortran code contributed to STATLIB by F. Murtagh.

### References

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (S version.)
- Everitt, B. (1974). *Cluster Analysis*. London: Heinemann Educ. Books.
- Hartigan, J. A. (1975). *Clustering Algorithms*. New York: Wiley.
- Sneath, P. H. A. and R. R. Sokal (1973). *Numerical Taxonomy*. San Francisco: Freeman.
- Anderberg, M. R. (1973). *Cluster Analysis for Applications*. Academic Press: New York.
- Gordon, A. D. (1999). *Classification*. Second Edition. London: Chapman and Hall / CRC
- Murtagh, F. (1985). "Multidimensional Clustering Algorithms", in *COMPSTAT Lectures 4*. Wuerzburg: Physica-Verlag (for algorithmic details of algorithms used).
- McQuitty, L.L. (1966). Similarity Analysis by Reciprocal Pairs for Discrete and Continuous Data. *Educational and Psychological Measurement*, **26**, 825–831.

### See Also

`identify.hclust`, `rect.hclust`, `cutree`, `dendrogram`, `kmeans`.

For the Lance–Williams formula and methods that apply it generally, see `agnes` from package `cluster`.

**Examples**

```
require(graphics)

hc <- hclust(dist(USArrests), "ave")
plot(hc)
plot(hc, hang = -1)

## Do the same with centroid clustering and squared Euclidean distance,
## cut the tree into ten clusters and reconstruct the upper part of the
## tree from the cluster centers.
hc <- hclust(dist(USArrests)^2, "cen")
memb <- cutree(hc, k = 10)
cent <- NULL
for(k in 1:10){
  cent <- rbind(cent, colMeans(USArrests[memb == k, , drop = FALSE]))
}
hcl <- hclust(dist(cent)^2, method = "cen", members = table(memb))
opar <- par(mfrow = c(1, 2))
plot(hc, labels = FALSE, hang = -1, main = "Original Tree")
plot(hcl, labels = FALSE, hang = -1, main = "Re-start from 10 clusters")
par(opar)
```

heatmap

*Draw a Heat Map***Description**

A heat map is a false color image (basically `image(t(x))`) with a dendrogram added to the left side and to the top. Typically, reordering of the rows and columns according to some set of values (row or column means) within the restrictions imposed by the dendrogram is carried out.

**Usage**

```
heatmap(x, Rowv=NULL, Colv=if(symm)"Rowv" else NULL,
        distfun = dist, hclustfun = hclust,
        reorderfun = function(d,w) reorder(d,w),
        add.expr, symm = FALSE, revC = identical(Colv, "Rowv"),
        scale=c("row", "column", "none"), na.rm = TRUE,
        margins = c(5, 5), ColSideColors, RowSideColors,
        cexRow = 0.2 + 1/log10(nr), cexCol = 0.2 + 1/log10(nc),
        labRow = NULL, labCol = NULL, main = NULL,
        xlab = NULL, ylab = NULL,
        keep.dendro = FALSE, verbose = getOption("verbose"), ...)
```

**Arguments**

`x` numeric matrix of the values to be plotted.

`Rowv` determines if and how the *row* dendrogram should be computed and reordered. Either a [dendrogram](#) or a vector of values used to reorder the row dendrogram or `NA` to suppress any row dendrogram (and reordering) or by default, `NULL`, see ‘Details’ below.

<code>Colv</code>	determines if and how the <i>column</i> dendrogram should be reordered. Has the same options as the <code>Rowv</code> argument above and <i>additionally</i> when <code>x</code> is a square matrix, <code>Colv = "Rowv"</code> means that columns should be treated identically to the rows (and so if there is to be no row dendrogram there will not be a column one either).
<code>distfun</code>	function used to compute the distance (dissimilarity) between both rows and columns. Defaults to <code>dist</code> .
<code>hclustfun</code>	function used to compute the hierarchical clustering when <code>Rowv</code> or <code>Colv</code> are not dendrograms. Defaults to <code>hclust</code> . Should take as argument a result of <code>distfun</code> and return an object to which <code>as.dendrogram</code> can be applied.
<code>reorderfun</code>	function( <code>d,w</code> ) of dendrogram and weights for reordering the row and column dendrograms. The default uses <code>reorder.dendrogram</code> .
<code>add.expr</code>	expression that will be evaluated after the call to <code>image</code> . Can be used to add components to the plot.
<code>symm</code>	logical indicating if <code>x</code> should be treated <b>symmetrically</b> ; can only be true when <code>x</code> is a square matrix.
<code>revC</code>	logical indicating if the column order should be <b>reversed</b> for plotting, such that e.g., for the symmetric case, the symmetry axis is as usual.
<code>scale</code>	character indicating if the values should be centered and scaled in either the row direction or the column direction, or none. The default is "row" if <code>symm</code> false, and "none" otherwise.
<code>na.rm</code>	logical indicating whether NA's should be removed.
<code>margins</code>	numeric vector of length 2 containing the margins (see <code>par(mar=*)</code> ) for column and row names, respectively.
<code>ColSideColors</code>	(optional) character vector of length <code>ncol(x)</code> containing the color names for a horizontal side bar that may be used to annotate the columns of <code>x</code> .
<code>RowSideColors</code>	(optional) character vector of length <code>nrow(x)</code> containing the color names for a vertical side bar that may be used to annotate the rows of <code>x</code> .
<code>cexRow, cexCol</code>	positive numbers, used as <code>cex.axis</code> in for the row or column axis labeling. The defaults currently only use number of rows or columns, respectively.
<code>labRow, labCol</code>	character vectors with row and column labels to use; these default to <code>rownames(x)</code> or <code>colnames(x)</code> , respectively.
<code>main, xlab, ylab</code>	main, x- and y-axis titles; defaults to none.
<code>keep.dendro</code>	logical indicating if the dendrogram(s) should be kept as part of the result (when <code>Rowv</code> and/or <code>Colv</code> are not NA).
<code>verbose</code>	logical indicating if information should be printed.
<code>...</code>	additional arguments passed on to <code>image</code> , e.g., <code>col</code> specifying the colors.

### Details

If either `Rowv` or `Colv` are dendrograms they are honored (and not reordered). Otherwise, dendrograms are computed as `dd <- as.dendrogram(hclustfun(distfun(X)))` where `X` is either `x` or `t(x)`.



If either is a vector (of ‘weights’) then the appropriate dendrogram is reordered according to the supplied values subject to the constraints imposed by the dendrogram, by `reorder` (`dd`, `Rowv`), in the row case. If either is missing, as by default, then the ordering of the corresponding dendrogram is by the mean value of the rows/columns, i.e., in the case of rows, `Rowv <- rowMeans(x, na.rm=na.rm)`. If either is `NULL`, no reordering will be done for the corresponding side.

By default (`scale = "row"`) the rows are scaled to have mean zero and standard deviation one. There is some empirical evidence from genomic plotting that this is useful.

The default colors are not pretty. Consider using enhancements such as the **RColorBrewer** package, <http://cran.r-project.org/package=RColorBrewer>.

### Value

Invisibly, a list with components

<code>rowInd</code>	row index permutation vector as returned by <code>order.dendrogram</code> .
<code>colInd</code>	column index permutation vector.
<code>Rowv</code>	the row dendrogram; only if input <code>Rowv</code> was not NA and <code>keep.dendro</code> is true.
<code>Colv</code>	the column dendrogram; only if input <code>Colv</code> was not NA and <code>keep.dendro</code> is true.

### Note

Unless `Rowv = NA` (or `Colv = NA`), the original rows and columns are reordered *in any case* to match the dendrogram, e.g., the rows by `order.dendrogram` (`Rowv`) where `Rowv` is the (possibly `reorder` () ed) row dendrogram.

`heatmap()` uses `layout` and draws the `image` in the lower right corner of a 2x2 layout. Consequentially, it can **not** be used in a multi column/row layout, i.e., when `par(mfrow=*)` or `(mfcol=*)` has been called.

### Author(s)

Andy Liaw, original; R. Gentleman, M. Maechler, W. Huber, revisions.

### See Also

`image`, `hclust`

### Examples

```
require(graphics); require(grDevices)
x <- as.matrix(mtcars)
rc <- rainbow(nrow(x), start=0, end=.3)
cc <- rainbow(ncol(x), start=0, end=.3)
hv <- heatmap(x, col = cm.colors(256), scale="column",
             RowSideColors = rc, ColSideColors = cc, margins=c(5,10),
             xlab = "specification variables", ylab = "Car Models",
             main = "heatmap(<Mtcars data>, ..., scale = \"column\")")
utils::str(hv) # the two re-ordering index vectors

## no column dendrogram (nor reordering) at all:
heatmap(x, Colv = NA, col = cm.colors(256), scale="column",
       RowSideColors = rc, margins=c(5,10),
```

```

xlab = "specification variables", ylab= "Car Models",
main = "heatmap(<Mtcars data>, ..., scale = \"column\")")

## "no nothing"
heatmap(x, Rowv = NA, Colv = NA, scale="column",
        main = "heatmap(*, NA, NA) ~ image(t(x))")

round(Ca <- cor(attitude), 2)
symnum(Ca) # simple graphic
heatmap(Ca,          symm = TRUE, margins=c(6,6))# with reorder()
heatmap(Ca, Rowv=FALSE, symm = TRUE, margins=c(6,6))# _NO_ reorder()

## For variable clustering, rather use distance based on cor():
symnum( cU <- cor(USJudgeRatings) )

hU <- heatmap(cU, Rowv = FALSE, symm = TRUE, col = topo.colors(16),
             distfun = function(c) as.dist(1 - c), keep.dendro = TRUE)
## The Correlation matrix with same reordering:
round(100 * cU[hU[[1]], hU[[2]])
## The column dendrogram:
utils::str(hU$Colv)

```

---

HoltWinters

*Holt-Winters Filtering*


---

## Description

Computes Holt-Winters Filtering of a given time series. Unknown parameters are determined by minimizing the squared prediction error.

## Usage

```

HoltWinters(x, alpha = NULL, beta = NULL, gamma = NULL,
           seasonal = c("additive", "multiplicative"),
           start.periods = 2, l.start = NULL, b.start = NULL,
           s.start = NULL,
           optim.start = c(alpha = 0.3, beta = 0.1, gamma = 0.1),
           optim.control = list())

```

## Arguments

<code>x</code>	An object of class <code>ts</code>
<code>alpha</code>	<i>alpha</i> parameter of Holt-Winters Filter.
<code>beta</code>	<i>beta</i> parameter of Holt-Winters Filter. If set to <code>FALSE</code> , the function will do exponential smoothing.
<code>gamma</code>	<i>gamma</i> parameter used for the seasonal component. If set to <code>FALSE</code> , a non-seasonal model is fitted.
<code>seasonal</code>	Character string to select an "additive" (the default) or "multiplicative" seasonal model. The first few characters are sufficient. (Only takes effect if <code>gamma</code> is non-zero).

<code>start.periods</code>	Start periods used in the autodetection of start values. Must be at least 2.
<code>l.start</code>	Start value for level ( <code>a[0]</code> ).
<code>b.start</code>	Start value for trend ( <code>b[0]</code> ).
<code>s.start</code>	Vector of start values for the seasonal component ( $s_1[0] \dots s_p[0]$ )
<code>optim.start</code>	Vector with named components <code>alpha</code> , <code>beta</code> , and <code>gamma</code> containing the starting values for the optimizer. Only the values needed must be specified. Ignored in the one-parameter case.
<code>optim.control</code>	Optional list with additional control parameters passed to <code>optim</code> if this is used. Ignored in the one-parameter case.

## Details

The additive Holt-Winters prediction function (for time series with period length `p`) is

$$\hat{Y}[t+h] = a[t] + hb[t] + s[t+1+(h-1) \bmod p],$$

where  $a[t]$ ,  $b[t]$  and  $s[t]$  are given by

$$a[t] = \alpha(Y[t] - s[t-p]) + (1 - \alpha)(a[t-1] + b[t-1])$$

$$b[t] = \beta(a[t] - a[t-1]) + (1 - \beta)b[t-1]$$

$$s[t] = \gamma(Y[t] - a[t]) + (1 - \gamma)s[t-p]$$

The multiplicative Holt-Winters prediction function (for time series with period length `p`) is

$$\hat{Y}[t+h] = (a[t] + hb[t]) \times s[t+1+(h-1) \bmod p].$$

where  $a[t]$ ,  $b[t]$  and  $s[t]$  are given by

$$a[t] = \alpha(Y[t]/s[t-p]) + (1 - \alpha)(a[t-1] + b[t-1])$$

$$b[t] = \beta(a[t] - a[t-1]) + (1 - \beta)b[t-1]$$

$$s[t] = \gamma(Y[t]/a[t]) + (1 - \gamma)s[t-p]$$

The data in `x` are required to be non-zero for a multiplicative model, but it makes most sense if they are all positive.

The function tries to find the optimal values of  $\alpha$  and/or  $\beta$  and/or  $\gamma$  by minimizing the squared one-step prediction error if they are `NULL` (the default). `optimize` will be used for the single-parameter case, and `optim` otherwise.

For seasonal models, start values for `a`, `b` and `s` are inferred by performing a simple decomposition in trend and seasonal component using moving averages (see function [decompose](#)) on the `start.periods` first periods (a simple linear regression on the trend component is used for starting level and trend.). For level/trend-models (no seasonal component), start values for `a` and `b` are `x[2]` and `x[2] - x[1]`, respectively. For level-only models (ordinary exponential smoothing), the start value for `a` is `x[1]`.

**Value**

An object of class "HoltWinters", a list with components:

fitted	A multiple time series with one column for the filtered series as well as for the level, trend and seasonal components, estimated contemporaneously (that is at time $t$ and not at the end of the series).
x	The original series
alpha	alpha used for filtering
beta	beta used for filtering
gamma	gamma used for filtering
coefficients	A vector with named components $a$ , $b$ , $s_1$ , ..., $s_p$ containing the estimated values for the level, trend and seasonal components
seasonal	The specified seasonal parameter
SSE	The final sum of squared errors achieved in optimizing
call	The call used

**Author(s)**

David Meyer <David.Meyer@wu.ac.at>

**References**

- C. C. Holt (1957) Forecasting trends and seasonals by exponentially weighted moving averages, *ONR Research Memorandum, Carnegie Institute of Technology* **52**.
- P. R. Winters (1960) Forecasting sales by exponentially weighted moving averages, *Management Science* **6**, 324–342.

**See Also**

[predict.HoltWinters](#), [optim](#).

**Examples**

```
require(graphics)

## Seasonal Holt-Winters
(m <- HoltWinters(co2))
plot(m)
plot(fitted(m))

(m <- HoltWinters(AirPassengers, seasonal = "mult"))
plot(m)

## Non-Seasonal Holt-Winters
x <- uspop + rnorm(uspop, sd = 5)
m <- HoltWinters(x, gamma = FALSE)
plot(m)

## Exponential Smoothing
m2 <- HoltWinters(x, gamma = FALSE, beta = FALSE)
lines(fitted(m2)[,1], col = 3)
```

**Description**

Density, distribution function, quantile function and random generation for the hypergeometric distribution.

**Usage**

```
dhyper(x, m, n, k, log = FALSE)
phyper(q, m, n, k, lower.tail = TRUE, log.p = FALSE)
qhyper(p, m, n, k, lower.tail = TRUE, log.p = FALSE)
rhyper(nn, m, n, k)
```

**Arguments**

<code>x, q</code>	vector of quantiles representing the number of white balls drawn without replacement from an urn which contains both black and white balls.
<code>m</code>	the number of white balls in the urn.
<code>n</code>	the number of black balls in the urn.
<code>k</code>	the number of balls drawn from the urn.
<code>p</code>	probability, it must be between 0 and 1.
<code>nn</code>	number of observations. If <code>length(nn) &gt; 1</code> , the length is taken to be the number required.
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .

**Details**

The hypergeometric distribution is used for sampling *without* replacement. The density of this distribution with parameters `m`, `n` and `k` (named  $Np$ ,  $N - Np$ , and  $n$ , respectively in the reference below) is given by

$$p(x) = \binom{m}{x} \binom{n}{k-x} / \binom{m+n}{k}$$

for  $x = 0, \dots, k$ .

The quantile is defined as the smallest value  $x$  such that  $F(x) \geq p$ , where  $F$  is the distribution function.

**Value**

`dhyper` gives the density, `phyper` gives the distribution function, `qhyper` gives the quantile function, and `rhyper` generates random deviates.

Invalid arguments will result in return value `NaN`, with a warning.

**Source**

dhyper computes via binomial probabilities, using code contributed by Catherine Loader (see [dbinom](#)).

phyper is based on calculating dhyper and phyper(. . .) / dhyper(. . .) (as a summation), based on ideas of Ian Smith and Morten Welinder.

qhyper is based on inversion.

rhyper is based on a corrected version of

Kachitvichyanukul, V. and Schmeiser, B. (1985). Computer generation of hypergeometric random variates. *Journal of Statistical Computation and Simulation*, **22**, 127–145.

**References**

Johnson, N. L., Kotz, S., and Kemp, A. W. (1992) *Univariate Discrete Distributions*, Second Edition. New York: Wiley.

**Examples**

```
m <- 10; n <- 7; k <- 8
x <- 0:(k+1)
rbind(phyper(x, m, n, k), dhyper(x, m, n, k))
all(phyper(x, m, n, k) == cumsum(dhyper(x, m, n, k)))# FALSE
## but error is very small:
signif(phyper(x, m, n, k) - cumsum(dhyper(x, m, n, k)), digits=3)
```

---

identify.hclust      *Identify Clusters in a Dendrogram*

---

**Description**

identify.hclust reads the position of the graphics pointer when the (first) mouse button is pressed. It then cuts the tree at the vertical position of the pointer and highlights the cluster containing the horizontal position of the pointer. Optionally a function is applied to the index of data points contained in the cluster.

**Usage**

```
## S3 method for class 'hclust':
identify(x, FUN = NULL, N = 20, MAXCLUSTER = 20, DEV.FUN = NULL,
        ...)
```

**Arguments**

x	an object of the type produced by hclust.
FUN	(optional) function to be applied to the index numbers of the data points in a cluster (see ‘Details’ below).
N	the maximum number of clusters to be identified.
MAXCLUSTER	the maximum number of clusters that can be produced by a cut (limits the effective vertical range of the pointer).
DEV.FUN	(optional) integer scalar. If specified, the corresponding graphics device is made active before FUN is applied.
...	further arguments to FUN.

**Details**

By default clusters can be identified using the mouse and an `invisible` list of indices of the respective data points is returned.

If `FUN` is not `NULL`, then the index vector of data points is passed to this function as first argument, see the examples below. The active graphics device for `FUN` can be specified using `DEV.FUN`.

The identification process is terminated by pressing any mouse button other than the first, see also `identify`.

**Value**

Either a list of data point index vectors or a list of return values of `FUN`.

**See Also**

`hclust`, `rect.hclust`

**Examples**

```
## Not run:
require(graphics)

hca <- hclust(dist(USArrests))
plot(hca)
(x <- identify(hca)) ## Terminate with 2nd mouse button !!

hci <- hclust(dist(iris[,1:4]))
plot(hci)
identify(hci, function(k) print(table(iris[k,5])))

# open a new device (one for dendrogram, one for bars):
get(getOption("device"))() # << make that narrow (& small)
# and *beside* 1st one
nD <- dev.cur() # to be for the barplot
dev.set(dev.prev()) # old one for dendrogram
plot(hci)
## select subtrees in dendrogram and "see" the species distribution:
identify(hci, function(k) barplot(table(iris[k,5]),col=2:4), DEV.FUN = nD)

## End(Not run)
```

---

influence.measures *Regression Deletion Diagnostics*

---

**Description**

This suite of functions can be used to compute some of the regression (leave-one-out deletion) diagnostics for linear and generalized linear models discussed in Belsley, Kuh and Welsch (1980), Cook and Weisberg (1982), etc.

**Usage**

```

influence.measures(model)

rstandard(model, ...)
## S3 method for class 'lm':
rstandard(model, infl = lm.influence(model, do.coef = FALSE),
          sd = sqrt(deviance(model)/df.residual(model)), ...)
## S3 method for class 'glm':
rstandard(model, infl = lm.influence(model, do.coef = FALSE),
          ...)

rstudent(model, ...)
## S3 method for class 'lm':
rstudent(model, infl = lm.influence(model, do.coef = FALSE),
          res = infl$wt.res, ...)
## S3 method for class 'glm':
rstudent(model, infl = influence(model, do.coef = FALSE), ...)

dffits(model, infl = , res = )

dfbeta(model, ...)
## S3 method for class 'lm':
dfbeta(model, infl = lm.influence(model, do.coef = TRUE), ...)

dfbetas(model, ...)
## S3 method for class 'lm':
dfbetas(model, infl = lm.influence(model, do.coef = TRUE), ...)

covratio(model, infl = lm.influence(model, do.coef = FALSE),
          res = weighted.residuals(model))

cooks.distance(model, ...)
## S3 method for class 'lm':
cooks.distance(model, infl = lm.influence(model, do.coef = FALSE),
              res = weighted.residuals(model),
              sd = sqrt(deviance(model)/df.residual(model)),
              hat = infl$hat, ...)
## S3 method for class 'glm':
cooks.distance(model, infl = influence(model, do.coef = FALSE),
              res = infl$pear.res,
              dispersion = summary(model)$dispersion,
              hat = infl$hat, ...)

hatvalues(model, ...)
## S3 method for class 'lm':
hatvalues(model, infl = lm.influence(model, do.coef = FALSE), ...)

hat(x, intercept = TRUE)

```

**Arguments**

model                    an R object, typically returned by `lm` or `glm`.



<code>infl</code>	influence structure as returned by <code>lm.influence</code> or <code>influence</code> (the latter only for the <code>glm</code> method of <code>rstudent</code> and <code>cooks.distance</code> ).
<code>res</code>	(possibly weighted) residuals, with proper default.
<code>sd</code>	standard deviation to use, see default.
<code>dispersion</code>	dispersion (for <code>glm</code> objects) to use, see default.
<code>hat</code>	hat values $H_{ii}$ , see default.
<code>x</code>	the $X$ or design matrix.
<code>intercept</code>	should an intercept column be prepended to <code>x</code> ?
<code>...</code>	further arguments passed to or from other methods.

### Details

The primary high-level function is `influence.measures` which produces a class "infl" object tabular display showing the DFBETAS for each model variable, DFFITS, covariance ratios, Cook's distances and the diagonal elements of the hat matrix. Cases which are influential with respect to any of these measures are marked with an asterisk.

The functions `dfbetas`, `dffits`, `covratio` and `cooks.distance` provide direct access to the corresponding diagnostic quantities. Functions `rstandard` and `rstudent` give the standardized and Studentized residuals respectively. (These re-normalize the residuals to have unit variance, using an overall and leave-one-out measure of the error variance respectively.)

Values for generalized linear models are approximations, as described in Williams (1987) (except that Cook's distances are scaled as  $F$  rather than as chi-square values). The approximations can be poor when some cases have large influence.

The optional `infl`, `res` and `sd` arguments are there to encourage the use of these direct access functions, in situations where, e.g., the underlying basic influence measures (from `lm.influence` or the generic `influence`) are already available.

Note that cases with `weights == 0` are *dropped* from all these functions, but that if a linear model has been fitted with `na.action = na.exclude`, suitable values are filled in for the cases excluded during fitting.

The function `hat()` exists mainly for S (version 2) compatibility; we recommend using `hatvalues()` instead.

### Note

For `hatvalues`, `dfbeta`, and `dfbetas`, the method for linear models also works for generalized linear models.

### Author(s)

Several R core team members and John Fox, originally in his 'car' package.

### References

- Belsley, D. A., Kuh, E. and Welsch, R. E. (1980) *Regression Diagnostics*. New York: Wiley.
- Cook, R. D. and Weisberg, S. (1982) *Residuals and Influence in Regression*. London: Chapman and Hall.
- Williams, D. A. (1987) Generalized linear model diagnostics using the deviance and single case deletions. *Applied Statistics* **36**, 181–191.
- Fox, J. (1997) *Applied Regression, Linear Models, and Related Methods*. Sage.

Fox, J. (2002) *An R and S-Plus Companion to Applied Regression*. Sage Publ.; <http://www.socsci.mcmaster.ca/jfox/Books/Companion/>.

### See Also

[influence](#) (containing [lm.influence](#)).  
[‘plotmath’](#) for the use of hat in plot annotation.

### Examples

```
require(graphics)

## Analysis of the life-cycle savings data
## given in Belsley, Kuh and Welsch.
lm.SR <- lm(sr ~ pop15 + pop75 + dpi + ddpi, data = LifeCycleSavings)

inflm.SR <- influence.measures(lm.SR)
which(apply(inflm.SR$sis.inf, 1, any))
# which observations 'are' influential
summary(inflm.SR) # only these
inflm.SR          # all
plot(rstudent(lm.SR) ~ hatvalues(lm.SR)) # recommended by some

## The 'infl' argument is not needed, but avoids recomputation:
rs <- rstandard(lm.SR)
iflSR <- influence(lm.SR)
identical(rs, rstandard(lm.SR, infl = iflSR))
## to "see" the larger values:
1000 * round(dfbetas(lm.SR, infl = iflSR), 3)

## Huber's data [Atkinson 1985]
xh <- c(-4:0, 10)
yh <- c(2.48, .73, -.04, -1.44, -1.32, 0)
summary(lmH <- lm(yh ~ xh))
(im <- influence.measures(lmH))
plot(xh,yh, main = "Huber's data: L.S. line and influential obs.")
abline(lmH); points(xh[im$sis.inf], yh[im$sis.inf], pch=20, col=2)

## Irwin's data [Williams 1987]
xi <- 1:5
yi <- c(0,2,14,19,30) # number of mice responding to does xi
mi <- rep(40, 5)      # number of mice exposed
summary(lmI <- glm(cbind(yi, mi -yi) ~ xi, family = binomial))
signif(cooks.distance(lmI), 3) # ~ = Ci in Table 3, p.184
(imI <- influence.measures(lmI))
stopifnot(all.equal(imI$infmtat[, "cook.d"],
                    cooks.distance(lmI)))
```

### Description

Adaptive quadrature of functions of one variable over a finite or infinite interval.

**Usage**

```
integrate(f, lower, upper, ..., subdivisions=100,
          rel.tol = .Machine$double.eps^0.25, abs.tol = rel.tol,
          stop.on.error = TRUE, keep.xy = FALSE, aux = NULL)
```

**Arguments**

<code>f</code>	an R function taking a numeric first argument and returning a numeric vector of the same length. Returning a non-finite element will generate an error.
<code>lower, upper</code>	the limits of integration. Can be infinite.
<code>...</code>	additional arguments to be passed to <code>f</code> .
<code>subdivisions</code>	the maximum number of subintervals.
<code>rel.tol</code>	relative accuracy requested.
<code>abs.tol</code>	absolute accuracy requested.
<code>stop.on.error</code>	logical. If true (the default) an error stops the function. If false some errors will give a result with a warning in the <code>message</code> component.
<code>keep.xy</code>	unused. For compatibility with S.
<code>aux</code>	unused. For compatibility with S.

**Details**

Note that arguments after `...` must be matched exactly.

If one or both limits are infinite, the infinite range is mapped onto a finite interval.

For a finite interval, globally adaptive interval subdivision is used in connection with extrapolation by the Epsilon algorithm.

`rel.tol` cannot be less than  $\max(50 \cdot \text{Machine\$double.eps}, 0.5e-28)$  if `abs.tol`  $\leq 0$ .

**Value**

A list of class "integrate" with components

<code>value</code>	the final estimate of the integral.
<code>abs.error</code>	estimate of the modulus of the absolute error.
<code>subdivisions</code>	the number of subintervals produced in the subdivision process.
<code>message</code>	"OK" or a character string giving the error message.
<code>call</code>	the matched call.

**Note**

Like all numerical integration routines, these evaluate the function on a finite set of points. If the function is approximately constant (in particular, zero) over nearly all its range it is possible that the result and error estimate may be seriously wrong.

When integrating over infinite intervals do so explicitly, rather than just using a large number as the endpoint. This increases the chance of a correct answer – any function whose integral over an infinite interval is finite must be near zero for most of that interval.

`f` must accept a vector of inputs and produce a vector of function evaluations at those points. The [Vectorize](#) function may be helpful to convert `f` to this form.

## References

Based on QUADPACK routines dqags and dqagi by R. Piessens and E. deDoncker-Kapenga, available from Netlib.

See

R. Piessens, E. deDoncker-Kapenga, C. Uberhuber, D. Kahaner (1983) *Quadpack: a Subroutine Package for Automatic Integration*; Springer Verlag.

## Examples

```
integrate(dnorm, -1.96, 1.96)
integrate(dnorm, -Inf, Inf)

## a slowly-convergent integral
integrand <- function(x) {1/((x+1)*sqrt(x))}
integrate(integrand, lower = 0, upper = Inf)

## don't do this if you really want the integral from 0 to Inf
integrate(integrand, lower = 0, upper = 10)
integrate(integrand, lower = 0, upper = 100000)
integrate(integrand, lower = 0, upper = 1000000, stop.on.error = FALSE)

## some functions do not handle vector input properly
f <- function(x) 2.0
try(integrate(f, 0, 1))
integrate(Vectorize(f), 0, 1) ## correct
integrate(function(x) rep(2.0, length(x)), 0, 1) ## correct

## integrate can fail if misused
integrate(dnorm, 0, 2)
integrate(dnorm, 0, 20)
integrate(dnorm, 0, 200)
integrate(dnorm, 0, 2000)
integrate(dnorm, 0, 20000) ## fails on many systems
integrate(dnorm, 0, Inf) ## works
```

---

interaction.plot     *Two-way Interaction Plot*

---

## Description

Plots the mean (or other summary) of the response for two-way combinations of factors, thereby illustrating possible interactions.

## Usage

```
interaction.plot(x.factor, trace.factor, response, fun = mean,
                type = c("l", "p", "b"), legend = TRUE,
                trace.label = deparse(substitute(trace.factor)),
                fixed = FALSE,
                xlab = deparse(substitute(x.factor)),
                ylab = ylabel,
                ylim = range(cells, na.rm=TRUE),
```

```
lty = nc:1, col = 1, pch = c(1:9, 0, letters),
xpd = NULL, leg.bg = par("bg"), leg.bty = "n",
xtick = FALSE, xaxt = par("xaxt"), axes = TRUE,
...)
```

### Arguments

<code>x.factor</code>	a factor whose levels will form the x axis.
<code>trace.factor</code>	another factor whose levels will form the traces.
<code>response</code>	a numeric variable giving the response
<code>fun</code>	the function to compute the summary. Should return a single real value.
<code>type</code>	the type of plot: lines or points.
<code>legend</code>	logical. Should a legend be included?
<code>trace.label</code>	overall label for the legend.
<code>fixed</code>	logical. Should the legend be in the order of the levels of <code>trace.factor</code> or in the order of the traces at their right-hand ends?
<code>xlab, ylab</code>	the x and y label of the plot each with a sensible default.
<code>ylim</code>	numeric of length 2 giving the y limits for the plot.
<code>lty</code>	line type for the lines drawn, with sensible default.
<code>col</code>	the color to be used for plotting.
<code>pch</code>	a vector of plotting symbols or characters, with sensible default.
<code>xpd</code>	determines clipping behaviour for the <code>legend</code> used, see <code>par(xpd)</code> . Per default, the legend is <i>not</i> clipped at the figure border.
<code>leg.bg, leg.bty</code>	arguments passed to <code>legend()</code> .
<code>xtick</code>	logical. Should tick marks be used on the x axis?
<code>xaxt, axes, ...</code>	graphics parameters to be passed to the plotting routines.

### Details

By default the levels of `x.factor` are plotted on the x axis in their given order, with extra space left at the right for the legend (if specified). If `x.factor` is an ordered factor and the levels are numeric, these numeric values are used for the x axis.

The response and hence its summary can contain missing values. If so, the missing values and the line segments joining them are omitted from the plot (and this can be somewhat disconcerting).

The graphics parameters `xlab`, `ylab`, `ylim`, `lty`, `col` and `pch` are given suitable defaults (and `xlim` and `xaxs` are set and cannot be overridden). The defaults are to cycle through the line types, use the foreground colour, and to use the symbols 1:9, 0, and the capital letters to plot the traces.

### Note

Some of the argument names and the precise behaviour are chosen for S-compatibility.

### References

Chambers, J. M., Freeny, A and Heiberger, R. M. (1992) *Analysis of variance; designed experiments*. Chapter 5 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**Examples**

```

require(graphics)

with(ToothGrowth, {
  interaction.plot(dose, supp, len, fixed=TRUE)
  dose <- ordered(dose)
  interaction.plot(dose, supp, len, fixed=TRUE, col = 2:3, leg.bty = "o")
  interaction.plot(dose, supp, len, fixed=TRUE, col = 2:3, type = "p")
})

with(OrchardSprays, {
  interaction.plot(treatment, rowpos, decrease)
  interaction.plot(rowpos, treatment, decrease, cex.axis=0.8)
  ## order the rows by their mean effect
  rowpos <- factor(rowpos,
                   levels = sort.list(tapply(decrease, rowpos, mean)))
  interaction.plot(rowpos, treatment, decrease, col = 2:9, lty = 1)
})

with(esoph, {
  interaction.plot(agegp, alcgp, ncases/ncontrols, main = "'esoph' Data")
  interaction.plot(agegp, tobgp, ncases/ncontrols, trace.label="tobacco",
                  fixed=TRUE, xaxt = "n")
})
## deal with NAs:
esoph[66,] # second to last age group: 65-74
esophNA <- esoph; esophNA$ncases[66] <- NA
with(esophNA, {
  interaction.plot(agegp, alcgp, ncases/ncontrols, col= 2:5)
  # doesn't show *last* group either
  interaction.plot(agegp, alcgp, ncases/ncontrols, col= 2:5, type = "b")
  ## alternative take non-NA's {"cheating"}
  interaction.plot(agegp, alcgp, ncases/ncontrols, col= 2:5,
                  fun = function(x) mean(x, na.rm=TRUE),
                  sub = "function(x) mean(x, na.rm=TRUE)")
})
rm(esophNA) # to clear up

```

**Description**

computes interquartile range of the  $x$  values.

**Usage**

```
IQR(x, na.rm = FALSE)
```

**Arguments**

$x$	a numeric vector.
<code>na.rm</code>	logical. Should missing values be removed?

## Details

Note that this function computes the quartiles using the `quantile` function rather than following Tukey's recommendations, i.e.,  $IQR(x) = \text{quantile}(x, 3/4) - \text{quantile}(x, 1/4)$ .

For normally  $N(m, 1)$  distributed  $X$ , the expected value of  $IQR(X)$  is  $2 * \text{qnorm}(3/4) = 1.3490$ , i.e., for a normal-consistent estimate of the standard deviation, use  $IQR(x) / 1.349$ .

## References

Tukey, J. W. (1977). *Exploratory Data Analysis*. Reading: Addison-Wesley.

## See Also

`fivenum`, `mad` which is more robust, `range`, `quantile`.

## Examples

```
IQR(rivers)
```

---

```
is.empty.model      Test if a Model's Formula is Empty
```

---

## Description

R's formula notation allows models with no intercept and no predictors. These require special handling internally. `is.empty.model()` checks whether an object describes an empty model.

## Usage

```
is.empty.model(x)
```

## Arguments

`x` A `terms` object or an object with a `terms` method.

## Value

TRUE if the model is empty

## See Also

`lm.glm`

## Examples

```
y <- rnorm(20)
is.empty.model(y ~ 0)
is.empty.model(y ~ -1)
is.empty.model(lm(y ~ 0))
```

isoreg

*Isotonic / Monotone Regression***Description**

Compute the isotonic (monotonely increasing nonparametric) least squares regression which is piecewise constant.

**Usage**

```
isoreg(x, y = NULL)
```

**Arguments**

`x`, `y` coordinate vectors of the regression points. Alternatively a single plotting structure can be specified: see [xy.coords](#).

**Details**

The algorithm determines the convex minorant  $m(x)$  of the *cumulative* data (i.e., `cumsum(y)`) which is piecewise linear and the result is  $m'(x)$ , a step function with level changes at locations where the convex  $m(x)$  touches the cumulative data polygon and changes slope.

`as.stepfun()` returns a [stepfun](#) object which can be more parsimonious.

**Value**

`isoreg()` returns an object of class `isoreg` which is basically a list with components

<code>x</code>	original (constructed) abscissa values <code>x</code> .
<code>y</code>	corresponding <code>y</code> values.
<code>yf</code>	fitted values corresponding to <i>ordered</i> <code>x</code> values.
<code>yc</code>	cumulative <code>y</code> values corresponding to <i>ordered</i> <code>x</code> values.
<code>iKnots</code>	integer vector giving indices where the fitted curve jumps, i.e., where the convex minorant has kinks.
<code>isOrd</code>	logical indicating if original <code>x</code> values were ordered increasingly already.
<code>ord</code>	<code>if(!isOrd)</code> : integer permutation <code>order(x)</code> of <i>original</i> <code>x</code> .
<code>call</code>	the <code>call</code> to <code>isoreg()</code> used.

**Note**

The code should be improved to accept *weights* additionally and solve the corresponding weighted least squares problem.

'Patches are welcome!'

**References**

Barlow, R. E., Bartholomew, D. J., Bremner, J. M., and Brunk, H. D. (1972) *Statistical inference under order restrictions*; Wiley, London.

Robertson, T., Wright, F. T. and Dykstra, R. L. (1988) *Order Restricted Statistical Inference*; Wiley, New York.



**See Also**

the plotting method `plot.isoreg` with more examples; `isoMDS()` from the **MASS** package internally uses isotonic regression.

**Examples**

```
require(graphics)

(ir <- isoreg(c(1,0,4,3,3,5,4,2,0)))
plot(ir, plot.type = "row")

(ir3 <- isoreg(y3 <- c(1,0,4,3,3,5,4,2, 3)))# last "3", not "0"
(fi3 <- as.stepfun(ir3))
(ir4 <- isoreg(1:10, y4 <- c(5, 9, 1:2, 5:8, 3, 8)))
cat(sprintf("R^2 = %.2f\n",
           1 - sum(residuals(ir4)^2) / ((10-1)*var(y4))))

## If you are interested in the knots alone :
with(ir4, cbind(iKnots, yf[iKnots]))

## Example of unordered x[] with ties:
x <- sample((0:30)/8)
y <- exp(x)
x. <- round(x) # ties!
plot(m <- isoreg(x., y))
stopifnot(all.equal(with(m, yf[iKnots]),
                    as.vector(tapply(y, x., mean))))
```

---

 KalmanLike

*Kalman Filtering*


---

**Description**

Use Kalman Filtering to find the (Gaussian) log-likelihood, or for forecasting or smoothing.

**Usage**

```
KalmanLike(y, mod, nit = 0, fast=TRUE)
KalmanRun(y, mod, nit = 0, fast=TRUE)
KalmanSmooth(y, mod, nit = 0)
KalmanForecast(n.ahead = 10, mod, fast=TRUE)
makeARIMA(phi, theta, Delta, kappa = 1e6)
```

**Arguments**

<code>y</code>	a univariate time series.
<code>mod</code>	A list describing the state-space model: see ‘Details’.
<code>nit</code>	The time at which the initialization is computed. <code>nit = 0</code> implies that the initialization is for a one-step prediction, so <code>Pn</code> should not be computed at the first step.
<code>n.ahead</code>	The number of steps ahead for which prediction is required.

phi, theta	numeric vectors of length $\geq 0$ giving AR and MA parameters.
Delta	vector of differencing coefficients, so an ARMA model is fitted to $y[t] - \text{Delta}[1]*y[t-1] - \dots$
kappa	the prior variance (as a multiple of the innovations variance) for the past observations in a differenced model.
fast	If TRUE the mod object may be modified.

### Details

These functions work with a general univariate state-space model with state vector 'a', transitions ' $a \leftarrow T a + R e$ ',  $e \sim \mathcal{N}(0, \kappa Q)$  and observation equation ' $y = Z'a + \text{eta}$ ', ( $\text{eta} \equiv \eta$ ),  $\eta \sim \mathcal{N}(0, \kappa h)$ . The likelihood is a profile likelihood after estimation of  $\kappa$ .

The model is specified as a list with at least components

- T the transition matrix
- Z the observation coefficients
- h the observation variance
- V 'RQR'
- a the current state estimate
- P the current estimate of the state uncertainty matrix
- Pn the estimate at time  $t - 1$  of the state uncertainty matrix

KalmanSmooth is the workhorse function for [tsSmooth](#).

makeARIMA constructs the state-space model for an ARIMA model.

### Value

For KalmanLike, a list with components Lik (the log-likelihood less some constants) and s2, the estimate of  $\kappa$ .

For KalmanRun, a list with components values, a vector of length 2 giving the output of KalmanLike, resid (the residuals) and states, the contemporaneous state estimates, a matrix with one row for each time.

For KalmanSmooth, a list with two components. Component smooth is a  $n$  by  $p$  matrix of state estimates based on all the observations, with one row for each time. Component var is a  $n$  by  $p$  by  $p$  array of variance matrices.

For KalmanForecast, a list with components pred, the predictions, and var, the unscaled variances of the prediction errors (to be multiplied by s2).

For makeARIMA, a model list including components for its arguments.

### Warning

These functions are designed to be called from other functions which check the validity of the arguments passed, so very little checking is done.

In particular, KalmanLike alters the objects passed as the elements a, P and Pn of mod, so these should not be shared. Use fast=FALSE to prevent this.

### References

Durbin, J. and Koopman, S. J. (2001) *Time Series Analysis by State Space Methods*. Oxford University Press.

**See Also**

[arima](#), [StructTS.tsSmooth](#).

---

kernapply

*Apply Smoothing Kernel*

---

**Description**

kernapply computes the convolution between an input sequence and a specific kernel.

**Usage**

```
kernapply(x, ...)  
  
## Default S3 method:  
kernapply(x, k, circular = FALSE, ...)  
## S3 method for class 'ts':  
kernapply(x, k, circular = FALSE, ...)  
## S3 method for class 'vector':  
kernapply(x, k, circular = FALSE, ...)  
  
## S3 method for class 'tskernel':  
kernapply(x, k, ...)
```

**Arguments**

x	an input vector, matrix, time series or kernel to be smoothed.
k	smoothing "tskernel" object.
circular	a logical indicating whether the input sequence to be smoothed is treated as circular, i.e., periodic.
...	arguments passed to or from other methods.

**Value**

A smoothed version of the input sequence.

**Author(s)**

A. Trapletti

**See Also**

[kernel](#), [convolve](#), [filter](#), [spectrum](#)

**Examples**

```
## see 'kernel' for examples
```

---

kernel *Smoothing Kernel Objects*


---

**Description**

The "tskernel" class is designed to represent discrete symmetric normalized smoothing kernels. These kernels can be used to smooth vectors, matrices, or time series objects.

There are `print`, `plot` and `[` methods for these kernel objects.

**Usage**

```
kernel(coef, m, r, name)

df.kernel(k)
bandwidth.kernel(k)
is.tskernel(k)

## S3 method for class 'tskernel':
plot(x, type = "h", xlab = "k", ylab = "W[k]",
      main = attr(x, "name"), ...)
```

**Arguments**

<code>coef</code>	the upper half of the smoothing kernel coefficients (including coefficient zero) <i>or</i> the name of a kernel (currently "daniell", "dirichlet", "fejer" or "modified.daniell").
<code>m</code>	the kernel dimension(s). When <code>m</code> has length larger than one, it means the convolution of kernels of dimension <code>m[j]</code> , for <code>j</code> in <code>1:length(m)</code> . Currently this is supported only for the named "*daniell" kernels.
<code>name</code>	the name the kernel will be called.
<code>r</code>	the kernel order for a Fejer kernel.
<code>k, x</code>	a "tskernel" object.
<code>type, xlab, ylab, main, ...</code>	arguments passed to <code>plot.default</code> .

**Details**

`kernel` is used to construct a general kernel or named specific kernels. The modified Daniell kernel halves the end coefficients (as used by S-PLUS).

The `[` method allows natural indexing of kernel objects with indices in  $(-m) : m$ . The normalization is such that for `k <- kernel(*)`, `sum(k[ -k$m : k$m ])` is one.

`df.kernel` returns the 'equivalent degrees of freedom' of a smoothing kernel as defined in Brockwell and Davis (1991), page 362, and `bandwidth.kernel` returns the equivalent bandwidth as defined in Bloomfield (1976), p. 201, with a continuity correction.

**Value**

`kernel()` returns an object of class "tskernel" which is basically a list with the two components `coef` and the kernel dimension `m`. An additional attribute is "name".

**Author(s)**

A. Trapletti; modifications by B.D. Ripley

**References**

- Bloomfield, P. (1976) *Fourier Analysis of Time Series: An Introduction*. Wiley.
- Brockwell, P.J. and Davis, R.A. (1991) *Time Series: Theory and Methods*. Second edition. Springer, pp. 350–365.

**See Also**

[kernapply](#)

**Examples**

```
require(graphics)

## Demonstrate a simple trading strategy for the
## financial time series German stock index DAX.
x <- EuStockMarkets[,1]
k1 <- kernel("daniell", 50) # a long moving average
k2 <- kernel("daniell", 10) # and a short one
plot(k1)
plot(k2)
x1 <- kernapply(x, k1)
x2 <- kernapply(x, k2)
plot(x)
lines(x1, col = "red") # go long if the short crosses the long upwards
lines(x2, col = "green") # and go short otherwise

## More interesting kernels
kd <- kernel("daniell", c(3,3))
kd # note the unusual indexing
kd[-2:2]
plot(kernel("fejjer", 100, r=6))
plot(kernel("modified.daniell", c(7,5,3)))

# Reproduce example 10.4.3 from Brockwell and Davis (1991)
spectrum(sunspot.year, kernel=kernel("daniell", c(11,7,3)), log="no")
```

---

kmeans

*K-Means Clustering*

---

**Description**

Perform k-means clustering on a data matrix.

**Usage**

```
kmeans(x, centers, iter.max = 10, nstart = 1,
       algorithm = c("Hartigan-Wong", "Lloyd", "Forgy",
                    "MacQueen"))
```

**Arguments**

<code>x</code>	A numeric matrix of data, or an object that can be coerced to such a matrix (such as a numeric vector or a data frame with all numeric columns).
<code>centers</code>	Either the number of clusters or a set of initial (distinct) cluster centres. If a number, a random set of (distinct) rows in <code>x</code> is chosen as the initial centres.
<code>iter.max</code>	The maximum number of iterations allowed.
<code>nstart</code>	If <code>centers</code> is a number, how many random sets should be chosen?
<code>algorithm</code>	character: may be abbreviated.

**Details**

The data given by `x` is clustered by the  $k$ -means method, which aims to partition the points into  $k$  groups such that the sum of squares from points to the assigned cluster centres is minimized. At the minimum, all cluster centres are at the mean of their Voronoi sets (the set of data points which are nearest to the cluster centre).

The algorithm of Hartigan and Wong (1979) is used by default. Note that some authors use  $k$ -means to refer to a specific algorithm rather than the general method: most commonly the algorithm given by MacQueen (1967) but sometimes that given by Lloyd (1957) and Forgy (1965). The Hartigan–Wong algorithm generally does a better job than either of those, but trying several random starts is often recommended.

Except for the Lloyd–Forgy method,  $k$  clusters will always be returned if a number is specified. If an initial matrix of centres is supplied, it is possible that no point will be closest to one or more centres, which is currently an error for the Hartigan–Wong method.

**Value**

An object of class "kmeans" which is a list with components:

<code>cluster</code>	A vector of integers indicating the cluster to which each point is allocated.
<code>centers</code>	A matrix of cluster centres.
<code>withinss</code>	The within-cluster sum of squares for each cluster.
<code>size</code>	The number of points in each cluster.

There is a `print` method for this class.

**References**

- Forgy, E. W. (1965) Cluster analysis of multivariate data: efficiency vs interpretability of classifications. *Biometrics* **21**, 768–769.
- Hartigan, J. A. and Wong, M. A. (1979). A K-means clustering algorithm. *Applied Statistics* **28**, 100–108.
- Lloyd, S. P. (1957, 1982) Least squares quantization in PCM. Technical Note, Bell Laboratories. Published in 1982 in *IEEE Transactions on Information Theory* **28**, 128–137.
- MacQueen, J. (1967) Some methods for classification and analysis of multivariate observations. In *Proceedings of the Fifth Berkeley Symposium on Mathematical Statistics and Probability*, eds L. M. Le Cam & J. Neyman, **1**, pp. 281–297. Berkeley, CA: University of California Press.

**Examples**

```
require(graphics)

# a 2-dimensional example
x <- rbind(matrix(rnorm(100, sd = 0.3), ncol = 2),
           matrix(rnorm(100, mean = 1, sd = 0.3), ncol = 2))
colnames(x) <- c("x", "y")
(cl <- kmeans(x, 2))
plot(x, col = cl$cluster)
points(cl$centers, col = 1:2, pch = 8, cex=2)

## random starts do help here with too many clusters
(cl <- kmeans(x, 5, nstart = 25))
plot(x, col = cl$cluster)
points(cl$centers, col = 1:5, pch = 8)
```

---

kruskal.test

*Kruskal-Wallis Rank Sum Test*


---

**Description**

Performs a Kruskal-Wallis rank sum test.

**Usage**

```
kruskal.test(x, ...)

## Default S3 method:
kruskal.test(x, g, ...)

## S3 method for class 'formula':
kruskal.test(formula, data, subset, na.action, ...)
```

**Arguments**

x	a numeric vector of data values, or a list of numeric data vectors.
g	a vector or factor object giving the group for the corresponding elements of x. Ignored if x is a list.
formula	a formula of the form lhs ~ rhs where lhs gives the data values and rhs the corresponding groups.
data	an optional matrix or data frame (or similar: see <a href="#">model.frame</a> ) containing the variables in the formula formula. By default the variables are taken from environment(formula).
subset	an optional vector specifying a subset of observations to be used.
na.action	a function which indicates what should happen when the data contain NAs. Defaults to <code>getOption("na.action")</code> .
...	further arguments to be passed to or from methods.

## Details

`kruskal.test` performs a Kruskal-Wallis rank sum test of the null that the location parameters of the distribution of `x` are the same in each group (sample). The alternative is that they differ in at least one.

If `x` is a list, its elements are taken as the samples to be compared, and hence have to be numeric data vectors. In this case, `g` is ignored, and one can simply use `kruskal.test(x)` to perform the test. If the samples are not yet contained in a list, use `kruskal.test(list(x, ...))`.

Otherwise, `x` must be a numeric data vector, and `g` must be a vector or factor object of the same length as `x` giving the group for the corresponding elements of `x`.

## Value

A list with class "htest" containing the following components:

<code>statistic</code>	the Kruskal-Wallis rank sum statistic.
<code>parameter</code>	the degrees of freedom of the approximate chi-squared distribution of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>method</code>	the character string "Kruskal-Wallis rank sum test".
<code>data.name</code>	a character string giving the names of the data.

## References

Myles Hollander and Douglas A. Wolfe (1973), *Nonparametric Statistical Methods*. New York: John Wiley & Sons. Pages 115–120.

## See Also

The Wilcoxon rank sum test ([wilcox.test](#)) as the special case for two samples; [lm](#) together with [anova](#) for performing one-way location analysis under normality assumptions; with Student's t test ([t.test](#)) as the special case for two samples.

[wilcox\\_test](#) in package **coin** for exact, asymptotic and Monte Carlo *conditional* p-values, including in the presence of ties.

## Examples

```
## Hollander & Wolfe (1973), 116.
## Mucociliary efficiency from the rate of removal of dust in normal
## subjects, subjects with obstructive airway disease, and subjects
## with asbestosis.
x <- c(2.9, 3.0, 2.5, 2.6, 3.2) # normal subjects
y <- c(3.8, 2.7, 4.0, 2.4)     # with obstructive airway disease
z <- c(2.8, 3.4, 3.7, 2.2, 2.0) # with asbestosis
kruskal.test(list(x, y, z))
## Equivalently,
x <- c(x, y, z)
g <- factor(rep(1:3, c(5, 4, 5)),
            labels = c("Normal subjects",
                      "Subjects with obstructive airway disease",
                      "Subjects with asbestosis"))
kruskal.test(x, g)
```



```
## Formula interface.
require(graphics)
boxplot(Ozone ~ Month, data = airquality)
kruskal.test(Ozone ~ Month, data = airquality)
```

ks.test

*Kolmogorov-Smirnov Tests***Description**

Performs one or two sample Kolmogorov-Smirnov tests.

**Usage**

```
ks.test(x, y, ...,
        alternative = c("two.sided", "less", "greater"),
        exact = NULL)
```

**Arguments**

x	a numeric vector of data values.
y	either a numeric vector of data values, or a character string naming a cumulative distribution function or an actual cumulative distribution function such as <code>pnorm</code> .
...	parameters of the distribution specified (as a character string) by <code>y</code> .
alternative	indicates the alternative hypothesis and must be one of "two.sided" (default), "less", or "greater". You can specify just the initial letter of the value, but the argument name must be give in full. See 'Details' for the meanings of the possible values.
exact	NULL or a logical indicating whether an exact p-value should be computed. See 'Details' for the meaning of NULL. Not used for the one-sided two-sample case.

**Details**

If `y` is numeric, a two-sample test of the null hypothesis that `x` and `y` were drawn from the same *continuous* distribution is performed.

Alternatively, `y` can be a character string naming a continuous (cumulative) distribution function, or such a function. In this case, a one-sample test is carried out of the null that the distribution function which generated `x` is distribution `y` with parameters specified by `...`

The presence of ties generates a warning, since continuous distributions do not generate them.

The possible values "two.sided", "less" and "greater" of `alternative` specify the null hypothesis that the true distribution function of `x` is equal to, not less than or not greater than the hypothesized distribution function (one-sample case) or the distribution function of `y` (two-sample case), respectively. This is a comparison of cumulative distribution functions, and the test statistic is the maximum difference in value, with the statistic in the "greater" alternative being  $D^+ = \max_u [F_x(u) - F_y(u)]$ . Thus in the two-sample case `alternative="greater"` includes distributions for which `x` is stochastically *smaller* than `y` (the CDF of `x` lies above and hence to the left of that for `y`), in contrast to `t.test` or `wilcox.test`.

Exact p-values are not available for the one-sided two-sample case, or in the case of ties. If `exact = NULL` (the default), an exact p-value is computed if the sample size is less than 100 in the one-sample case, and if the product of the sample sizes is less than 10000 in the two-sample case. Otherwise, asymptotic distributions are used whose approximations may be inaccurate in small samples. In the one-sample two-sided case, exact p-values are obtained as described in Marsaglia, Tsang & Wang (2003). The formula of Birnbaum & Tingey (1951) is used for the one-sample one-sided case.

If a single-sample test is used, the parameters specified in `. . .` must be pre-specified and not estimated from the data. There is some more refined distribution theory for the KS test with estimated parameters (see Durbin, 1973), but that is not implemented in `ks.test`.

### Value

A list with class `"htest"` containing the following components:

<code>statistic</code>	the value of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>alternative</code>	a character string describing the alternative hypothesis.
<code>method</code>	a character string indicating what type of test was performed.
<code>data.name</code>	a character string giving the name(s) of the data.

### References

- Z. W. Birnbaum and Fred H. Tingey (1951), One-sided confidence contours for probability distribution functions. *The Annals of Mathematical Statistics*, **22**/4, 592–596.
- William J. Conover (1971), *Practical Nonparametric Statistics*. New York: John Wiley & Sons. Pages 295–301 (one-sample Kolmogorov test), 309–314 (two-sample Smirnov test).
- Durbin, J. (1973) *Distribution theory for tests based on the sample distribution function*. SIAM.
- George Marsaglia, Wai Wan Tsang and Jingbo Wang (2003), Evaluating Kolmogorov's distribution. *Journal of Statistical Software*, **8**/18. <http://www.jstatsoft.org/v08/i18/>.

### See Also

[shapiro.test](#) which performs the Shapiro-Wilk test for normality.

### Examples

```
require(graphics)

x <- rnorm(50)
y <- runif(30)
# Do x and y come from the same distribution?
ks.test(x, y)
# Does x come from a shifted gamma distribution with shape 3 and rate 2?
ks.test(x+2, "pgamma", 3, 2) # two-sided, exact
ks.test(x+2, "pgamma", 3, 2, exact = FALSE)
ks.test(x+2, "pgamma", 3, 2, alternative = "gr")

# test if x is stochastically larger than x2
x2 <- rnorm(50, -1)
plot(ecdf(x), xlim=range(c(x, x2)))
plot(ecdf(x2), add=TRUE, lty="dashed")
```

```
t.test(x, x2, alternative="g")
wilcox.test(x, x2, alternative="g")
ks.test(x, x2, alternative="l")
```

ksmooth

*Kernel Regression Smoother***Description**

The Nadaraya–Watson kernel regression estimate.

**Usage**

```
ksmooth(x, y, kernel = c("box", "normal"), bandwidth = 0.5,
        range.x = range(x),
        n.points = max(100, length(x)), x.points)
```

**Arguments**

x	input x values
y	input y values
kernel	the kernel to be used.
bandwidth	the bandwidth. The kernels are scaled so that their quartiles (viewed as probability densities) are at $\pm 0.25 \cdot \text{bandwidth}$ .
range.x	the range of points to be covered in the output.
n.points	the number of points at which to evaluate the fit.
x.points	points at which to evaluate the smoothed fit. If missing, n.points are chosen uniformly to cover range.x.

**Value**

A list with components

x	values at which the smoothed fit is evaluated. Guaranteed to be in increasing order.
y	fitted values corresponding to x.

**Note**

This function is implemented purely for compatibility with S, although it is nowhere near as slow as the S function. Better kernel smoothers are available in other packages.

**Examples**

```
require(graphics)

with(cars, {
  plot(speed, dist)
  lines(ksmooth(speed, dist, "normal", bandwidth=2), col=2)
  lines(ksmooth(speed, dist, "normal", bandwidth=5), col=3)
})
```

---

`lag`*Lag a Time Series*

---

**Description**

Compute a lagged version of a time series, shifting the time base back by a given number of observations.

**Usage**

```
lag(x, ...)  
  
## Default S3 method:  
lag(x, k = 1, ...)
```

**Arguments**

<code>x</code>	A vector or matrix or univariate or multivariate time series
<code>k</code>	The number of lags (in units of observations).
<code>...</code>	further arguments to be passed to or from methods.

**Details**

Vector or matrix arguments `x` are coerced to time series.

`lag` is a generic function; this page documents its default method.

**Value**

A time series object.

**Note**

Note the sign of `k`: a series lagged by a positive `k` starts *earlier*.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[diff](#), [deltat](#)

**Examples**

```
lag(1deaths, 12) # starts one year earlier
```

lag.plot

*Time Series Lag Plots***Description**

Plot time series against lagged versions of themselves. Helps visualizing ‘auto-dependence’ even when auto-correlations vanish.

**Usage**

```
lag.plot(x, lags = 1, layout = NULL, set.lags = 1:lags,
        main = NULL, asp = 1,
        diag = TRUE, diag.col = "gray", type = "p", oma = NULL,
        ask = NULL, do.lines = (n <= 150), labels = do.lines,
        ...)
```

**Arguments**

x	time-series (univariate or multivariate)
lags	number of lag plots desired, see arg <code>set.lags</code> .
layout	the layout of multiple plots, basically the <code>mfrow</code> <code>par()</code> argument. The default uses about a square layout (see <code>n2mfrow</code> such that all plots are on one page.
set.lags	vector of positive integers allowing specification of the set of lags used; defaults to <code>1:lags</code> .
main	character with a main header title to be done on the top of each page.
asp	Aspect ratio to be fixed, see <code>plot.default</code> .
diag	logical indicating if the $x=y$ diagonal should be drawn.
diag.col	color to be used for the diagonal if <code>(diag)</code> .
type	plot type to be used, but see <code>plot.ts</code> about its restricted meaning.
oma	outer margins, see <code>par</code> .
ask	logical or <code>NULL</code> ; if true, the user is asked to confirm before a new page is started.
do.lines	logical indicating if lines should be drawn.
labels	logical indicating if labels should be used.
...	Further arguments to <code>plot.ts</code> . Several graphical parameters are set in this function and so cannot be changed: these include <code>xlab</code> , <code>ylab</code> , <code>mgp</code> , <code>col.lab</code> and <code>font.lab</code> : this also applies to the arguments <code>xy.labels</code> and <code>xy.lines</code> .

**Details**

If just one plot is produced, this is a conventional plot. If more than one plot is to be produced, `par(mfrow)` and several other graphics parameters will be set, so it is not (easily) possible to mix such lag plots with other plots on the same page.

If `ask = NULL`, `par(ask = TRUE)` will be called if more than one page of plots is to be produced and the device is interactive.

**Note**

It is more flexible and has different default behaviour than the S version. We use `main =` instead of `head =` for internal consistency.

**Author(s)**

Martin Maechler

**See Also**

`plot.ts` which is the basic work horse.

**Examples**

```
require(graphics)

lag.plot(nhtemp, 8, diag.col = "forest green")
lag.plot(nhtemp, 5, main="Average Temperatures in New Haven")
## ask defaults to TRUE when we have more than one page:
lag.plot(nhtemp, 6, layout = c(2,1), asp = NA,
         main = "New Haven Temperatures", col.main = "blue")

## Multivariate (but non-stationary! ...)
lag.plot(freeny.x, lags = 3)
## Not run:
no lines for long series :
lag.plot(sqrt(sunspots), set = c(1:4, 9:12), pch = ".", col = "gold")

## End(Not run)
```

---

line

*Robust Line Fitting*

---

**Description**

Fit a line robustly as recommended in *Exploratory Data Analysis*.

**Usage**

```
line(x, y)
```

**Arguments**

`x, y` the arguments can be any way of specifying x-y pairs.

**Value**

An object of class "tukeyline".

Methods are available for the generic functions `coef`, `residuals`, `fitted`, and `print`.

**References**

Tukey, J. W. (1977). *Exploratory Data Analysis*, Reading Massachusetts: Addison-Wesley.

**See Also**[lm](#).**Examples**

```
require(graphics)

plot(cars)
(z <- line(cars))
abline(coef(z))
## Tukey-Anscombe Plot :
plot(residuals(z) ~ fitted(z), main = deparse(z$call))
```

lm

*Fitting Linear Models***Description**

`lm` is used to fit linear models. It can be used to carry out regression, single stratum analysis of variance and analysis of covariance (although [aov](#) may provide a more convenient interface for these).

**Usage**

```
lm(formula, data, subset, weights, na.action,
   method = "qr", model = TRUE, x = FALSE, y = FALSE, qr = TRUE,
   singular.ok = TRUE, contrasts = NULL, offset, ...)
```

**Arguments**

<code>formula</code>	an object of class " <a href="#">formula</a> " (or one that can be coerced to that class): a symbolic description of the model to be fitted. The details of model specification are given under ‘Details’.
<code>data</code>	an optional data frame, list or environment (or object coercible by <a href="#">as.data.frame</a> to a data frame) containing the variables in the model. If not found in <code>data</code> , the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>lm</code> is called.
<code>subset</code>	an optional vector specifying a subset of observations to be used in the fitting process.
<code>weights</code>	an optional vector of weights to be used in the fitting process. Should be <code>NULL</code> or a numeric vector. If non- <code>NULL</code> , weighted least squares is used with weights <code>weights</code> (that is, minimizing $\sum(w * e^2)$ ); otherwise ordinary least squares is used. See also ‘Details’.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. The default is set by the <code>na.action</code> setting of <a href="#">options</a> , and is <code>na.fail</code> if that is unset. The ‘factory-fresh’ default is <code>na.omit</code> . Another possible value is <code>NULL</code> , no action. Value <code>na.exclude</code> can be useful.
<code>method</code>	the method to be used; for fitting, currently only <code>method = "qr"</code> is supported; <code>method = "model.frame"</code> returns the model frame (the same as with <code>model = TRUE</code> , see below).

<code>model, x, y, qr</code>	logicals. If <code>TRUE</code> the corresponding components of the fit (the model frame, the model matrix, the response, the QR decomposition) are returned.
<code>singular.ok</code>	logical. If <code>FALSE</code> (the default in <code>S</code> but not in <code>R</code> ) a singular fit is an error.
<code>contrasts</code>	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
<code>offset</code>	this can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting. This should be <code>NULL</code> or a numeric vector of length equal to the number of cases. One or more <code>offset</code> terms can be included in the formula instead or as well, and if more than one are specified their sum is used. See <code>model.offset</code> .
<code>...</code>	additional arguments to be passed to the low level regression fitting functions (see below).

## Details

Models for `lm` are specified symbolically. A typical model has the form `response ~ terms` where `response` is the (numeric) response vector and `terms` is a series of terms which specifies a linear predictor for `response`. A terms specification of the form `first + second` indicates all the terms in `first` together with all the terms in `second` with duplicates removed. A specification of the form `first:second` indicates the set of terms obtained by taking the interactions of all terms in `first` with all terms in `second`. The specification `first*second` indicates the *cross* of `first` and `second`. This is the same as `first + second + first:second`.

If the formula includes an `offset`, this is evaluated and subtracted from the response.

If `response` is a matrix a linear model is fitted separately by least-squares to each column of the matrix.

See `model.matrix` for some further details. The terms in the formula will be re-ordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on: to avoid this pass a `terms` object as the formula (see `av` and `demo(glm.vr)` for an example).

A formula has an implied intercept term. To remove this use either `y ~ x - 1` or `y ~ 0 + x`. See `formula` for more details of allowed formulae.

Non-`NULL` `weights` can be used to indicate that different observations have different variances (with the values in `weights` being inversely proportional to the variances); or equivalently, when the elements of `weights` are positive integers  $w_i$ , that each response  $y_i$  is the mean of  $w_i$  unit-weight observations (including the case that there are  $w_i$  observations equal to  $y_i$  and the data have been summarized).

`lm` calls the lower level functions `lm.fit`, etc, see below, for the actual numerical computations. For programming only, you may consider doing likewise.

All of `weights`, `subset` and `offset` are evaluated in the same way as variables in `formula`, that is first in `data` and then in the environment of `formula`.

## Value

`lm` returns an object of class `"lm"` or for multiple responses of class `c("mlm", "lm")`.

The functions `summary` and `anova` are used to obtain and print a summary and analysis of variance table of the results. The generic accessor functions `coefficients`, `effects`, `fitted.values` and `residuals` extract various useful features of the value returned by `lm`.

An object of class `"lm"` is a list containing at least the following components:

`coefficients` a named vector of coefficients



<code>residuals</code>	the residuals, that is response minus fitted values.
<code>fitted.values</code>	the fitted mean values.
<code>rank</code>	the numeric rank of the fitted linear model.
<code>weights</code>	(only for weighted fits) the specified weights.
<code>df.residual</code>	the residual degrees of freedom.
<code>call</code>	the matched call.
<code>terms</code>	the <code>terms</code> object used.
<code>contrasts</code>	(only where relevant) the contrasts used.
<code>xlevels</code>	(only where relevant) a record of the levels of the factors used in fitting.
<code>offset</code>	the offset used (missing if none were used).
<code>y</code>	if requested, the response used.
<code>x</code>	if requested, the model matrix used.
<code>model</code>	if requested (the default), the model frame used.
<code>na.action</code>	(where relevant) information returned by <code>model.frame</code> on the special handling of NAs.

In addition, non-null fits will have components `assign`, `effects` and (unless not requested) `qr` relating to the linear fit, for use by extractor functions such as `summary` and `effects`.

### Using time series

Considerable care is needed when using `lm` with time series.

Unless `na.action = NULL`, the time series attributes are stripped from the variables before the regression is done. (This is necessary as omitting NAs would invalidate the time series attributes, and if NAs are omitted in the middle of the series the result would no longer be a regular time series.)

Even if the time series attributes are retained, they are not used to line up series, so that the time shift of a lagged or differenced regressor would be ignored. It is good practice to prepare a `data` argument by `ts.intersect(..., dframe = TRUE)`, then apply a suitable `na.action` to that data frame and call `lm` with `na.action = NULL` so that residuals and fitted values are time series.

### Note

Offsets specified by `offset` will not be included in predictions by `predict.lm`, whereas those specified by an offset term in the formula will be.

### Author(s)

The design was inspired by the S function of the same name described in Chambers (1992). The implementation of model formula by Ross Ihaka was based on Wilkinson & Rogers (1973).

### References

- Chambers, J. M. (1992) *Linear models*. Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.
- Wilkinson, G. N. and Rogers, C. E. (1973) Symbolic descriptions of factorial models for analysis of variance. *Applied Statistics*, **22**, 392–9.

**See Also**

[summary.lm](#) for summaries and [anova.lm](#) for the ANOVA table; [aov](#) for a different interface.

The generic functions [coef](#), [effects](#), [residuals](#), [fitted](#), [vcov](#).

[predict.lm](#) (via [predict](#)) for prediction, including confidence and prediction intervals; [confint](#) for confidence intervals of *parameters*.

[lm.influence](#) for regression diagnostics, and [glm](#) for **generalized** linear models.

The underlying low level functions, [lm.fit](#) for plain, and [lm.wfit](#) for weighted regression fitting.

More `lm()` examples are available e.g., in [anscombe](#), [attitude](#), [freeny](#), [LifeCycleSavings](#), [longley](#), [stackloss](#), [swiss](#).

`biglm` in package **biglm** for an alternative way to fit linear models to large datasets (especially those with many cases).

**Examples**

```
require(graphics)

## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.
ctl <- c(4.17,5.58,5.18,6.11,4.50,4.61,5.17,4.53,5.33,5.14)
trt <- c(4.81,4.17,4.41,3.59,5.87,3.83,6.03,4.89,4.32,4.69)
group <- gl(2,10,20, labels=c("Ctl","Trt"))
weight <- c(ctl, trt)
anova(lm.D9 <- lm(weight ~ group))
summary(lm.D90 <- lm(weight ~ group - 1))# omitting intercept
summary(resid(lm.D9) - resid(lm.D90)) #- residuals almost identical

opar <- par(mfrow = c(2,2), oma = c(0, 0, 1.1, 0))
plot(lm.D9, las = 1)      # Residuals, Fitted, ...
par(opar)

## model frame :
stopifnot(identical(lm(weight ~ group, method = "model.frame"),
                    model.frame(lm.D9)))

### less simple examples in "See Also" above
```

lm.fit

*Fitter Functions for Linear Models***Description**

These are the basic computing engines called by `lm` used to fit linear models. These should usually *not* be used directly unless by experienced users.

**Usage**

```
lm.fit(x, y,      offset = NULL, method = "qr", tol = 1e-7,
       singular.ok = TRUE, ...)
```

```
lm.wfit(x, y, w, offset = NULL, method = "qr", tol = 1e-7,
       singular.ok = TRUE, ...)
```

**Arguments**

<code>x</code>	design matrix of dimension $n * p$ .
<code>y</code>	vector of observations of length $n$ , or a matrix with $n$ rows.
<code>w</code>	vector of weights (length $n$ ) to be used in the fitting process for the <code>wfit</code> functions. Weighted least squares is used with weights $w$ , i.e., $\sum(w * e^2)$ is minimized.
<code>offset</code>	numeric of length $n$ ). This can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting.
<code>method</code>	currently, only <code>method="qr"</code> is supported.
<code>tol</code>	tolerance for the <code>qr</code> decomposition. Default is $1e-7$ .
<code>singular.ok</code>	logical. If <code>FALSE</code> , a singular model is an error.
<code>...</code>	currently disregarded.

**Value**

a list with components

<code>coefficients</code>	$p$ vector
<code>residuals</code>	$n$ vector or matrix
<code>fitted.values</code>	$n$ vector or matrix
<code>effects</code>	(not null fits) $n$ vector of orthogonal single-df effects. The first <code>rank</code> of them correspond to non-aliased coefficients, and are named accordingly.
<code>weights</code>	$n$ vector — <i>only</i> for the <code>*wfit*</code> functions.
<code>rank</code>	integer, giving the rank
<code>df.residual</code>	degrees of freedom of residuals
<code>qr</code>	(not null fits) the QR decomposition, see <code>qr</code> .

**See Also**

`lm` which you should use for linear least squares regression, unless you know better.

**Examples**

```
require(utils)

set.seed(129)
n <- 7 ; p <- 2
X <- matrix(rnorm(n * p), n,p) # no intercept!
y <- rnorm(n)
w <- rnorm(n)^2

str(lmw <- lm.wfit(x=X, y=y, w=w))

str(lm. <- lm.fit (x=X, y=y))
```

---

lm.influence                      *Regression Diagnostics*


---

### Description

This function provides the basic quantities which are used in forming a wide variety of diagnostics for checking the quality of regression fits.

### Usage

```
influence(model, ...)
## S3 method for class 'lm':
influence(model, do.coef = TRUE, ...)
## S3 method for class 'glm':
influence(model, do.coef = TRUE, ...)

lm.influence(model, do.coef = TRUE)
```

### Arguments

model	an object as returned by <code>lm</code> or <code>glm</code> .
do.coef	logical indicating if the changed coefficients (see below) are desired. These need $O(n^2p)$ computing time.
...	further arguments passed to or from other methods.

### Details

The `influence.measures()` and other functions listed in **See Also** provide a more user oriented way of computing a variety of regression diagnostics. These all build on `lm.influence`. Note that for GLMs (other than the Gaussian family with identity link) these are based on one-step approximations which may be inadequate if a case has high influence.

An attempt is made to ensure that computed hat values that are probably one are treated as one, and the corresponding rows in `sigma` and `coefficients` are NaN. (Dropping such a case would normally result in a variable being dropped, so it is not possible to give simple drop-one diagnostics.)

`naresid` is applied to the results and so will fill in with NAs if the fit had `na.action = na.exclude`.

### Value

A list containing the following components of the same length or number of rows  $n$ , which is the number of non-zero weights. Cases omitted in the fit are omitted unless a `na.action` method was used (such as `na.exclude`) which restores them.

hat	a vector containing the diagonal of the 'hat' matrix.
coefficients	(unless <code>do.coef</code> is false) a matrix whose $i$ -th row contains the change in the estimated coefficients which results when the $i$ -th case is dropped from the regression. Note that aliased coefficients are not included in the matrix.

<code>sigma</code>	a vector whose <i>i</i> -th element contains the estimate of the residual standard deviation obtained when the <i>i</i> -th case is dropped from the regression. (The approximations needed for GLMs can result in this being NaN.)
<code>wt.res</code>	a vector of <i>weighted</i> (or for class <code>glm</code> rather <i>deviance</i> ) residuals.

### Note

The coefficients returned by the R version of `lm.influence` differ from those computed by S. Rather than returning the coefficients which result from dropping each case, we return the changes in the coefficients. This is more directly useful in many diagnostic measures. Since these need  $O(n^2p)$  computing time, they can be omitted by `do.coef = FALSE`.

Note that cases with `weights == 0` are *dropped* (contrary to the situation in S).

If a model has been fitted with `na.action=na.exclude` (see `na.exclude`), cases excluded in the fit *are* considered here.

### References

See the list in the documentation for `influence.measures`.

Chambers, J. M. (1992) *Linear models*. Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

### See Also

`summary.lm` for `summary` and related methods;  
`influence.measures`,  
`hat` for the hat matrix diagonals,  
`dfbetas`, `dffits`, `covratio`, `cooks.distance`, `lm`.

### Examples

```
## Analysis of the life-cycle savings data
## given in Belsley, Kuh and Welsch.
summary(lm.SR <- lm(sr ~ pop15 + pop75 + dpi + ddpi,
                  data = LifeCycleSavings),
        corr = TRUE)
utils::str(lmI <- lm.influence(lm.SR))

## For more "user level" examples, use example(influence.measures)
```

### Description

All these functions are `methods` for class "lm" objects.

**Usage**

```
## S3 method for class 'lm':
family(object, ...)

## S3 method for class 'lm':
formula(x, ...)

## S3 method for class 'lm':
residuals(object,
           type = c("working", "response", "deviance", "pearson",
                   "partial"),
           ...)

## S3 method for class 'lm':
labels(object, ...)

weights(object, ...)
```

**Arguments**

`object`, `x`     an object inheriting from class `lm`, usually the result of a call to `lm` or `aov`.  
`...`            further arguments passed to or from other methods.  
`type`            the type of residuals which should be returned.

**Details**

The generic accessor functions `coef`, `effects`, `fitted` and `residuals` can be used to extract various useful features of the value returned by `lm`.

The `working` and `response` residuals are ‘observed - fitted’. The `deviance` and `pearson` residuals are weighted residuals, scaled by the square root of the weights used in fitting. The `partial` residuals are a matrix with each column formed by omitting a term from the model. In all these, zero weight cases are never omitted (as opposed to the standardized `rstudent` residuals, and the `weighted.residuals`).

How `residuals` treats cases with missing values in the original fit is determined by the `na.action` argument of that fit. If `na.action = na.omit` omitted cases will not appear in the residuals, whereas if `na.action = na.exclude` they will appear, with residual value `NA`. See also `naresid`.

The "`lm`" method for generic `labels` returns the term labels for estimable terms, that is the names of the terms with an least one estimable coefficient.

**References**

Chambers, J. M. (1992) *Linear models*. Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

The model fitting function `lm`, `anova.lm`.  
[coef](#), [deviance](#), [df.residual](#), [effects](#), [fitted](#), [glm](#) for **generalized** linear models, [influence](#) (etc on that page) for regression diagnostics, [weighted.residuals](#), [residuals](#), [residuals.glm](#), [summary.lm](#).

[influence.measures](#) for deletion diagnostics, including standardized ([rstandard](#)) and studentized ([rstudent](#)) residuals.

### Examples

```
##-- Continuing the lm(.) example:
coef(lm.D90) # the bare coefficients

## The 2 basic regression diagnostic plots [plot.lm(.) is preferred]
plot(resid(lm.D90), fitted(lm.D90)) # Tukey-Anscombe's
abline(h=0, lty=2, col = 'gray')

qqnorm(residuals(lm.D90))
```

---

loadings

*Print Loadings in Factor Analysis*

---

### Description

Extract or print loadings in factor analysis (or principal components analysis).

### Usage

```
loadings(x)

## S3 method for class 'loadings':
print(x, digits = 3, cutoff = 0.1, sort = FALSE, ...)

## S3 method for class 'factanal':
print(x, digits = 3, ...)
```

### Arguments

x	an object of class " <a href="#">factanal</a> " or " <a href="#">princomp</a> " or the loadings component of such an object.
digits	number of decimal places to use in printing uniquenesses and loadings.
cutoff	loadings smaller than this (in absolute value) are suppressed.
sort	logical. If true, the variables are sorted by their importance on each factor. Each variable with any loading larger than 0.5 (in modulus) is assigned to the factor with the largest loading, and the variables are printed in the order of the factor they are assigned to, then those unassigned.
...	further arguments for other methods.

### Details

'Loadings' is a term from *factor analysis*, but because factor analysis and principal component analysis (PCA) are often conflated in the social science literature, it was used for PCA by SPSS and hence by [princomp](#) in S-PLUS to help SPSS users.

Small loadings are conventionally not printed (replaced by spaces), to draw the eye to the pattern of the larger loadings.

The print method for class "[factanal](#)" calls the "loadings" method to print the loadings, and so passes down arguments such as `cutoff` and `sort`.

**See Also**

[factanal](#), [princomp](#)

---

 loess

*Local Polynomial Regression Fitting*


---

**Description**

Fit a polynomial surface determined by one or more numerical predictors, using local fitting.

**Usage**

```
loess(formula, data, weights, subset, na.action, model = FALSE,
      span = 0.75, enp.target, degree = 2,
      parametric = FALSE, drop.square = FALSE, normalize = TRUE,
      family = c("gaussian", "symmetric"),
      method = c("loess", "model.frame"),
      control = loess.control(...), ...)
```

**Arguments**

formula	a <a href="#">formula</a> specifying the numeric response and one to four numeric predictors (best specified via an interaction, but can also be specified additively). Will be coerced to a formula if necessary.
data	an optional data frame, list or environment (or object coercible by <a href="#">as.data.frame</a> to a data frame) containing the variables in the model. If not found in <code>data</code> , the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>loess</code> is called.
weights	optional weights for each case.
subset	an optional specification of a subset of the data to be used.
na.action	the action to be taken with missing values in the response or predictors. The default is given by <code>getOption("na.action")</code> .
model	should the model frame be returned?
span	the parameter $\alpha$ which controls the degree of smoothing.
enp.target	an alternative way to specify <code>span</code> , as the approximate equivalent number of parameters to be used.
degree	the degree of the polynomials to be used, normally 1 or 2. (Degree 0 is also allowed, but see the ‘Note’.)
parametric	should any terms be fitted globally rather than locally? Terms can be specified by name, number or as a logical vector of the same length as the number of predictors.
drop.square	for fits with more than one predictor and <code>degree=2</code> , should the quadratic term be dropped for particular predictors? Terms are specified in the same way as for <code>parametric</code> .
normalize	should the predictors be normalized to a common scale if there is more than one? The normalization used is to set the 10% trimmed standard deviation to one. Set to false for spatial coordinate predictors and others know to be a common scale.



family	if "gaussian" fitting is by least-squares, and if "symmetric" a re-descending M estimator is used with Tukey's biweight function.
method	fit the model or just extract the model frame.
control	control parameters: see <code>loess.control</code> .
...	control parameters can also be supplied directly.

### Details

Fitting is done locally. That is, for the fit at point  $x$ , the fit is made using points in a neighbourhood of  $x$ , weighted by their distance from  $x$  (with differences in 'parametric' variables being ignored when computing the distance). The size of the neighbourhood is controlled by  $\alpha$  (set by `span` or `enp.target`). For  $\alpha < 1$ , the neighbourhood includes proportion  $\alpha$  of the points, and these have tricubic weighting (proportional to  $(1 - (\text{dist}/\text{maxdist})^3)^3$ ). For  $\alpha > 1$ , all points are used, with the 'maximum distance' assumed to be  $\alpha^{1/p}$  times the actual maximum distance for  $p$  explanatory variables.

For the default family, fitting is by (weighted) least squares. For `family="symmetric"` a few iterations of an M-estimation procedure with Tukey's biweight are used. Be aware that as the initial value is the least-squares fit, this need not be a very resistant fit.

It can be important to tune the control list to achieve acceptable speed. See `loess.control` for details.

### Value

An object of class "loess".

### Note

As this is based on `cloess`, it is similar to but not identical to the `loess` function of S. In particular, conditioning is not implemented.

The memory usage of this implementation of `loess` is roughly quadratic in the number of points, with 1000 points taking about 10Mb.

`degree = 0`, local constant fitting, is allowed in this implementation but not documented in the reference. It seems very little tested, so use with caution.

### Author(s)

B. D. Ripley, based on the `cloess` package of Cleveland, Grosse and Shyu (currently available as `dloess` at <http://www.netlib.org/a>: the R implementation is based on an 1998 version).

### References

W. S. Cleveland, E. Grosse and W. M. Shyu (1992) Local regression models. Chapter 8 of *Statistical Models in S* eds J.M. Chambers and T.J. Hastie, Wadsworth & Brooks/Cole.

### See Also

`loess.control`, `predict.loess`.

`lowess`, the ancestor of `loess` (with different defaults!).

**Examples**

```
cars.lo <- loess(dist ~ speed, cars)
predict(cars.lo, data.frame(speed = seq(5, 30, 1)), se = TRUE)
# to allow extrapolation
cars.lo2 <- loess(dist ~ speed, cars,
  control = loess.control(surface = "direct"))
predict(cars.lo2, data.frame(speed = seq(5, 30, 1)), se = TRUE)
```

---

loess.control      *Set Parameters for Loess*

---

**Description**

Set control parameters for loess fits.

**Usage**

```
loess.control(surface = c("interpolate", "direct"),
  statistics = c("approximate", "exact"),
  trace.hat = c("exact", "approximate"),
  cell = 0.2, iterations = 4, ...)
```

**Arguments**

surface	should the fitted surface be computed exactly or via interpolation from a kd tree?
statistics	should the statistics be computed exactly or approximately? Exact computation can be very slow.
trace.hat	should the trace of the smoother matrix be computed exactly or approximately? It is recommended to use the approximation for more than about 1000 data points.
cell	if interpolation is used this controls the accuracy of the approximation via the maximum number of points in a cell in the kd tree. Cells with more than $\text{floor}(n \cdot \text{span} \cdot \text{cell})$ points are subdivided.
iterations	the number of iterations used in robust fitting.
...	further arguments which are ignored.

**Value**

A list with components

```
surface
statistics
trace.hat
cell
iterations
```

with meanings as explained under ‘Arguments’.

**See Also**

[loess](#)

Logistic

*The Logistic Distribution***Description**

Density, distribution function, quantile function and random generation for the logistic distribution with parameters `location` and `scale`.

**Usage**

```
dlogis(x, location = 0, scale = 1, log = FALSE)
plogis(q, location = 0, scale = 1, lower.tail = TRUE, log.p = FALSE)
qlogis(p, location = 0, scale = 1, lower.tail = TRUE, log.p = FALSE)
rlogis(n, location = 0, scale = 1)
```

**Arguments**

`x`, `q`            vector of quantiles.  
`p`                    vector of probabilities.  
`n`                    number of observations. If `length(n) > 1`, the length is taken to be the number required.  
`location`, `scale`    location and scale parameters.  
`log`, `log.p`        logical; if TRUE, probabilities `p` are given as `log(p)`.  
`lower.tail`        logical; if TRUE (default), probabilities are  $P[X \leq x]$ , otherwise,  $P[X > x]$ .

**Details**

If `location` or `scale` are omitted, they assume the default values of 0 and 1 respectively.

The Logistic distribution with `location` =  $\mu$  and `scale` =  $\sigma$  has distribution function

$$F(x) = \frac{1}{1 + e^{-(x-\mu)/\sigma}}$$

and density

$$f(x) = \frac{1}{\sigma} \frac{e^{(x-\mu)/\sigma}}{(1 + e^{(x-\mu)/\sigma})^2}$$

It is a long-tailed distribution with mean  $\mu$  and variance  $\pi^2/3\sigma^2$ .

**Value**

`dlogis` gives the density, `plogis` gives the distribution function, `qlogis` gives the quantile function, and `rlogis` generates random deviates.

**Note**

`qlogis(p)` is the same as the well known ‘*logit*’ function,  $\text{logit}(p) = \log p/(1 - p)$ , and `plogis(x)` has consequently been called the ‘inverse logit’.

The distribution function is a rescaled hyperbolic tangent, `plogis(x) == (1 + tanh(x/2)) / 2`, and it is called a *sigmoid function* in contexts such as neural networks.

**Source**

[dpr]logis are calculated directly from the definitions.  
rlogis uses inversion.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 2, chapter 23. Wiley, New York.

**Examples**

```
var(rlogis(4000, 0, scale = 5))# approximately (+/- 3)
pi^2/3 * 5^2
```

logLik

*Extract Log-Likelihood***Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which have methods for this function include: "glm", "lm", "nls", "Arima" and "gls", "lme" and others in package **nlme**.

**Usage**

```
logLik(object, ...)
```

```
## S3 method for class 'lm':
logLik(object, REML = FALSE, ...)
```

**Arguments**

object	any object from which a log-likelihood value, or a contribution to a log-likelihood value, can be extracted.
...	some methods for this generic function require additional arguments.
REML	an optional logical value. If TRUE the restricted log-likelihood is returned, else, if FALSE, the log-likelihood is returned. Defaults to FALSE.

**Details**

For a "glm" fit the `family` does not have to specify how to calculate the log-likelihood, so this is based on using the family's `aic()` function to compute the AIC. For the `gaussian`, `Gamma` and `inverse.gaussian` families it assumed that the dispersion of the GLM is estimated has been counted as a parameter in the AIC value, and for all other families it is assumed that the dispersion is known. Note that this procedure does not give the maximized likelihood for "glm" fits from the Gamma and inverse gaussian families, as the estimate of dispersion used is not the MLE.

For "lm" fits it is assumed that the scale has been estimated (by maximum likelihood or REML), and all the constants in the log-likelihood are included.

**Value**

Returns an object of class `logLik`. This is a number with at least one attribute, "df" (**d**egrees of **f**reedom), giving the number of (estimated) parameters in the model.

There is a simple `print` method for "logLik" objects.

There may be other attributes depending on the method used: see the appropriate documentation. One that is used by several methods is "nobs", the number of observations used in estimation (after the restrictions if `REML = TRUE`).

**Author(s)**

José Pinheiro and Douglas Bates

**References**

For `logLik.lm`:

Harville, D.A. (1974). Bayesian inference for variance components using only error contrasts. *Biometrika*, **61**, 383–385.

**See Also**

[logLik.gls](#), [logLik.lme](#), in package **nlme**, etc.

**Examples**

```
x <- 1:5
lmx <- lm(x ~ 1)
logLik(lmx) # using print.logLik() method
utils::str(logLik(lmx))

## lm method
(fm1 <- lm(rating ~ ., data = attitude))
logLik(fm1)
logLik(fm1, REML = TRUE)

utils::data(Orthodont, package="nlme")
fm1 <- lm(distance ~ Sex * age, Orthodont)
logLik(fm1)
logLik(fm1, REML = TRUE)
```

---

loglin

*Fitting Log-Linear Models*


---

**Description**

`loglin` is used to fit log-linear models to multidimensional contingency tables by Iterative Proportional Fitting.

**Usage**

```
loglin(table, margin, start = rep(1, length(table)), fit = FALSE,
       eps = 0.1, iter = 20, param = FALSE, print = TRUE)
```

**Arguments**

<code>table</code>	a contingency table to be fit, typically the output from <code>table</code> .
<code>margin</code>	a list of vectors with the marginal totals to be fit. (Hierarchical) log-linear models can be specified in terms of these marginal totals which give the 'maximal' factor subsets contained in the model. For example, in a three-factor model, <code>list(c(1, 2), c(1, 3))</code> specifies a model which contains parameters for the grand mean, each factor, and the 1-2 and 1-3 interactions, respectively (but no 2-3 or 1-2-3 interaction), i.e., a model where factors 2 and 3 are independent conditional on factor 1 (sometimes represented as '[12][13]'). The names of factors (i.e., <code>names(dimnames(table))</code> ) may be used rather than numeric indices.
<code>start</code>	a starting estimate for the fitted table. This optional argument is important for incomplete tables with structural zeros in <code>table</code> which should be preserved in the fit. In this case, the corresponding entries in <code>start</code> should be zero and the others can be taken as one.
<code>fit</code>	a logical indicating whether the fitted values should be returned.
<code>eps</code>	maximum deviation allowed between observed and fitted margins.
<code>iter</code>	maximum number of iterations.
<code>param</code>	a logical indicating whether the parameter values should be returned.
<code>print</code>	a logical. If <code>TRUE</code> , the number of iterations and the final deviation are printed.

**Details**

The Iterative Proportional Fitting algorithm as presented in Haberman (1972) is used for fitting the model. At most `iter` iterations are performed, convergence is taken to occur when the maximum deviation between observed and fitted margins is less than `eps`. All internal computations are done in double precision; there is no limit on the number of factors (the dimension of the table) in the model.

Assuming that there are no structural zeros, both the Likelihood Ratio Test and Pearson test statistics have an asymptotic chi-squared distribution with `df` degrees of freedom.

Note that the IPF steps are applied to the factors in the order given in `margin`. Hence if the model is decomposable and the order given in `margin` is a running intersection property ordering then IPF will converge in one iteration.

Package **MASS** contains `loglm`, a front-end to `loglin` which allows the log-linear model to be specified and fitted in a formula-based manner similar to that of other fitting functions such as `lm` or `glm`.

**Value**

A list with the following components.

<code>lrt</code>	the Likelihood Ratio Test statistic.
<code>pearson</code>	the Pearson test statistic (X-squared).
<code>df</code>	the degrees of freedom for the fitted model. There is no adjustment for structural zeros.
<code>margin</code>	list of the margins that were fit. Basically the same as the input <code>margin</code> , but with numbers replaced by names where possible.

<code>fit</code>	An array like <code>table</code> containing the fitted values. Only returned if <code>fit</code> is <code>TRUE</code> .
<code>param</code>	A list containing the estimated parameters of the model. The ‘standard’ constraints of zero marginal sums (e.g., zero row and column sums for a two factor parameter) are employed. Only returned if <code>param</code> is <code>TRUE</code> .

**Author(s)**

Kurt Hornik

**References**

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- Haberman, S. J. (1972) Log-linear fit for contingency tables—Algorithm AS51. *Applied Statistics*, **21**, 218–225.
- Agresti, A. (1990) *Categorical data analysis*. New York: Wiley.

**See Also**

[table](#).

[loglm](#) in package **MASS** for a user-friendly wrapper.

[glm](#) for another way to fit log-linear models.

**Examples**

```
## Model of joint independence of sex from hair and eye color.
fm <- loglin(HairEyeColor, list(c(1, 2), c(1, 3), c(2, 3)))
fm
1 - pchisq(fm$lrt, fm$df)
## Model with no three-factor interactions fits well.
```

---

Lognormal

*The Log Normal Distribution*


---

**Description**

Density, distribution function, quantile function and random generation for the log normal distribution whose logarithm has mean equal to `meanlog` and standard deviation equal to `sdlog`.

**Usage**

```
dlnorm(x, meanlog = 0, sdlog = 1, log = FALSE)
plnorm(q, meanlog = 0, sdlog = 1, lower.tail = TRUE, log.p = FALSE)
qlnorm(p, meanlog = 0, sdlog = 1, lower.tail = TRUE, log.p = FALSE)
rlnorm(n, meanlog = 0, sdlog = 1)
```

**Arguments**

<code>x, q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
<code>meanlog, sdlog</code>	mean and standard deviation of the distribution on the log scale with default values of 0 and 1 respectively.
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .

**Details**

The log normal distribution has density

$$f(x) = \frac{1}{\sqrt{2\pi}\sigma x} e^{-(\log(x)-\mu)^2/2\sigma^2}$$

where  $\mu$  and  $\sigma$  are the mean and standard deviation of the logarithm. The mean is  $E(X) = \exp(\mu + 1/2\sigma^2)$ , the median is  $med(X) = \exp(\mu)$ , and the variance  $Var(X) = \exp(2\mu + \sigma^2)(\exp(\sigma^2) - 1)$  and hence the coefficient of variation is  $\sqrt{\exp(\sigma^2) - 1}$  which is approximately  $\sigma$  when that is small (e.g.,  $\sigma < 1/2$ ).

**Value**

`dlnorm` gives the density, `plnorm` gives the distribution function, `qlnorm` gives the quantile function, and `rlnorm` generates random deviates.

**Note**

The cumulative hazard  $H(t) = -\log(1 - F(t))$  is `-plnorm(t, r, lower = FALSE, log = TRUE)`.

**Source**

`dlnorm` is calculated from the definition (in ‘Details’). `[pqr]lnorm` are based on the relationship to the normal.

**References**

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 1, chapter 14. Wiley, New York.

**See Also**

[dnorm](#) for the normal distribution.

**Examples**

```
dlnorm(1) == dnorm(0)
```



lowess

*Scatter Plot Smoothing***Description**

This function performs the computations for the *LOWESS* smoother which uses locally-weighted polynomial regression (see the references).

**Usage**

```
lowess(x, y = NULL, f = 2/3, iter = 3,
       delta = 0.01 * diff(range(xy$x[o])))
```

**Arguments**

<code>x</code> , <code>y</code>	vectors giving the coordinates of the points in the scatter plot. Alternatively a single plotting structure can be specified – see <a href="#">xy.coords</a> .
<code>f</code>	the smoother span. This gives the proportion of points in the plot which influence the smooth at each value. Larger values give more smoothness.
<code>iter</code>	the number of ‘robustifying’ iterations which should be performed. Using smaller values of <code>iter</code> will make <code>lowess</code> run faster.
<code>delta</code>	See ‘Details’. Defaults to 1/100th of the range of <code>x</code> .

**Details**

`lowess` is defined by a complex algorithm, the Ratfor original of which (by W. S. Cleveland) can be found in the R sources as file ‘`src/appl/lowess.doc`’. Normally a local linear polynomial fit is used, but under some circumstances (see the file) a local constant fit can be used. ‘Local’ is defined by the distance to the `floor(f*n)` th nearest neighbour, and tricubic weighting is used for `x` which fall within the neighbourhood.

The initial fit is done using weighted least squares. If `iter > 0`, further weighted fits are done using the product of the weights from the proximity of the `x` values and case weights derived from the residuals at the previous iteration. Specifically, the case weight is Tukey’s biweight, with cutoff 6 times the MAD of the residuals. (The current R implementation differs from the original in stopping iteration if the MAD is effectively zero since the algorithm is highly unstable in that case.)

`delta` is used to speed up computation: instead of computing the local polynomial fit at each data point it is not computed for points within `delta` of the last computed point, and linear interpolation is used to fill in the fitted values for the skipped points.

**Value**

`lowess` returns a list containing components `x` and `y` which give the coordinates of the smooth. The smooth can be added to a plot of the original points with the function `lines`: see the examples.

**References**

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- Cleveland, W. S. (1979) Robust locally weighted regression and smoothing scatterplots. *J. Amer. Statist. Assoc.* **74**, 829–836.

Cleveland, W. S. (1981) LOWESS: A program for smoothing scatterplots by robust locally weighted regression. *The American Statistician*, **35**, 54.

### See Also

`loess`, a newer formula based version of `lowess` (with different defaults!).

### Examples

```
require(graphics)

plot(cars, main = "lowess(cars)")
lines(lowess(cars), col = 2)
lines(lowess(cars, f=.2), col = 3)
legend(5, 120, c(paste("f = ", c("2/3", ".2"))), lty = 1, col = 2:3)
```

---

ls.diag

*Compute Diagnostics for 'lsfit' Regression Results*

---

### Description

Computes basic statistics, including standard errors, t- and p-values for the regression coefficients.

### Usage

```
ls.diag(ls.out)
```

### Arguments

ls.out            Typically the result of `lsfit()`

### Value

A list with the following numeric components.

std.dev	The standard deviation of the errors, an estimate of $\sigma$ .
hat	diagonal entries $h_{ii}$ of the hat matrix $H$
std.res	standardized residuals
stud.res	studentized residuals
cooks	Cook's distances
dfits	DFITS statistics
correlation	correlation matrix
std.err	standard errors of the regression coefficients
cov.scaled	Scaled covariance matrix of the coefficients
cov.unscaled	Unscaled covariance matrix of the coefficients

### References

Belsley, D. A., Kuh, E. and Welsch, R. E. (1980) *Regression Diagnostics*. New York: Wiley.

**See Also**

[hat](#) for the hat matrix diagonals, [ls.print](#), [lm.influence](#), [summary.lm](#), [anova](#).

**Examples**

```
##-- Using the same data as the lm(.) example:
lsD9 <- lsfit(x = as.numeric(gl(2, 10, 20)), y = weight)
dlsD9 <- ls.diag(lsD9)
utils::str(dlsD9, give.attr=FALSE)
abs(1 - sum(dlsD9$hat) / 2) < 10*.Machine$double.eps # sum(h.ii) = p
plot(dlsD9$hat, dlsD9$stud.res, xlim=c(0,0.11))
abline(h = 0, lty = 2, col = "lightgray")
```

---

ls.print

*Print 'lsfit' Regression Results*

---

**Description**

Computes basic statistics, including standard errors, t- and p-values for the regression coefficients and prints them if `print.it` is TRUE.

**Usage**

```
ls.print(ls.out, digits = 4, print.it = TRUE)
```

**Arguments**

<code>ls.out</code>	Typically the result of <code>lsfit()</code>
<code>digits</code>	The number of significant digits used for printing
<code>print.it</code>	a logical indicating whether the result should also be printed

**Value**

A list with the components

<code>summary</code>	The ANOVA table of the regression
<code>coef.table</code>	matrix with regression coefficients, standard errors, t- and p-values

**Note**

Usually you would use `summary(lm(...))` and `anova(lm(...))` to obtain similar output.

**See Also**

[ls.diag](#), [lsfit](#), also for examples; [lm](#), [lm.influence](#) which usually are preferable.

---

 lsfit

*Find the Least Squares Fit*


---

### Description

The least squares estimate of  $\beta$  in the model

$$Y = X\beta + \epsilon$$

is found.

### Usage

```
lsfit(x, y, wt = NULL, intercept = TRUE, tolerance = 1e-07,
      yname = NULL)
```

### Arguments

x	a matrix whose rows correspond to cases and whose columns correspond to variables.
y	the responses, possibly a matrix if you want to fit multiple left hand sides.
wt	an optional vector of weights for performing weighted least squares.
intercept	whether or not an intercept term should be used.
tolerance	the tolerance to be used in the matrix decomposition.
yname	names to be used for the response variables.

### Details

If weights are specified then a weighted least squares is performed with the weight given to the  $j$ th case specified by the  $j$ th entry in `wt`.

If any observation has a missing value in any field, that observation is removed before the analysis is carried out. This can be quite inefficient if there is a lot of missing data.

The implementation is via a modification of the LINPACK subroutines which allow for multiple left-hand sides.

### Value

A list with the following named components:

coef	the least squares estimates of the coefficients in the model ( $\beta$ as stated above).
residuals	residuals from the fit.
intercept	indicates whether an intercept was fitted.
qr	the QR decomposition of the design matrix.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`lm` which usually is preferable; `ls.print`, `ls.diag`.

**Examples**

```
##-- Using the same data as the lm(.) example:
lsD9 <- lsfit(x = unclass(gl(2,10)), y = weight)
ls.print(lsD9)
```

---

mad

---

*Median Absolute Deviation*


---

**Description**

Compute the median absolute deviation, i.e., the (lo-/hi-) median of the absolute deviations from the median, and (by default) adjust by a factor for asymptotically normal consistency.

**Usage**

```
mad(x, center = median(x), constant = 1.4826, na.rm = FALSE,
    low = FALSE, high = FALSE)
```

**Arguments**

<code>x</code>	a numeric vector.
<code>center</code>	Optionally, the centre: defaults to the median.
<code>constant</code>	scale factor.
<code>na.rm</code>	if TRUE then NA values are stripped from <code>x</code> before computation takes place.
<code>low</code>	if TRUE, compute the ‘lo-median’, i.e., for even sample size, do not average the two middle values, but take the smaller one.
<code>high</code>	if TRUE, compute the ‘hi-median’, i.e., take the larger of the two middle values for even sample size.

**Details**

The actual value calculated is `constant * cMedian(abs(x - center))` with the default value of `center` being `median(x)`, and `cMedian` being the usual, the ‘low’ or ‘high’ median, see the arguments description for `low` and `high` above.

The default `constant = 1.4826` (approximately  $1/\Phi^{-1}(\frac{3}{4}) = 1/\text{qnorm}(3/4)$ ) ensures consistency, i.e.,

$$E[\text{mad}(X_1, \dots, X_n)] = \sigma$$

for  $X_i$  distributed as  $N(\mu, \sigma^2)$  and large  $n$ .

If `na.rm` is TRUE then NA values are stripped from `x` before computation takes place. If this is not done then an NA value in `x` will cause `mad` to return NA.

**See Also**

`IQR` which is simpler but less robust, `median`, `var`.

**Examples**

```

mad(c(1:9))
print(mad(c(1:9), constant=1)) ==
      mad(c(1:8,100), constant=1) # = 2 ; TRUE
x <- c(1,2,3, 5,7,8)
sort(abs(x - median(x)))
c(mad(x, constant=1),
  mad(x, constant=1, low = TRUE),
  mad(x, constant=1, high = TRUE))

```

mahalanobis

*Mahalanobis Distance***Description**

Returns the squared Mahalanobis distance of all rows in `x` and the vector  $\mu = \text{center}$  with respect to  $\Sigma = \text{cov}$ . This is (for vector  $x$ ) defined as

$$D^2 = (x - \mu)' \Sigma^{-1} (x - \mu)$$

**Usage**

```

mahalanobis(x, center, cov, inverted=FALSE, ...)

```

**Arguments**

<code>x</code>	vector or matrix of data with, say, $p$ columns.
<code>center</code>	mean vector of the distribution or second data vector of length $p$ .
<code>cov</code>	covariance matrix ( $p \times p$ ) of the distribution.
<code>inverted</code>	logical. If TRUE, <code>cov</code> is supposed to contain the <i>inverse</i> of the covariance matrix.
<code>...</code>	passed to <code>solve</code> for computing the inverse of the covariance matrix (if <code>inverted</code> is false).

**See Also**

`cov`, `var`

**Examples**

```

require(graphics)

ma <- cbind(1:6, 1:3)
(S <- var(ma))
mahalanobis(c(0,0), 1:2, S)

x <- matrix(rnorm(100*3), ncol = 3)
stopifnot(mahalanobis(x, 0, diag(ncol(x))) == rowSums(x*x))
          # #- Here, D^2 = usual squared Euclidean distances

Sx <- cov(x)
D2 <- mahalanobis(x, colMeans(x), Sx)

```

```
plot(density(D2, bw=.5),
      main="Squared Mahalanobis distances, n=100, p=3") ; rug(D2)
qqplot(qchisq(ppoints(100), df=3), D2,
        main = expression("Q-Q plot of Mahalanobis" * ~D^2 *
                           " vs. quantiles of" * ~ chi[3]^2))
abline(0, 1, col = 'gray')
```

---

make.link

*Create a Link for GLM Families*


---

### Description

This function is used with the [family](#) functions in `glm()`. Given the name of a link, it returns a link function, an inverse link function, the derivative  $d\mu/d\eta$  and a function for domain checking.

### Usage

```
make.link(link)
```

### Arguments

`link` character; one of "logit", "probit", "cauchit", "cloglog", "identity", "log", "sqrt", "1/mu^2", "inverse".

### Value

A object of class "link-glm", a list with components

<code>linkfun</code>	Link function <code>function(mu)</code>
<code>linkinv</code>	Inverse link function <code>function(eta)</code>
<code>mu.eta</code>	Derivative function <code>function(eta) dμ/dη</code>
<code>valideta</code>	<code>function(eta) { TRUE if eta is in the domain of linkinv }</code> .
<code>name</code>	a name to be used for the link

.

### See Also

[power](#), [glm](#), [family](#).

### Examples

```
utils::str(make.link("logit"))
```

---

makepredictcall      *Utility Function for Safe Prediction*

---

### Description

A utility to help `model.frame.default` create the right matrices when predicting from models with terms like `poly` or `ns`.

### Usage

```
makepredictcall(var, call)
```

### Arguments

<code>var</code>	A variable.
<code>call</code>	The term in the formula, as a call.

### Details

This is a generic function with methods for `poly`, `bs` and `ns`: the default method handles `scale`. If `model.frame.default` encounters such a term when creating a model frame, it modifies the `predvars` attribute of the terms supplied by replacing the term with one which will work for predicting new data. For example `makepredictcall.ns` adds arguments for the knots and intercept.

To make use of this, have your model-fitting function return the `terms` attribute of the model frame, or copy the `predvars` attribute of the `terms` attribute of the model frame to your `terms` object.

To extend this, make sure the term creates variables with a class, and write a suitable method for that class.

### Value

A replacement for `call` for the `predvars` attribute of the terms.

### See Also

`model.frame`, `poly`, `scale`; `bs` and `ns` in package **splines**.  
`cars` for an example of prediction from a polynomial fit.

### Examples

```
require(graphics)

## using poly: this did not work in R < 1.5.0
fm <- lm(weight ~ poly(height, 2), data = women)
plot(women, xlab = "Height (in)", ylab = "Weight (lb)")
ht <- seq(57, 73, len = 200)
lines(ht, predict(fm, data.frame(height=ht)))

## see also example(cars)

## see bs and ns for spline examples.
```



---

`manova`*Multivariate Analysis of Variance*

---

**Description**

A class for the multivariate analysis of variance.

**Usage**

```
manova(...)
```

**Arguments**

... Arguments to be passed to [aov](#).

**Details**

Class "manova" differs from class "aov" in selecting a different `summary` method. Function `manova` calls [aov](#) and then add class "manova" to the result object for each stratum.

**Value**

See [aov](#) and the comments in ‘Details’ here.

**Note**

`manova` does not support multistratum analysis of variance, so the formula should not include an `Error` term.

**References**

Krzanowski, W. J. (1988) *Principles of Multivariate Analysis. A User's Perspective*. Oxford.

Hand, D. J. and Taylor, C. C. (1987) *Multivariate Analysis of Variance and Repeated Measures*. Chapman and Hall.

**See Also**

[aov](#), [summary.manova](#), the latter containing examples.

---

mantelhaen.test      *Cochran-Mantel-Haenszel Chi-Squared Test for Count Data*

---

### Description

Performs a Cochran-Mantel-Haenszel chi-squared test of the null that two nominal variables are conditionally independent in each stratum, assuming that there is no three-way interaction.

### Usage

```
mantelhaen.test(x, y = NULL, z = NULL,
                alternative = c("two.sided", "less", "greater"),
                correct = TRUE, exact = FALSE, conf.level = 0.95)
```

### Arguments

<code>x</code>	either a 3-dimensional contingency table in array form where each dimension is at least 2 and the last dimension corresponds to the strata, or a factor object with at least 2 levels.
<code>y</code>	a factor object with at least 2 levels; ignored if <code>x</code> is an array.
<code>z</code>	a factor object with at least 2 levels identifying to which stratum the corresponding elements in <code>x</code> and <code>y</code> belong; ignored if <code>x</code> is an array.
<code>alternative</code>	indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter. Only used in the 2 by 2 by $K$ case.
<code>correct</code>	a logical indicating whether to apply continuity correction when computing the test statistic. Only used in the 2 by 2 by $K$ case.
<code>exact</code>	a logical indicating whether the Mantel-Haenszel test or the exact conditional test (given the strata margins) should be computed. Only used in the 2 by 2 by $K$ case.
<code>conf.level</code>	confidence level for the returned confidence interval. Only used in the 2 by 2 by $K$ case.

### Details

If `x` is an array, each dimension must be at least 2, and the entries should be nonnegative integers. NA's are not allowed. Otherwise, `x`, `y` and `z` must have the same length. Triples containing NA's are removed. All variables must take at least two different values.

### Value

A list with class "htest" containing the following components:

<code>statistic</code>	Only present if no exact test is performed. In the classical case of a 2 by 2 by $K$ table (i.e., of dichotomous underlying variables), the Mantel-Haenszel chi-squared statistic; otherwise, the generalized Cochran-Mantel-Haenszel statistic.
<code>parameter</code>	the degrees of freedom of the approximate chi-squared distribution of the test statistic (1 in the classical case). Only present if no exact test is performed.
<code>p.value</code>	the p-value of the test.

conf.int	a confidence interval for the common odds ratio. Only present in the 2 by 2 by $K$ case.
estimate	an estimate of the common odds ratio. If an exact test is performed, the conditional Maximum Likelihood Estimate is given; otherwise, the Mantel-Haenszel estimate. Only present in the 2 by 2 by $K$ case.
null.value	the common odds ratio under the null of independence, 1. Only present in the 2 by 2 by $K$ case.
alternative	a character string describing the alternative hypothesis. Only present in the 2 by 2 by $K$ case.
method	a character string indicating the method employed, and whether or not continuity correction was used.
data.name	a character string giving the names of the data.

### Note

The asymptotic distribution is only valid if there is no three-way interaction. In the classical 2 by 2 by  $K$  case, this is equivalent to the conditional odds ratios in each stratum being identical. Currently, no inference on homogeneity of the odds ratios is performed.

See also the example below.

### References

Alan Agresti (1990). *Categorical data analysis*. New York: Wiley. Pages 230–235.

Alan Agresti (2002). *Categorical data analysis* (second edition). New York: Wiley.

### Examples

```
## Agresti (1990), pages 231--237, Penicillin and Rabbits
## Investigation of the effectiveness of immediately injected or 1.5
## hours delayed penicillin in protecting rabbits against a lethal
## injection with beta-hemolytic streptococci.
Rabbits <-
array(c(0, 0, 6, 5,
        3, 0, 3, 6,
        6, 2, 0, 4,
        5, 6, 1, 0,
        2, 5, 0, 0),
      dim = c(2, 2, 5),
      dimnames = list(
        Delay = c("None", "1.5h"),
        Response = c("Cured", "Died"),
        Penicillin.Level = c("1/8", "1/4", "1/2", "1", "4")))
Rabbits
## Classical Mantel-Haenszel test
mantelhaen.test(Rabbits)
## => p = 0.047, some evidence for higher cure rate of immediate
## injection
## Exact conditional test
mantelhaen.test(Rabbits, exact = TRUE)
## => p = 0.040
## Exact conditional test for one-sided alternative of a higher
## cure rate for immediate injection
mantelhaen.test(Rabbits, exact = TRUE, alternative = "greater")
```

```
## => p = 0.020

## UC Berkeley Student Admissions
mantelhaen.test(UCBAdmissions)
## No evidence for association between admission and gender
## when adjusted for department. However,
apply(UCBAdmissions, 3, function(x) (x[1,1]*x[2,2])/(x[1,2]*x[2,1]))
## This suggests that the assumption of homogeneous (conditional)
## odds ratios may be violated. The traditional approach would be
## using the Woolf test for interaction:
woolf <- function(x) {
  x <- x + 1 / 2
  k <- dim(x)[3]
  or <- apply(x, 3, function(x) (x[1,1]*x[2,2])/(x[1,2]*x[2,1]))
  w <- apply(x, 3, function(x) 1 / sum(1 / x))
  1 - pchisq(sum(w * (log(or) - weighted.mean(log(or), w)) ^ 2), k - 1)
}
woolf(UCBAdmissions)
## => p = 0.003, indicating that there is significant heterogeneity.
## (And hence the Mantel-Haenszel test cannot be used.)

## Agresti (2002), p. 287f and p. 297.
## Job Satisfaction example.
Satisfaction <-
  as.table(array(c(1, 2, 0, 0, 3, 3, 1, 2,
                  11, 17, 8, 4, 2, 3, 5, 2,
                  1, 0, 0, 0, 1, 3, 0, 1,
                  2, 5, 7, 9, 1, 1, 3, 6),
                dim = c(4, 4, 2),
                dimnames =
                  list(Income =
                     c("<5000", "5000-15000",
                       "15000-25000", ">25000"),
                     "Job Satisfaction" =
                     c("V_D", "L_S", "M_S", "V_S"),
                     Gender = c("Female", "Male"))))
## (Satisfaction categories abbreviated for convenience.)
ftable(. ~ Gender + Income, Satisfaction)
## Table 7.8 in Agresti (2002), p. 288.
mantelhaen.test(Satisfaction)
## See Table 7.12 in Agresti (2002), p. 297.
```

---

mauchly.test

*Mauchly's Test of Sphericity*


---

### Description

Tests whether a Wishart-distributed covariance matrix (or transformation thereof) is proportional to a given matrix.

### Usage

```
mauchly.test(object, ...)
## S3 method for class 'mlm':
```

```
mauchly.test(object,...)
## S3 method for class 'SSD':
mauchly.test(object, Sigma = diag(nrow = p),
  T = Thin.row(proj(M) - proj(X)), M = diag(nrow = p), X = ~0,
  idata = data.frame(index = seq_len(p)), ...)
```

### Arguments

object	object of class <code>SSD</code> or <code>mlm</code> .
Sigma	matrix to be proportional to.
T	transformation matrix. By default computed from <code>M</code> and <code>X</code> .
M	formula or matrix describing the outer projection (see below).
X	formula or matrix describing the inner projection (see below).
idata	data frame describing intra-block design.
...	arguments to be passed to or from other methods.

### Details

Mauchly's test test for whether a covariance matrix can be assumed to be proportional to a given matrix.

This is a generic function with methods for classes `"mlm"` and `"SSD"`.

The basic method is for objects of class `SSD` the method for `mlm` objects just extracts the `SSD` matrix and invokes the corresponding method with the same options and arguments.

The `T` argument is used to transform the observations prior to testing. This typically involves transformation to intra-block differences, but more complicated within-block designs can be encountered, making more elaborate transformations necessary. A matrix `T` can be given directly or specified as the difference between two projections onto the spaces spanned by `M` and `X`, which in turn can be given as matrices or as model formulas with respect to `idata` (the tests will be invariant to parametrization of the quotient space  $M/X$ ).

The common use of this test is in repeated measurements designs, with  $X \sim 1$ . This is almost, but not quite the same as testing for compound symmetry in the untransformed covariance matrix.

Notice that the defaults involve `p`, which is calculated internally as the dimension of the `SSD` matrix, and a couple of hidden functions in the `stats` name space, namely `proj` which calculates projection matrices from design matrices or model formulas and `Thin.row` which removes linearly dependent rows from a matrix until it has full row rank.

### Value

An object of class `"htest"`

### Note

The p-value differs slightly from that of SAS because a second order term is included in the asymptotic approximation in `R`.

### References

T. W. Anderson (1958). *An Introduction to Multivariate Statistical Analysis*. Wiley.

**See Also**

[SSD](#), [anova.mlm](#)

**Examples**

```
utils::example(SSD) # Brings in the mlmfit and reacttime objects

### traditional test of intrasubj. contrasts
mauchly.test(mlmfit, X=~1)

### tests using intra-subject 3x2 design
idata <- data.frame(deg=gl(3,1,6, labels=c(0,4,8)),
                    noise=gl(2,3,6, labels=c("A","P")))
mauchly.test(mlmfit, X = ~ deg + noise, idata = idata)
mauchly.test(mlmfit, M = ~ deg + noise, X = ~ noise, idata=idata)
```

---

mcnemar.test

*McNemar's Chi-squared Test for Count Data*


---

**Description**

Performs McNemar's chi-squared test for symmetry of rows and columns in a two-dimensional contingency table.

**Usage**

```
mcnemar.test(x, y = NULL, correct = TRUE)
```

**Arguments**

<code>x</code>	either a two-dimensional contingency table in matrix form, or a factor object.
<code>y</code>	a factor object; ignored if <code>x</code> is a matrix.
<code>correct</code>	a logical indicating whether to apply continuity correction when computing the test statistic.

**Details**

The null is that the probabilities of being classified into cells  $[i, j]$  and  $[j, i]$  are the same.

If `x` is a matrix, it is taken as a two-dimensional contingency table, and hence its entries should be nonnegative integers. Otherwise, both `x` and `y` must be vectors or factors of the same length. Incomplete cases are removed, vectors are coerced into factors, and the contingency table is computed from these.

Continuity correction is only used in the 2-by-2 case if `correct` is TRUE.

**Value**

A list with class "htest" containing the following components:

statistic	the value of McNemar's statistic.
parameter	the degrees of freedom of the approximate chi-squared distribution of the test statistic.
p.value	the p-value of the test.
method	a character string indicating the type of test performed, and whether continuity correction was used.
data.name	a character string giving the name(s) of the data.

**References**

Alan Agresti (1990). *Categorical data analysis*. New York: Wiley. Pages 350–354.

**Examples**

```
## Agresti (1990), p. 350.
## Presidential Approval Ratings.
## Approval of the President's performance in office in two surveys,
## one month apart, for a random sample of 1600 voting-age Americans.
Performance <-
matrix(c(794, 86, 150, 570),
       nrow = 2,
       dimnames = list("1st Survey" = c("Approve", "Disapprove"),
                       "2nd Survey" = c("Approve", "Disapprove")))
Performance
mcnemar.test(Performance)
## => significant change (in fact, drop) in approval ratings
```

---

median

*Median Value*

---

**Description**

Compute the sample median.

**Usage**

```
median(x, na.rm = FALSE)
```

**Arguments**

x	an object for which a method has been defined, or a numeric vector containing the values whose median is to be computed.
na.rm	a logical value indicating whether NA values should be stripped before the computation proceeds.

## Details

This is a generic function for which methods can be written. However, the default method makes use of `sort` and `mean` from package **base** both of which are generic, and so the default method will work for most classes (e.g. "`Date`") for which a median is a reasonable concept.

## Value

The default method returns a length-one object of the same type as `x`, except when `x` is integer of even length, when the result will be double.

If there are no values or if `na.rm = FALSE` and there are `NA` values the result is `NA` of the same type as `x` (or more generally the result of `x[FALSE][NA]`).

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[quantile](#) for general quantiles.

## Examples

```
median(1:4)# = 2.5 [even number]
median(c(1:3,100,1000))# = 3 [odd, robust]
```

---

medpolish

*Median Polish of a Matrix*

---

## Description

Fits an additive model using Tukey's *median polish* procedure.

## Usage

```
medpolish(x, eps = 0.01, maxiter = 10, trace.iter = TRUE,
          na.rm = FALSE)
```

## Arguments

<code>x</code>	a numeric matrix.
<code>eps</code>	real number greater than 0. A tolerance for convergence: see 'Details'.
<code>maxiter</code>	the maximum number of iterations
<code>trace.iter</code>	logical. Should progress in convergence be reported?
<code>na.rm</code>	logical. Should missing values be removed?



## Details

The model fitted is additive (constant + rows + columns). The algorithm works by alternately removing the row and column medians, and continues until the proportional reduction in the sum of absolute residuals is less than `eps` or until there have been `maxiter` iterations. The sum of absolute residuals is printed at each iteration of the fitting process, if `trace.iter` is TRUE. If `na.rm` is FALSE the presence of any NA value in `x` will cause an error, otherwise NA values are ignored.

`medpolish` returns an object of class `medpolish` (see below). There are printing and plotting methods for this class, which are invoked via by the generics `print` and `plot`.

## Value

An object of class `medpolish` with the following named components:

<code>overall</code>	the fitted constant term.
<code>row</code>	the fitted row effects.
<code>col</code>	the fitted column effects.
<code>residuals</code>	the residuals.
<code>name</code>	the name of the dataset.

## References

Tukey, J. W. (1977). *Exploratory Data Analysis*, Reading Massachusetts: Addison-Wesley.

## See Also

`median`; `ao` for a *mean* instead of *median* decomposition.

## Examples

```
require(graphics)

## Deaths from sport parachuting; from ABC of EDA, p.224:
deaths <-
  rbind(c(14,15,14),
        c( 7, 4, 7),
        c( 8, 2,10),
        c(15, 9,10),
        c( 0, 2, 0))
dimnames(deaths) <- list(c("1-24", "25-74", "75-199", "200++", "NA"),
                        paste(1973:1975))

deaths
(med.d <- medpolish(deaths))
plot(med.d)
## Check decomposition:
all(deaths ==
    med.d$overall + outer(med.d$row,med.d$col, "+") + med.d$residuals)
```

---

model.extract	<i>Extract Components from a Model Frame</i>
---------------	--

---

### Description

Returns the response, offset, subset, weights or other special components of a model frame passed as optional arguments to `model.frame`.

### Usage

```
model.extract(frame, component)
model.offset(x)
model.response(data, type = "any")
model.weights(x)
```

### Arguments

frame, x, data	A model frame.
component	literal character string or name. The name of a component to extract, such as "weights", "subset".
type	One of "any", "numeric", "double". Using either of latter two coerces the result to have storage mode "double".

### Details

`model.extract` is provided for compatibility with S, which does not have the more specific functions. It is also useful to extract e.g. the `etastart` and `mustart` components of a `glm` fit.

`model.offset` and `model.response` are equivalent to `model.extract(, "offset")` and `model.extract(, "response")` respectively. `model.offset` sums any terms specified by `offset` terms in the formula or by `offset` arguments in the call producing the model frame: it does check that the offset is numeric.

`model.weights` is slightly different from `model.frame(, "weights")` in not naming the vector it returns.

### Value

The specified component of the model frame, usually a vector.

### See Also

`model.frame`, `offset`

### Examples

```
a <- model.frame(cbind(ncases,ncontrols) ~ agegp+tobgp+alcgp, data=esoph)
model.extract(a, "response")
stopifnot(model.extract(a, "response") == model.response(a))

a <- model.frame(ncases/(ncases+ncontrols) ~ agegp+tobgp+alcgp,
                 data = esoph, weights = ncases+ncontrols)
```

```

model.response(a)
model.extract(a, "weights")

a <- model.frame(cbind(ncases, ncontrols) ~ agegp,
                 something = tobgp, data = esoph)
names(a)
stopifnot(model.extract(a, "something") == esoph$tobgp)

```

---

model.frame	<i>Extracting the “Environment” of a Model Formula</i>
-------------	--

---

## Description

`model.frame` (a generic function) and its methods return a `data.frame` with the variables needed to use `formula` and any `...` arguments.

## Usage

```

model.frame(formula, ...)

## Default S3 method:
model.frame(formula, data = NULL,
            subset = NULL, na.action = na.fail,
            drop.unused.levels = FALSE, xlev = NULL, ...)

## S3 method for class 'aovlist':
model.frame(formula, data = NULL, ...)

## S3 method for class 'glm':
model.frame(formula, ...)

## S3 method for class 'lm':
model.frame(formula, ...)

get_all_vars(formula, data, ...)

```

## Arguments

<code>formula</code>	a model <code>formula</code> or <code>terms</code> object or an R object.
<code>data</code>	a <code>data.frame</code> , list or environment (or object coercible by <code>as.data.frame</code> to a <code>data.frame</code> ), containing the variables in <code>formula</code> . Neither a matrix nor an array will be accepted.
<code>subset</code>	a specification of the rows to be used: defaults to all rows. This can be any valid indexing vector (see <code>[.data.frame]</code> ) for the rows of <code>data</code> or if that is not supplied, a data frame made up of the variables used in <code>formula</code> .
<code>na.action</code>	how NAs are treated. The default is first, any <code>na.action</code> attribute of <code>data</code> , second a <code>na.action</code> setting of <code>options</code> , and third <code>na.fail</code> if that is unset. The ‘factory-fresh’ default is <code>na.omit</code> . Another possible value is <code>NULL</code> .
<code>drop.unused.levels</code>	should factors have unused levels dropped? Defaults to <code>FALSE</code> .

xlev	a named list of character vectors giving the full set of levels to be assumed for each factor.
...	further arguments such as <code>data</code> , <code>na.action</code> , <code>subset</code> . Any additional arguments such as <code>offset</code> and <code>weights</code> which reach the default method are used to create further columns in the model frame, with parenthesised names such as <code>"(offset)"</code> .

## Details

Exactly what happens depends on the class and attributes of the object `formula`. If this is an object of fitted-model class such as `"lm"`, the method will either return the saved model frame used when fitting the model (if any, often selected by argument `model = TRUE`) or pass the call used when fitting on to the default method. The default method itself can cope with rather standard model objects such as those of class `"lqs"` from package **MASS** if no other arguments are supplied.

The rest of this section applies only to the default method.

If either `formula` or `data` is already a model frame (a data frame with a `"terms"` attribute) and the other is missing, the model frame is returned. Unless `formula` is a terms object, `as.formula` and then `terms` is called on it. (If you wish to use the `keep.order` argument of `terms.formula`, pass a terms object rather than a formula.)

Row names for the model frame are taken from the `data` argument if present, then from the names of the response in the formula (or `rownames` if it is a matrix), if there is one.

All the variables in `formula`, `subset` and in `...` are looked for first in `data` and then in the environment of `formula` (see the help for `formula()` for further details) and collected into a data frame. Then the `subset` expression is evaluated, and it is used as a row index to the data frame. Then the `na.action` function is applied to the data frame (and may well add attributes). The levels of any factors in the data frame are adjusted according to the `drop.unused.levels` and `xlev` arguments: if `xlev` specifies a factor and a character variable is found, it is converted to a factor (as from R 2.10.0).

Unless `na.action = NULL`, time-series attributes will be removed from the variables found (since they will be wrong if NAs are removed).

Note that *all* the variables in the formula are included in the data frame, even those preceded by `-`.

Only variables whose type is raw, logical, integer, real, complex or character can be included in a model frame: this includes classed variables such as factors (whose underlying type is integer), but excludes lists.

`get_all_vars` returns a `data.frame` containing the variables used in `formula` plus those specified `...`. Unlike `model.frame.default`, it returns the input variables and not those resulting from function calls in `formula`.

## Value

A `data.frame` containing the variables used in `formula` plus those specified in `...`. It will have additional attributes, including `"terms"` for an object of class `"terms"` derived from `formula`, and possibly `"na.action"` giving information on the handling of NAs (which will not be present if no special handling was done, e.g. by `na.pass`).

## References

Chambers, J. M. (1992) *Data for models*. Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

`model.matrix` for the ‘design matrix’, `formula` for formulas and `expand.model.frame` for model.frame manipulation.

**Examples**

```
data.class(model.frame(dist ~ speed, data = cars))
```

---

model.matrix                      *Construct Design Matrices*

---

**Description**

`model.matrix` creates a design matrix.

**Usage**

```
model.matrix(object, ...)

## Default S3 method:
model.matrix(object, data = environment(object),
             contrasts.arg = NULL, xlev = NULL, ...)
```

**Arguments**

<code>object</code>	an object of an appropriate class. For the default method, a model <a href="#">formula</a> or a <a href="#">terms</a> object.
<code>data</code>	a data frame created with <code>model.frame</code> . If another sort of object, <code>model.frame</code> is called first.
<code>contrasts.arg</code>	A list, whose entries are values (numeric matrices or character strings naming functions) to be used as replacement values for the <code>contrasts</code> replacement function and whose names are the names of columns of <code>data</code> containing <a href="#">factors</a> .
<code>xlev</code>	to be used as argument of <code>model.frame</code> if <code>data</code> has no "terms" attribute.
<code>...</code>	further arguments passed to or from other methods.

**Details**

`model.matrix` creates a design matrix from the description given in `terms(object)`, using the data in `data` which must supply variables with the same names as would be created by a call to `model.frame(object)` or, more precisely, by evaluating `attr(terms(object), "variables")`. If `data` is a data frame, there may be other columns and the order of columns is not important. Any character variables are coerced to factors, with a warning. After coercion, all the variables used on the right-hand side of the formula must be logical, integer, numeric or factor.

If `contrasts.arg` is specified for a factor it overrides the default factor coding for that variable and any "contrasts" attribute set by `C` or `contrasts`.

In an interaction term, the variable whose levels vary fastest is the first one to appear in the formula (and not in the term), so in `~ a + b + b:a` the interaction will have `a` varying fastest.

By convention, if the response variable also appears on the right-hand side of the formula it is dropped (with a warning), although interactions involving the term are retained.

**Value**

The design matrix for a regression model with the specified formula and data.

There is an attribute "assign", an integer vector with an entry for each column in the matrix giving the term in the formula which gave rise to the column. Value 0 corresponds to the intercept (if any), and positive values to terms in the order given by the `terms.labels` attribute of the `terms` structure corresponding to `object`.

If there are any factors in terms in the model, there is an attribute "contrasts", a named list with an entry for each factor. This specifies the contrasts that would be used in terms in which the factor is coded by contrasts (in some terms dummy coding may be used), either as a character vector naming a function or as a numeric matrix.

**References**

Chambers, J. M. (1992) *Data for models*. Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

`model.frame`, `model.extract`, `terms`

**Examples**

```
ff <- log(Volume) ~ log(Height) + log(Girth)
utils::str(m <- model.frame(ff, trees))
mat <- model.matrix(ff, m)

dd <- data.frame(a = gl(3,4), b = gl(4,1,12)) # balanced 2-way
options("contrasts")
model.matrix(~ a + b, dd)
model.matrix(~ a + b, dd, contrasts = list(a="contr.sum"))
model.matrix(~ a + b, dd, contrasts = list(a="contr.sum", b="contr.poly"))
m.orth <- model.matrix(~a+b, dd, contrasts = list(a="contr.helmert"))
crossprod(m.orth) # m.orth is ALMOST orthogonal
```

---

model.tables

*Compute Tables of Results from an Aov Model Fit*

---

**Description**

Computes summary tables for model fits, especially complex aov fits.

**Usage**

```
model.tables(x, ...)

## S3 method for class 'aov':
model.tables(x, type = "effects", se = FALSE, cterms, ...)

## S3 method for class 'aovlist':
model.tables(x, type = "effects", se = FALSE, ...)
```

**Arguments**

x	a model object, usually produced by <code>aov</code>
type	type of table: currently only "effects" and "means" are implemented.
se	should standard errors be computed?
cterm	A character vector giving the names of the terms for which tables should be computed. The default is all tables.
...	further arguments passed to or from other methods.

**Details**

For `type = "effects"` give tables of the coefficients for each term, optionally with standard errors.

For `type = "means"` give tables of the mean response for each combinations of levels of the factors in a term.

The "aov" method cannot be applied to components of a "aovlist" fit.

**Value**

An object of class "tables.aov", as list which may contain components

tables	A list of tables for each requested term.
n	The replication information for each term.
se	Standard error information.

**Warning**

The implementation is incomplete, and only the simpler cases have been tested thoroughly.

Weighted `aov` fits are not supported.

**See Also**

[aov](#), [proj](#), [replications](#), [TukeyHSD](#), [se.contrast](#)

**Examples**

```
## From Venables and Ripley (2002) p.165.
N <- c(0,1,0,1,1,1,0,0,0,1,1,0,1,1,0,0,1,0,0,1,0,1,0,1,1,0,0)
P <- c(1,1,0,0,0,1,0,1,1,1,0,0,0,1,0,1,1,0,0,1,0,1,0,1,1,0)
K <- c(1,0,0,1,0,1,1,0,0,1,0,1,0,1,1,0,0,0,1,1,0,0,0,1,1,0,1,0)
yield <- c(49.5,62.8,46.8,57.0,59.8,58.5,55.5,56.0,62.8,55.8,69.5,
55.0, 62.0,48.8,45.5,44.2,52.0,51.5,49.8,48.8,57.2,59.0,53.2,56.0)

npk <- data.frame(block=gl(6,4), N=factor(N), P=factor(P),
                  K=factor(K), yield=yield)
options(contrasts=c("contr.helmert", "contr.treatment"))
npk.aov <- aov(yield ~ block + N*P*K, npk)
model.tables(npk.aov, "means", se = TRUE)

## as a test, not particularly sensible statistically
npk.aovE <- aov(yield ~ N*P*K + Error(block), npk)
model.tables(npk.aovE, se=TRUE)
model.tables(npk.aovE, "means")
```

---

 monthplot

*Plot a Seasonal or other Subseries from a Time Series*


---

### Description

These functions plot seasonal (or other) subseries of a time series. For each season (or other category), a time series is plotted.

### Usage

```
monthplot(x, ...)

## S3 method for class 'stl':
monthplot(x, labels = NULL, ylab = choice, choice = "seasonal",
          ...)

## S3 method for class 'StructTS':
monthplot(x, labels = NULL, ylab = choice, choice = "sea", ...)

## S3 method for class 'ts':
monthplot(x, labels = NULL, times = time(x), phase = cycle(x),
          ylab = deparse(substitute(x)), ...)

## Default S3 method:
monthplot(x, labels = 1L:12L,
          ylab = deparse(substitute(x)),
          times = seq_along(x),
          phase = (times - 1L)%%length(labels) + 1L, base = mean,
          axes = TRUE, type = c("l", "h"), box = TRUE,
          add = FALSE, ...)
```

### Arguments

x	Time series or related object.
labels	Labels to use for each 'season'.
ylab	y label.
times	Time of each observation.
phase	Indicator for each 'season'.
base	Function to use for reference line for subseries.
choice	Which series of an stl or StructTS object?
...	Arguments to be passed to the default method or graphical parameters.
axes	Should axes be drawn (ignored if add=TRUE)?
type	Type of plot. The default is to join the points with lines, and "h" is for histogram-like vertical lines.
box	Should a box be drawn (ignored if add=TRUE)?
add	Should thus just add on an existing plot.



## Details

These functions extract subseries from a time series and plot them all in one frame. The `ts`, `stl`, and `StructTS` methods use the internally recorded frequency and start and finish times to set the scale and the seasons. The default method assumes observations come in groups of 12 (though this can be changed).

If the `labels` are not given but the `phase` is given, then the `labels` default to the unique values of the `phase`. If both are given, then the `phase` values are assumed to be indices into the `labels` array, i.e., they should be in the range from 1 to `length(labels)`.

## Value

These functions are executed for their side effect of drawing a seasonal subseries plot on the current graphical window.

## Author(s)

Duncan Murdoch

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

`ts`, `stl`, `StructTS`

## Examples

```
require(graphics)

## The CO2 data
fit <- stl(log(co2), s.window = 20, t.window = 20)
plot(fit)
op <- par(mfrow = c(2,2))
monthplot(co2, ylab = "data", cex.axis = 0.8)
monthplot(fit, choice = "seasonal", cex.axis = 0.8)
monthplot(fit, choice = "trend", cex.axis = 0.8)
monthplot(fit, choice = "remainder", type = "h", cex.axis = 0.8)
par(op)

## The CO2 data, grouped quarterly
quarter <- (cycle(co2) - 1) %/% 3
monthplot(co2, phase = quarter)

## see also JohnsonJohnson
```

---

mood.test *Mood Two-Sample Test of Scale*


---

### Description

Performs Mood's two-sample test for a difference in scale parameters.

### Usage

```
mood.test(x, ...)

## Default S3 method:
mood.test(x, y,
          alternative = c("two.sided", "less", "greater"), ...)

## S3 method for class 'formula':
mood.test(formula, data, subset, na.action, ...)
```

### Arguments

<code>x, y</code>	numeric vectors of data values.
<code>alternative</code>	indicates the alternative hypothesis and must be one of "two.sided" (default), "greater" or "less" all of which can be abbreviated.
<code>formula</code>	a formula of the form <code>lhs ~ rhs</code> where <code>lhs</code> is a numeric variable giving the data values and <code>rhs</code> a factor with two levels giving the corresponding groups.
<code>data</code>	an optional matrix or data frame (or similar: see <code>model.frame</code> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>subset</code>	an optional vector specifying a subset of observations to be used.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. Defaults to <code>getOption("na.action")</code> .
<code>...</code>	further arguments to be passed to or from methods.

### Details

The underlying model is that the two samples are drawn from  $f(x-l)$  and  $f((x-l)/s)/s$ , respectively, where  $l$  is a common location parameter and  $s$  is a scale parameter.

The null hypothesis is  $s = 1$ .

There are more useful tests for this problem.

In the case of ties, the formulation of Mielke (1967) is employed.

### Value

A list with class "htest" containing the following components:

<code>statistic</code>	the value of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>alternative</code>	a character string describing the alternative hypothesis.
<code>method</code>	the character string "Mood two-sample test of scale".
<code>data.name</code>	a character string giving the names of the data.

## References

William J. Conover (1971), *Practical nonparametric statistics*. New York: John Wiley & Sons. Pages 234f.

Paul W. Mielke, Jr. (1967), Note on some squared rank tests with existing ties. *Technometrics*, **9/2**, 312–314.

## See Also

`fligner.test` for a rank-based (nonparametric) k-sample test for homogeneity of variances; `ansari.test` for another rank-based two-sample test for a difference in scale parameters; `var.test` and `bartlett.test` for parametric tests for the homogeneity in variance.

## Examples

```
## Same data as for the Ansari-Bradley test:
## Serum iron determination using Hyland control sera
ramsay <- c(111, 107, 100, 99, 102, 106, 109, 108, 104, 99,
           101, 96, 97, 102, 107, 113, 116, 113, 110, 98)
jung.parekh <- c(107, 108, 106, 98, 105, 103, 110, 105, 104,
               100, 96, 108, 103, 104, 114, 114, 113, 108, 106, 99)
mood.test(ramsay, jung.parekh)
## Compare this to ansari.test(ramsay, jung.parekh)
```

---

Multinom

*The Multinomial Distribution*

---

## Description

Generate multinomially distributed random number vectors and compute multinomial probabilities.

## Usage

```
rmultinom(n, size, prob)
dmultinom(x, size = NULL, prob, log = FALSE)
```

## Arguments

<code>x</code>	vector of length $K$ of integers in $0 : \text{size}$ .
<code>n</code>	number of random vectors to draw.
<code>size</code>	integer, say $N$ , specifying the total number of objects that are put into $K$ boxes in the typical multinomial experiment. For <code>dmultinom</code> , it defaults to $\text{sum}(x)$ .
<code>prob</code>	numeric non-negative vector of length $K$ , specifying the probability for the $K$ classes; is internally normalized to sum 1.
<code>log</code>	logical; if TRUE, log probabilities are computed.

**Details**

If  $\mathbf{x}$  is a  $K$ -component vector, `dmultinom(x, prob)` is the probability

$$P(X_1 = x_1, \dots, X_K = x_k) = C \times \prod_{j=1}^K \pi_j^{x_j}$$

where  $C$  is the ‘multinomial coefficient’  $C = N!/(x_1! \cdots x_K!)$  and  $N = \sum_{j=1}^K x_j$ .

By definition, each component  $X_j$  is binomially distributed as `Bin(size, prob[j])` for  $j = 1, \dots, K$ .

The `rmultinom()` algorithm draws binomials  $X_j$  from  $Bin(n_j, P_j)$  sequentially, where  $n_1 = N$  ( $N := \text{size}$ ),  $P_1 = \pi_1$  ( $\pi$  is `prob` scaled to sum 1), and for  $j \geq 2$ , recursively,  $n_j = N - \sum_{k=1}^{j-1} X_k$  and  $P_j = \pi_j / (1 - \sum_{k=1}^{j-1} \pi_k)$ .

**Value**

For `rmultinom()`, an integer  $K \times n$  matrix where each column is a random vector generated according to the desired multinomial law, and hence summing to `size`. Whereas the *transposed* result would seem more natural at first, the returned matrix is more efficient because of columnwise storage.

**Note**

`dmultinom` is currently *not vectorized* at all and has no C interface (API); this may be amended in the future.

**See Also**

[rbinom](#) which is a special case conceptually.

**Examples**

```
rmultinom(10, size = 12, prob=c(0.1,0.2,0.8))

pr <- c(1,3,6,10) # normalization not necessary for generation
rmultinom(10, 20, prob = pr)

## all possible outcomes of Multinom(N = 3, K = 3)
X <- t(as.matrix(expand.grid(0:3, 0:3))); X <- X[, colSums(X) <= 3]
X <- rbind(X, 3:3 - colSums(X)); dimnames(X) <- list(letters[1:3], NULL)
X
round(apply(X, 2, function(x) dmultinom(x, prob = c(1,2,5))), 3)
```

---

na.action

NA Action

---

**Description**

Extract information on the NA action used to create an object.

**Usage**

```
na.action(object, ...)
```

**Arguments**

`object` any object whose NA action is given.  
`...` further arguments special methods could require.

**Details**

`na.action` is a generic function, and `na.action.default` its default method. The latter extracts the "`na.action`" component of a list if present, otherwise the "`na.action`" attribute.

When `model.frame` is called, it records any information on NA handling in a "`na.action`" attribute. Most model-fitting functions return this as a component of their result.

**Value**

Information from the action which was applied to `object` if NAs were handled specially, or NULL.

**References**

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

**See Also**

`options("na.action")`, `na.omit`, `na.fail`, also for `na.exclude`, `na.pass`.

**Examples**

```
na.action(na.omit(c(1, NA)))
```

---

`na.contiguous` *Find Longest Contiguous Stretch of non-NAs*

---

**Description**

Find the longest consecutive stretch of non-missing values in a time series object. (In the event of a tie, the first such stretch.)

**Usage**

```
na.contiguous(object, ...)
```

**Arguments**

`object` a univariate or multivariate time series.  
`...` further arguments passed to or from other methods.

**Value**

A time series without missing values. The class of `object` will be preserved.

**See Also**

`na.omit` and `na.omit.ts`; `na.fail`

## Examples

```
na.contiguous(presidents)
```

---

na.fail

*Handle Missing Values in Objects*

---

## Description

These generic functions are useful for dealing with [NAs](#) in e.g., data frames. `na.fail` returns the object if it does not contain any missing values, and signals an error otherwise. `na.omit` returns the object with incomplete cases removed. `na.pass` returns the object unchanged.

## Usage

```
na.fail(object, ...)  
na.omit(object, ...)  
na.exclude(object, ...)  
na.pass(object, ...)
```

## Arguments

<code>object</code>	an R object, typically a data frame
<code>...</code>	further arguments special methods could require.

## Details

At present these will handle vectors, matrices and data frames comprising vectors and matrices (only).

If `na.omit` removes cases, the row numbers of the cases form the "`na.action`" attribute of the result, of class "omit".

`na.exclude` differs from `na.omit` only in the class of the "`na.action`" attribute of the result, which is "exclude". This gives different behaviour in functions making use of `naresid` and `napredict`: when `na.exclude` is used the residuals and predictions are padded to the correct length by inserting NAs for cases omitted by `na.exclude`.

## References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

## See Also

`na.action`; `options` with argument `na.action` for setting NA actions; and `lm` and `glm` for functions using these. `na.contiguous` as alternative for time series.

**Examples**

```
DF <- data.frame(x = c(1, 2, 3), y = c(0, 10, NA))
na.omit(DF)
m <- as.matrix(DF)
na.omit(m)
stopifnot(all(na.omit(1:3) == 1:3)) # does not affect objects with no NA's
try(na.fail(DF))#> Error: missing values in ...

options("na.action")
```

---

`naprint`*Adjust for Missing Values*

---

**Description**

Use missing value information to report the effects of an `na.action`.

**Usage**

```
naprint(x, ...)
```

**Arguments**

`x` An object produced by an `na.action` function.  
`...` further arguments passed to or from other methods.

**Details**

This is a generic function, and the exact information differs by method. `naprint.omit` reports the number of rows omitted: `naprint.default` reports an empty string.

**Value**

A character string providing information on missing values, for example the number.

---

`naresid`*Adjust for Missing Values*

---

**Description**

Use missing value information to adjust residuals and predictions.

**Usage**

```
naresid(omit, x, ...)
napredict(omit, x, ...)
```

**Arguments**

<code>omit</code>	an object produced by an <code>na.action</code> function, typically the <code>"na.action"</code> attribute of the result of <code>na.omit</code> or <code>na.exclude</code> .
<code>x</code>	a vector, data frame, or matrix to be adjusted based upon the missing value information.
<code>...</code>	further arguments passed to or from other methods.

**Details**

These are utility functions used to allow `predict`, `fitted` and `residuals` methods for modelling functions to compensate for the removal of NAs in the fitting process. They are used by the default, `"lm"`, `"glm"` and `"nls"` methods, and by further methods in packages **MASS**, **rpart** and **survival**. Also used for the scores returned by `factanal`, `prcomp` and `princomp`.

The default methods do nothing. The default method for the `na.exclude` action is to pad the object with NAs in the correct positions to have the same number of rows as the original data frame.

Currently `naresid` and `napredict` are identical, but future methods need not be. `naresid` is used for residuals, and `napredict` for fitted values and predictions.

**Value**

These return a similar object to `x`.

**Note**

Packages `rpart` and `survival5` used to contain versions of these functions that had an `na.omit` action equivalent to that now used for `na.exclude`.

---

 NegBinomial

*The Negative Binomial Distribution*


---

**Description**

Density, distribution function, quantile function and random generation for the negative binomial distribution with parameters `size` and `prob`.

**Usage**

```
dnbinom(x, size, prob, mu, log = FALSE)
pnbinom(q, size, prob, mu, lower.tail = TRUE, log.p = FALSE)
qnbinom(p, size, prob, mu, lower.tail = TRUE, log.p = FALSE)
rnbinom(n, size, prob, mu)
```

**Arguments**

<code>x</code>	vector of (non-negative integer) quantiles.
<code>q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.



<code>size</code>	target for number of successful trials, or dispersion parameter (the shape parameter of the gamma mixing distribution). Must be strictly positive, need not be integer.
<code>prob</code>	probability of success in each trial. $0 < \text{prob} \leq 1$ .
<code>mu</code>	alternative parametrization via mean: see 'Details'.
<code>log, log.p</code>	logical; if TRUE, probabilities $p$ are given as $\log(p)$ .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .

### Details

The negative binomial distribution with `size =  $n$`  and `prob =  $p$`  has density

$$p(x) = \frac{\Gamma(x+n)}{\Gamma(n)x!} p^n (1-p)^x$$

for  $x = 0, 1, 2, \dots, n > 0$  and  $0 < p \leq 1$ .

This represents the number of failures which occur in a sequence of Bernoulli trials before a target number of successes is reached.

A negative binomial distribution can arise as a mixture of Poisson distributions with mean distributed as a gamma distribution (see [pgamma](#)) with scale parameter  $(1 - \text{prob})/\text{prob}$  and shape parameter `size`. (This definition allows non-integer values of `size`.) In this model `prob =  $1/(1+\text{size})$` , and the mean is `size *  $(1 - \text{prob})/\text{prob}$` .

The alternative parametrization (often used in ecology) is by the *mean* `mu`, and `size`, the *dispersion parameter*, where `prob =  $\text{size}/(\text{size}+\text{mu})$` . The variance is `mu +  $\text{mu}^2/\text{size}$`  in this parametrization or  `$n(1-p)/p^2$`  in the first one.

If an element of `x` is not integer, the result of `dnbinom` is zero, with a warning.

The quantile is defined as the smallest value  $x$  such that  $F(x) \geq p$ , where  $F$  is the distribution function.

### Value

`dnbinom` gives the density, `pnbinom` gives the distribution function, `qnbinom` gives the quantile function, and `rnbinom` generates random deviates.

Invalid `size` or `prob` will result in return value NaN, with a warning.

### Source

`dnbinom` computes via binomial probabilities, using code contributed by Catherine Loader (see [dbinom](#)).

`pnbinom` uses [pbeta](#).

`qnbinom` uses the Cornish–Fisher Expansion to include a skewness correction to a normal approximation, followed by a search.

`rnbinom` uses the derivation as a gamma mixture of Poissons, see

Devroye, L. (1986) *Non-Uniform Random Variate Generation*. Springer-Verlag, New York. Page 480.

### See Also

[dbinom](#) for the binomial, [dpois](#) for the Poisson and [dgeom](#) for the geometric distribution, which is a special case of the negative binomial.

**Examples**

```

require(graphics)
x <- 0:11
dnbinom(x, size = 1, prob = 1/2) * 2^(1 + x) # == 1
126 / dnbinom(0:8, size = 2, prob = 1/2) #- theoretically integer

## Cumulative ('p') = Sum of discrete prob.s ('d'); Relative error :
summary(1 - cumsum(dnbinom(x, size = 2, prob = 1/2)) /
        pnbinom(x, size = 2, prob = 1/2))

x <- 0:15
size <- (1:20)/4
persp(x,size, dnb <- outer(x, size, function(x,s) dnbinom(x,s, prob= 0.4)),
      xlab = "x", ylab = "s", zlab="density", theta = 150)
title(tit <- "negative binomial density(x,s, pr = 0.4) vs. x & s")

image (x,size, log10(dnb), main= paste("log [",tit,"]")
contour(x,size, log10(dnb),add=TRUE)

## Alternative parametrization
x1 <- rnbinom(500, mu = 4, size = 1)
x2 <- rnbinom(500, mu = 4, size = 10)
x3 <- rnbinom(500, mu = 4, size = 100)
h1 <- hist(x1, breaks = 20, plot = FALSE)
h2 <- hist(x2, breaks = h1$breaks, plot = FALSE)
h3 <- hist(x3, breaks = h1$breaks, plot = FALSE)
barplot(rbind(h1$counts, h2$counts, h3$counts),
        beside = TRUE, col = c("red", "blue", "cyan"),
        names.arg = round(h1$breaks[-length(h1$breaks)]))

```

---

nextn

*Highly Composite Numbers*


---

**Description**

nextn returns the smallest integer, greater than or equal to n, which can be obtained as a product of powers of the values contained in factors. nextn is intended to be used to find a suitable length to zero-pad the argument of fft to so that the transform is computed quickly. The default value for factors ensures this.

**Usage**

```
nextn(n, factors = c(2, 3, 5))
```

**Arguments**

n                    an integer.  
factors              a vector of positive integer factors.

**See Also**

[convolve](#), [fft](#).

**Examples**

```
nextn(1001) # 1024
table(sapply(599:630, nextn))
```

nlm

*Non-Linear Minimization***Description**

This function carries out a minimization of the function  $f$  using a Newton-type algorithm. See the references for details.

**Usage**

```
nlm(f, p, ..., hessian = FALSE, typsize = rep(1, length(p)),
     fscale = 1, print.level = 0, ndigit = 12, gradtol = 1e-6,
     stepmax = max(1000 * sqrt(sum((p/typsize)^2)), 1000),
     steptol = 1e-6, iterlim = 100, check.analyticals = TRUE)
```

**Arguments**

<code>f</code>	the function to be minimized. If the function value has an attribute called <code>gradient</code> or both <code>gradient</code> and <code>hessian</code> attributes, these will be used in the calculation of updated parameter values. Otherwise, numerical derivatives are used. <code>deriv</code> returns a function with suitable <code>gradient</code> attribute. This should be a function of a vector of the length of <code>p</code> followed by any other arguments specified by the <code>...</code> argument.
<code>p</code>	starting parameter values for the minimization.
<code>...</code>	additional arguments to <code>f</code> .
<code>hessian</code>	if TRUE, the hessian of $f$ at the minimum is returned.
<code>typsize</code>	an estimate of the size of each parameter at the minimum.
<code>fscale</code>	an estimate of the size of $f$ at the minimum.
<code>print.level</code>	this argument determines the level of printing which is done during the minimization process. The default value of 0 means that no printing occurs, a value of 1 means that initial and final details are printed and a value of 2 means that full tracing information is printed.
<code>ndigit</code>	the number of significant digits in the function $f$ .
<code>gradtol</code>	a positive scalar giving the tolerance at which the scaled gradient is considered close enough to zero to terminate the algorithm. The scaled gradient is a measure of the relative change in $f$ in each direction $p[i]$ divided by the relative change in $p[i]$ .
<code>stepmax</code>	a positive scalar which gives the maximum allowable scaled step length. <code>stepmax</code> is used to prevent steps which would cause the optimization function to overflow, to prevent the algorithm from leaving the area of interest in parameter space, or to detect divergence in the algorithm. <code>stepmax</code> would be chosen small enough to prevent the first two of these occurrences, but should be larger than any anticipated reasonable step.
<code>steptol</code>	A positive scalar providing the minimum allowable relative step length.

<code>iterlim</code>	a positive integer specifying the maximum number of iterations to be performed before the program is terminated.
<code>check.analyticals</code>	a logical scalar specifying whether the analytic gradients and Hessians, if they are supplied, should be checked against numerical derivatives at the initial parameter values. This can help detect incorrectly formulated gradients or Hessians.

### Details

Note that arguments after `. . .` must be matched exactly.

If a gradient or hessian is supplied but evaluates to the wrong mode or length, it will be ignored if `check.analyticals = TRUE` (the default) with a warning. The hessian is not even checked unless the gradient is present and passes the sanity checks.

From the three methods available in the original source, we always use method “1” which is line search.

The functions supplied must always return finite (including not NA and not NaN) values.

### Value

A list containing the following components:

<code>minimum</code>	the value of the estimated minimum of $f$ .
<code>estimate</code>	the point at which the minimum value of $f$ is obtained.
<code>gradient</code>	the gradient at the estimated minimum of $f$ .
<code>hessian</code>	the hessian at the estimated minimum of $f$ (if requested).
<code>code</code>	an integer indicating why the optimization process terminated. <ol style="list-style-type: none"> <li><b>1:</b> relative gradient is close to zero, current iterate is probably solution.</li> <li><b>2:</b> successive iterates within tolerance, current iterate is probably solution.</li> <li><b>3:</b> last global step failed to locate a point lower than <code>estimate</code>. Either <code>estimate</code> is an approximate local minimum of the function or <code>steptol</code> is too small.</li> <li><b>4:</b> iteration limit exceeded.</li> <li><b>5:</b> maximum step size <code>stepmax</code> exceeded five consecutive times. Either the function is unbounded below, becomes asymptotic to a finite value from above in some direction or <code>stepmax</code> is too small.</li> </ol>
<code>iterations</code>	the number of iterations performed.

### References

- Dennis, J. E. and Schnabel, R. B. (1983) *Numerical Methods for Unconstrained Optimization and Nonlinear Equations*. Prentice-Hall, Englewood Cliffs, NJ.
- Schnabel, R. B., Koontz, J. E. and Weiss, B. E. (1985) A modular system of algorithms for unconstrained minimization. *ACM Trans. Math. Software*, **11**, 419–440.

### See Also

[optim](#) and [nlminb](#).

[constrOptim](#) for constrained optimization, [optimize](#) for one-dimensional minimization and [uniroot](#) for root finding. [deriv](#) to calculate analytical derivatives.

For nonlinear regression, [nls](#) may be better.

**Examples**

```
f <- function(x) sum((x-1:length(x))^2)
nlm(f, c(10,10))
nlm(f, c(10,10), print.level = 2)
utils::str(nlm(f, c(5), hessian = TRUE))

f <- function(x, a) sum((x-a)^2)
nlm(f, c(10,10), a=c(3,5))
f <- function(x, a)
{
  res <- sum((x-a)^2)
  attr(res, "gradient") <- 2*(x-a)
  res
}
nlm(f, c(10,10), a=c(3,5))

## more examples, including the use of derivatives.
## Not run: demo(nlm)
```

nlminb

*Optimization using PORT routines***Description**

Unconstrained and constrained optimization using PORT routines.

**Usage**

```
nlminb(start, objective, gradient = NULL, hessian = NULL, ...,
       scale = 1, control = list(), lower = -Inf, upper = Inf)
```

**Arguments**

start	numeric vector, initial values for the parameters to be optimized.
objective	Function to be minimized. Must return a scalar value (possibly NA/Inf). The first argument to <code>objective</code> is the vector of parameters to be optimized, whose initial values are supplied through <code>start</code> . Further arguments (fixed during the course of the optimization) to <code>objective</code> may be specified as well (see ...).
gradient	Optional function that takes the same arguments as <code>objective</code> and evaluates the gradient of <code>objective</code> at its first argument. Must return a vector as long as <code>start</code> .
hessian	Optional function that takes the same arguments as <code>objective</code> and evaluates the hessian of <code>objective</code> at its first argument. Must return a square matrix of order <code>length(start)</code> . Only the lower triangle is used.
...	Further arguments to be supplied to <code>objective</code> .
scale	See PORT documentation (or leave alone).
control	A list of control parameters. See below for details.
lower, upper	vectors of lower and upper bounds, replicated to be as long as <code>start</code> . If unspecified, all parameters are assumed to be unconstrained.

## Details

Any names of `start` are (as from R 2.8.1) passed on to `objective` and where applicable, `gradient` and `hessian`. The parameter vector will be coerced to double.

The PORT documentation is at <http://netlib.bell-labs.com/cm/cs/cstr/153.pdf>.

## Value

A list with components:

<code>par</code>	The best set of parameters found.
<code>objective</code>	The value of <code>objective</code> corresponding to <code>par</code> .
<code>convergence</code>	An integer code. 0 indicates successful convergence.
<code>message</code>	A character string giving any additional information returned by the optimizer, or NULL. For details, see PORT documentation.
<code>iterations</code>	Number of iterations performed.
<code>evaluations</code>	Number of objective function and gradient function evaluations

## Control parameters

Possible names in the `control` list and their default values are:

<code>eval.max</code>	Maximum number of evaluations of the objective function allowed. Defaults to 200.
<code>iter.max</code>	Maximum number of iterations allowed. Defaults to 150.
<code>trace</code>	The value of the objective function and the parameters is printed every <code>trace</code> 'th iteration. Defaults to 0 which indicates no trace information is to be printed.
<code>abs.tol</code>	Absolute tolerance. Defaults to $1e-20$ .
<code>rel.tol</code>	Relative tolerance. Defaults to $1e-10$ .
<code>x.tol</code>	X tolerance. Defaults to $1.5e-8$ .
<code>step.min</code>	Minimum step size. Defaults to $2.2e-14$ .

## Author(s)

(of R port) Douglas Bates and Deepayan Sarkar.

## References

<http://netlib.bell-labs.com/netlib/port/>

## See Also

[optim](#) and [nlm](#).

[optimize](#) for one-dimensional minimization and [constrOptim](#) for constrained optimization.

**Examples**

```

x <- rnbinom(100, mu = 10, size = 10)
hdev <- function(par) {
  -sum(dnbinom(x, mu = par[1], size = par[2], log = TRUE))
}
nlminb(c(9, 12), hdev)
nlminb(c(20, 20), hdev, lower = 0, upper = Inf)
nlminb(c(20, 20), hdev, lower = 0.001, upper = Inf)

## slightly modified from the S-PLUS help page for nlminb
# this example minimizes a sum of squares with known solution y
sumsq <- function( x, y) {sum((x-y)^2)}
y <- rep(1,5)
x0 <- rnorm(length(y))
nlminb(start = x0, sumsq, y = y)
# now use bounds with a y that has some components outside the bounds
y <- c( 0, 2, 0, -2, 0)
nlminb(start = x0, sumsq, lower = -1, upper = 1, y = y)
# try using the gradient
sumsq.g <- function(x,y) 2*(x-y)
nlminb(start = x0, sumsq, sumsq.g,
        lower = -1, upper = 1, y = y)
# now use the hessian, too
sumsq.h <- function(x,y) diag(2, nrow = length(x))
nlminb(start = x0, sumsq, sumsq.g, sumsq.h,
        lower = -1, upper = 1, y = y)

## Rest lifted from optim help page

fr <- function(x) { ## Rosenbrock Banana function
  x1 <- x[1]
  x2 <- x[2]
  100 * (x2 - x1 * x1)^2 + (1 - x1)^2
}
grr <- function(x) { ## Gradient of 'fr'
  x1 <- x[1]
  x2 <- x[2]
  c(-400 * x1 * (x2 - x1 * x1) - 2 * (1 - x1),
    200 * (x2 - x1 * x1))
}
nlminb(c(-1.2,1), fr)
nlminb(c(-1.2,1), fr, grr)

flb <- function(x)
  { p <- length(x); sum(c(1, rep(4, p-1)) * (x - c(1, x[-p]))^2)^2 }
## 25-dimensional box constrained
## par[24] is *not* at boundary
nlminb(rep(3, 25), flb,
        lower=rep(2, 25),
        upper=rep(4, 25))
## trying to use a too small tolerance:
r <- nlminb(rep(3, 25), flb, control = list(rel.tol=1e-16))
stopifnot(grepl("rel.tol", r$message))

```

---

nls *Nonlinear Least Squares*


---

**Description**

Determine the nonlinear (weighted) least-squares estimates of the parameters of a nonlinear model.

**Usage**

```
nls(formula, data, start, control, algorithm,
     trace, subset, weights, na.action, model,
     lower, upper, ...)
```

**Arguments**

formula	a nonlinear model <a href="#">formula</a> including variables and parameters. Will be coerced to a formula if necessary.
data	an optional data frame in which to evaluate the variables in <a href="#">formula</a> and <a href="#">weights</a> . Can also be a list or an environment, but not a matrix.
start	a named list or named numeric vector of starting estimates. When <a href="#">start</a> is missing, a very cheap guess for <a href="#">start</a> is tried (if <code>algorithm != "plinear"</code> ).
control	an optional list of control settings. See <a href="#">nls.control</a> for the names of the settable control values and their effect.
algorithm	character string specifying the algorithm to use. The default algorithm is a Gauss-Newton algorithm. Other possible values are "plinear" for the Golub-Pereyra algorithm for partially linear least-squares models and "port" for the 'nl2sol' algorithm from the Port library – see the references.
trace	logical value indicating if a trace of the iteration progress should be printed. Default is FALSE. If TRUE the residual (weighted) sum-of-squares and the parameter values are printed at the conclusion of each iteration. When the "plinear" algorithm is used, the conditional estimates of the linear parameters are printed after the nonlinear parameters. When the "port" algorithm is used the objective function value printed is half the residual (weighted) sum-of-squares.
subset	an optional vector specifying a subset of observations to be used in the fitting process.
weights	an optional numeric vector of (fixed) weights. When present, the objective function is weighted least squares.
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the <code>na.action</code> setting of <a href="#">options</a> , and is <code>na.fail</code> if that is unset. The 'factory-fresh' default is <code>na.omit</code> . Value <code>na.exclude</code> can be useful.
model	logical. If true, the model frame is returned as part of the object. Default is FALSE.
lower, upper	vectors of lower and upper bounds, replicated to be as long as <a href="#">start</a> . If unspecified, all parameters are assumed to be unconstrained. Bounds can only be used with the "port" algorithm. They are ignored, with a warning, if given for other algorithms.
...	Additional optional arguments. None are used at present.



## Details

An `nls` object is a type of fitted model object. It has methods for the generic functions `anova`, `coef`, `confint`, `deviance`, `df.residual`, `fitted`, `formula`, `logLik`, `predict`, `print`, `profile`, `residuals`, `summary`, `vcov` and `weights`.

Variables in `formula` (and `weights` if not missing) are looked for first in `data`, then the environment of `formula` and finally along the search path. Functions in `formula` are searched for first in the environment of `formula` and then along the search path.

Arguments `subset` and `na.action` are supported only when all the variables in the formula taken from `data` are of the same length: other cases give a warning.

Note that the `anova` method does not check that the models are nested: this cannot easily be done automatically, so use with care.

## Value

A list of

<code>m</code>	an <code>nlsModel</code> object incorporating the model.
<code>data</code>	the expression that was passed to <code>nls</code> as the <code>data</code> argument. The actual data values are present in the environment of the <code>m</code> component.
<code>call</code>	the matched call with several components, notably <code>algorithm</code> .
<code>na.action</code>	the <code>"na.action"</code> attribute (if any) of the model frame.
<code>dataClasses</code>	the <code>"dataClasses"</code> attribute (if any) of the <code>"terms"</code> attribute of the model frame.
<code>model</code>	if <code>model = TRUE</code> , the model frame.
<code>weights</code>	if <code>weights</code> is supplied, the weights.
<code>convInfo</code>	when <code>algorithm</code> is not <code>"port"</code> , a list with convergence information.
<code>control</code>	the control list used, see the <code>control</code> argument.
<code>convergence,</code> <code>message,</code>	for an <code>algorithm = "port"</code> fit only, a convergence code (0 for convergence) and message.

**Note** that setting `warnOnly = TRUE` in the `control` argument (see `nls.control`) returns a non-converged object (since R version 2.5.0) which might be useful for further convergence analysis, *but not for inference*.

## Warning

**Do not use `nls` on artificial "zero-residual" data.**

The `nls` function uses a relative-offset convergence criterion that compares the numerical imprecision at the current parameter estimates to the residual sum-of-squares. This performs well on data of the form

$$y = f(x, \theta) + \epsilon$$

(with `var(eps) > 0`). It fails to indicate convergence on data of the form

$$y = f(x, \theta)$$

because the criterion amounts to comparing two components of the round-off error. If you wish to test `nls` on artificial data please add a noise component, as shown in the example below.

The `algorithm = "port"` code appears unfinished, and does not even check that the starting value is within the bounds. Use with caution, especially where bounds are supplied.

**Author(s)**

Douglas M. Bates and Saikat DebRoy

**References**

Bates, D. M. and Watts, D. G. (1988) *Nonlinear Regression Analysis and Its Applications*, Wiley

Bates, D. M. and Chambers, J. M. (1992) *Nonlinear models*. Chapter 10 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

<http://www.netlib.org/port/> for the Port library documentation.

**See Also**

[summary.nls](#), [predict.nls](#), [profile.nls](#).

**Examples**

```
require(graphics)

DNase1 <- subset(DNase, Run == 1)

## using a selfStart model
fm1DNase1 <- nls(density ~ SSlogis(log(conc), Asym, xmid, scal), DNase1)
summary(fm1DNase1)
## the coefficients only:
coef(fm1DNase1)
## including their SE, etc:
coef(summary(fm1DNase1))

## using conditional linearity
fm2DNase1 <- nls(density ~ 1/(1 + exp((xmid - log(conc))/scal)),
               data = DNase1,
               start = list(xmid = 0, scal = 1),
               algorithm = "plinear", trace = TRUE)
summary(fm2DNase1)

## without conditional linearity
fm3DNase1 <- nls(density ~ Asym/(1 + exp((xmid - log(conc))/scal)),
               data = DNase1,
               start = list(Asym = 3, xmid = 0, scal = 1),
               trace = TRUE)
summary(fm3DNase1)

## using Port's nl2sol algorithm
fm4DNase1 <- nls(density ~ Asym/(1 + exp((xmid - log(conc))/scal)),
               data = DNase1,
               start = list(Asym = 3, xmid = 0, scal = 1),
               trace = TRUE, algorithm = "port")
summary(fm4DNase1)

## weighted nonlinear regression
Treated <- Puromycin[Puromycin$state == "treated", ]
weighted.MM <- function(resp, conc, Vm, K)
{
  ## Purpose: exactly as white book p. 451 -- RHS for nls()
  ## Weighted version of Michaelis-Menten model
```

```

## -----
## Arguments: 'y', 'x' and the two parameters (see book)
## -----
## Author: Martin Maechler, Date: 23 Mar 2001

pred <- (Vm * conc)/(K + conc)
(resp - pred) / sqrt(pred)
}

Pur.wt <- nls( ~ weighted.MM(rate, conc, Vm, K), data = Treated,
             start = list(Vm = 200, K = 0.1),
             trace = TRUE)
summary(Pur.wt)

## Passing arguments using a list that can not be coerced to a data.frame
lisTreat <- with(Treated,
                list(conc1 = conc[1], conc.1 = conc[-1], rate = rate))

weighted.MM1 <- function(resp, conc1, conc.1, Vm, K)
{
  conc <- c(conc1, conc.1)
  pred <- (Vm * conc)/(K + conc)
  (resp - pred) / sqrt(pred)
}
Pur.wt1 <- nls( ~ weighted.MM1(rate, conc1, conc.1, Vm, K),
              data = lisTreat, start = list(Vm = 200, K = 0.1))
stopifnot(all.equal(coef(Pur.wt), coef(Pur.wt1)))

## Chambers and Hastie (1992) Statistical Models in S (p. 537):
## If the value of the right side [of formula] has an attribute called
## 'gradient' this should be a matrix with the number of rows equal
## to the length of the response and one column for each parameter.

weighted.MM.grad <- function(resp, conc1, conc.1, Vm, K)
{
  conc <- c(conc1, conc.1)

  K.conc <- K+conc
  dy.dV <- conc/K.conc
  dy.dK <- -Vm*dy.dV/K.conc
  pred <- Vm*dy.dV
  pred.5 <- sqrt(pred)
  dev <- (resp - pred) / pred.5
  Ddev <- -0.5*(resp+pred)/(pred.5*pred)
  attr(dev, "gradient") <- Ddev * cbind(Vm = dy.dV, K = dy.dK)
  dev
}

Pur.wt.grad <- nls( ~ weighted.MM.grad(rate, conc1, conc.1, Vm, K),
                  data = lisTreat, start = list(Vm = 200, K = 0.1))

rbind(coef(Pur.wt), coef(Pur.wt1), coef(Pur.wt.grad))

## In this example, there seems no advantage to providing the gradient.
## In other cases, there might be.

```

```

## The two examples below show that you can fit a model to
## artificial data with noise but not to artificial data
## without noise.
x <- 1:10
y <- 2*x + 3 # perfect fit
yeps <- y + rnorm(length(y), sd = 0.01) # added noise
nls(yeps ~ a + b*x, start = list(a = 0.12345, b = 0.54321),
    trace = TRUE)
## Not run:
## terminates in an error, because convergence cannot be confirmed:
nls(y ~ a + b*x, start = list(a = 0.12345, b = 0.54321),
    trace = TRUE)

## End(Not run)

## the nls() internal cheap guess for starting values can be sufficient:

x <- -(1:100)/10
y <- 100 + 10 * exp(x / 2) + rnorm(x)/10
nlmod <- nls(y ~ Const + A * exp(B * x), trace=TRUE)

plot(x,y, main = "nls(*)", data, true function and fit, n=100")
curve(100 + 10 * exp(x / 2), col=4, add = TRUE)
lines(x, predict(nlmod), col=2)

## The muscle dataset in MASS is from an experiment on muscle
## contraction on 21 animals. The observed variables are Strip
## (identifier of muscle), Conc (Cacl concentration) and Length
## (resulting length of muscle section).
utils::data(muscle, package = "MASS")

## The non linear model considered is
## Length = alpha + beta*exp(-Conc/theta) + error
## where theta is constant but alpha and beta may vary with Strip.

with(muscle, table(Strip)) # 2,3 or 4 obs per strip

## We first use the plinear algorithm to fit an overall model,
## ignoring that alpha and beta might vary with Strip.

musc.1 <- nls(Length ~ cbind(1, exp(-Conc/th)), muscle,
             start = list(th=1), algorithm="plinear")
summary(musc.1)

## Then we use nls' indexing feature for parameters in non-linear
## models to use the conventional algorithm to fit a model in which
## alpha and beta vary with Strip. The starting values are provided
## by the previously fitted model.
## Note that with indexed parameters, the starting values must be
## given in a list (with names):
b <- coef(musc.1)
musc.2 <- nls(Length ~ a[Strip] + b[Strip]*exp(-Conc/th),
             muscle,
             start = list(a=rep(b[2],21), b=rep(b[3],21), th=b[1]))
summary(musc.2)

```

---

nls.control                      *Control the Iterations in nls*

---

**Description**

Allow the user to set some characteristics of the `nls` nonlinear least squares algorithm.

**Usage**

```
nls.control(maxiter = 50, tol = 1e-05, minFactor = 1/1024,  
           printEval = FALSE, warnOnly = FALSE)
```

**Arguments**

<code>maxiter</code>	A positive integer specifying the maximum number of iterations allowed.
<code>tol</code>	A positive numeric value specifying the tolerance level for the relative offset convergence criterion.
<code>minFactor</code>	A positive numeric value specifying the minimum step-size factor allowed on any step in the iteration. The increment is calculated with a Gauss-Newton algorithm and successively halved until the residual sum of squares has been decreased or until the step-size factor has been reduced below this limit.
<code>printEval</code>	a logical specifying whether the number of evaluations (steps in the gradient direction taken each iteration) is printed.
<code>warnOnly</code>	a logical specifying whether <code>nls()</code> should return instead of signalling an error in the case of termination before convergence. Termination before convergence happens upon completion of <code>maxiter</code> iterations, in the case of a singular gradient, and in the case that the step-size factor is reduced below <code>minFactor</code> .

**Value**

A list with exactly five components:

```
maxiter  
tol  
minFactor  
printEval  
warnOnly
```

with meanings as explained under ‘Arguments’.

**Author(s)**

Douglas Bates and Saikat DebRoy

**References**

Bates, D. M. and Watts, D. G. (1988), *Nonlinear Regression Analysis and Its Applications*, Wiley.

**See Also**

[nls](#)

**Examples**

```
nls.control(minFactor = 1/2048)
```

---

NLSstAsymptotic     *Fit the Asymptotic Regression Model*

---

**Description**

Fits the asymptotic regression model, in the form  $b_0 + b_1 \cdot (1 - \exp(-\exp(\text{lrc}) \cdot x))$  to the `xy` data. This can be used as a building block in determining starting estimates for more complicated models.

**Usage**

```
NLSstAsymptotic(xy)
```

**Arguments**

`xy`                    a sortedXyData object

**Value**

A numeric value of length 3 with components labelled `b0`, `b1`, and `lrc`. `b0` is the estimated intercept on the `y`-axis, `b1` is the estimated difference between the asymptote and the `y`-intercept, and `lrc` is the estimated logarithm of the rate constant.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

[SSasymp](#)

**Examples**

```
Lob.329 <- Loblolly[ Loblolly$Seed == "329", ]  
NLSstAsymptotic(sortedXyData(expression(age), expression(height), Lob.329))
```

---

NLSstClosestX      *Inverse Interpolation*

---

**Description**

Use inverse linear interpolation to approximate the  $x$  value at which the function represented by `xy` is equal to `yval`.

**Usage**

```
NLSstClosestX(xy, yval)
```

**Arguments**

<code>xy</code>	a <code>sortedXyData</code> object
<code>yval</code>	a numeric value on the $y$ scale

**Value**

A single numeric value on the  $x$  scale.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

[sortedXyData](#), [NLSstLfAsymptote](#), [NLSstRtAsymptote](#), [selfStart](#)

**Examples**

```
DNase.2 <- DNase[ DNase$Run == "2", ]
DN.srt <- sortedXyData(expression(log(conc)), expression(density), DNase.2)
NLSstClosestX(DN.srt, 1.0)
```

---

NLSstLfAsymptote      *Horizontal Asymptote on the Left Side*

---

**Description**

Provide an initial guess at the horizontal asymptote on the left side (i.e., small values of  $x$ ) of the graph of  $y$  versus  $x$  from the `xy` object. Primarily used within `initial` functions for self-starting nonlinear regression models.

**Usage**

```
NLSstLfAsymptote(xy)
```

**Arguments**

<code>xy</code>	a <code>sortedXyData</code> object
-----------------	------------------------------------

**Value**

A single numeric value estimating the horizontal asymptote for small  $x$ .

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

[sortedXyData](#), [NLSstClosestX](#), [NLSstRtAsymptote](#), [selfStart](#)

**Examples**

```
DNase.2 <- DNase[ DNase$Run == "2", ]
DN.srt <- sortedXyData( expression(log(conc)), expression(density), DNase.2 )
NLSstLfAsymptote( DN.srt )
```

---

NLSstRtAsymptote     *Horizontal Asymptote on the Right Side*

---

**Description**

Provide an initial guess at the horizontal asymptote on the right side (i.e., large values of  $x$ ) of the graph of  $y$  versus  $x$  from the `xy` object. Primarily used within `initial` functions for self-starting nonlinear regression models.

**Usage**

```
NLSstRtAsymptote(xy)
```

**Arguments**

`xy`                    a `sortedXyData` object

**Value**

A single numeric value estimating the horizontal asymptote for large  $x$ .

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

[sortedXyData](#), [NLSstClosestX](#), [NLSstRtAsymptote](#), [selfStart](#)

**Examples**

```
DNase.2 <- DNase[ DNase$Run == "2", ]
DN.srt <- sortedXyData( expression(log(conc)), expression(density), DNase.2 )
NLSstRtAsymptote( DN.srt )
```



Normal

*The Normal Distribution***Description**

Density, distribution function, quantile function and random generation for the normal distribution with mean equal to `mean` and standard deviation equal to `sd`.

**Usage**

```
dnorm(x, mean = 0, sd = 1, log = FALSE)
pnorm(q, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
qnorm(p, mean = 0, sd = 1, lower.tail = TRUE, log.p = FALSE)
rnorm(n, mean = 0, sd = 1)
```

**Arguments**

<code>x, q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
<code>mean</code>	vector of means.
<code>sd</code>	vector of standard deviations.
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ otherwise, $P[X > x]$ .

**Details**

If `mean` or `sd` are not specified they assume the default values of 0 and 1, respectively.

The normal distribution has density

$$f(x) = \frac{1}{\sqrt{2\pi}\sigma} e^{-(x-\mu)^2/2\sigma^2}$$

where  $\mu$  is the mean of the distribution and  $\sigma$  the standard deviation.

`qnorm` is based on Wichura's algorithm AS 241 which provides precise results up to about 16 digits.

**Value**

`dnorm` gives the density, `pnorm` gives the distribution function, `qnorm` gives the quantile function, and `rnorm` generates random deviates.

**Source**

For `pnorm`, based on

Cody, W. D. (1993) Algorithm 715: SPECFUN – A portable FORTRAN package of special function routines and test drivers. *ACM Transactions on Mathematical Software* **19**, 22–32.

For `qnorm`, the code is a C translation of

Wichura, M. J. (1988) Algorithm AS 241: The Percentage Points of the Normal Distribution. *Applied Statistics*, **37**, 477–484.

For `rnorm`, see [RNG](#) for how to select the algorithm and for references to the supplied methods.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 1, chapter 13. Wiley, New York.

**See Also**

[runif](#) and [.Random.seed](#) about random number generation, and [dlnorm](#) for the Lognormal distribution.

**Examples**

```
require(graphics)

dnorm(0) == 1/ sqrt(2*pi)
dnorm(1) == exp(-1/2)/ sqrt(2*pi)
dnorm(1) == 1/ sqrt(2*pi*exp(1))

## Using "log = TRUE" for an extended range :
par(mfrow=c(2,1))
plot(function(x) dnorm(x, log=TRUE), -60, 50,
      main = "log { Normal density }")
curve(log(dnorm(x)), add=TRUE, col="red", lwd=2)
mtext("dnorm(x, log=TRUE)", adj=0)
mtext("log(dnorm(x))", col="red", adj=1)

plot(function(x) pnorm(x, log.p=TRUE), -50, 10,
      main = "log { Normal Cumulative }")
curve(log(pnorm(x)), add=TRUE, col="red", lwd=2)
mtext("pnorm(x, log=TRUE)", adj=0)
mtext("log(pnorm(x))", col="red", adj=1)

## if you want the so-called 'error function'
erf <- function(x) 2 * pnorm(x * sqrt(2)) - 1
## (see Abramowitz and Stegun 29.2.29)
## and the so-called 'complementary error function'
erfc <- function(x) 2 * pnorm(x * sqrt(2), lower = FALSE)
## and the inverses
erfinv <- function(x) qnorm((1 + x)/2)/sqrt(2)
erfcinv <- function(x) qnorm(x/2, lower = FALSE)/sqrt(2)
```

---

numericDeriv	<i>Evaluate Derivatives Numerically</i>
--------------	---

---

## Description

`numericDeriv` numerically evaluates the gradient of an expression.

## Usage

```
numericDeriv(expr, theta, rho = parent.frame(), dir = 1.0)
```

## Arguments

<code>expr</code>	The expression to be differentiated. The value of this expression should be a numeric vector.
<code>theta</code>	A character vector of names of numeric variables used in <code>expr</code> .
<code>rho</code>	An environment containing all the variables needed to evaluate <code>expr</code> .
<code>dir</code>	A numeric vector of directions to use for the finite differences.

## Details

This is a front end to the C function `numeric_deriv`, which is described in *Writing R Extensions*. The numeric variables must be of type `real` and not `integer`.

## Value

The value of `eval(expr, envir = rho)` plus a matrix attribute called `gradient`. The columns of this matrix are the derivatives of the value with respect to the variables listed in `theta`.

## Author(s)

Saikat DebRoy <saikat@stat.wisc.edu>

## Examples

```
myenv <- new.env()
assign("mean", 0., envir = myenv)
assign("sd", 1., envir = myenv)
assign("x", seq(-3., 3., len = 31), envir = myenv)
numericDeriv(quote(pnorm(x, mean, sd)), c("mean", "sd"), myenv)
```

---

`offset`*Include an Offset in a Model Formula*

---

**Description**

An offset is a term to be added to a linear predictor, such as in a generalised linear model, with known coefficient 1 rather than an estimated coefficient.

**Usage**

```
offset(object)
```

**Arguments**

`object`      An offset to be included in a model frame

**Details**

There can be more than one offset in a model formula, but `-` is not supported for `offset` terms (and is equivalent to `+`).

**Value**

The input value.

**See Also**

[model.offset](#), [model.frame](#).

For examples see [glm](#) and [Insurance](#) in package **MASS**.

---

`oneway.test`*Test for Equal Means in a One-Way Layout*

---

**Description**

Test whether two or more samples from normal distributions have the same means. The variances are not necessarily assumed to be equal.

**Usage**

```
oneway.test(formula, data, subset, na.action, var.equal = FALSE)
```

**Arguments**

<code>formula</code>	a formula of the form <code>lhs ~ rhs</code> where <code>lhs</code> gives the sample values and <code>rhs</code> the corresponding groups.
<code>data</code>	an optional matrix or data frame (or similar: see <a href="#">model.frame</a> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>subset</code>	an optional vector specifying a subset of observations to be used.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. Defaults to <code>getOption("na.action")</code> .
<code>var.equal</code>	a logical variable indicating whether to treat the variances in the samples as equal. If <code>TRUE</code> , then a simple F test for the equality of means in a one-way analysis of variance is performed. If <code>FALSE</code> , an approximate method of Welch (1951) is used, which generalizes the commonly known 2-sample Welch test to the case of arbitrarily many samples.

**Value**

A list with class "htest" containing the following components:

<code>statistic</code>	the value of the test statistic.
<code>parameter</code>	the degrees of freedom of the exact or approximate F distribution of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>method</code>	a character string indicating the test performed.
<code>data.name</code>	a character string giving the names of the data.

**References**

B. L. Welch (1951), On the comparison of several mean values: an alternative approach. *Biometrika*, **38**, 330–336.

**See Also**

The standard t test ([t.test](#)) as the special case for two samples; the Kruskal-Wallis test [kruskal.test](#) for a nonparametric test for equal location parameters in a one-way layout.

**Examples**

```
## Not assuming equal variances
oneway.test(extra ~ group, data = sleep)
## Assuming equal variances
oneway.test(extra ~ group, data = sleep, var.equal = TRUE)
## which gives the same result as
anova(lm(extra ~ group, data = sleep))
```

optim

*General-purpose Optimization***Description**

General-purpose optimization based on Nelder–Mead, quasi-Newton and conjugate-gradient algorithms. It includes an option for box-constrained optimization and simulated annealing.

**Usage**

```
optim(par, fn, gr = NULL, ...,
      method = c("Nelder-Mead", "BFGS", "CG", "L-BFGS-B", "SANN"),
      lower = -Inf, upper = Inf,
      control = list(), hessian = FALSE)
```

**Arguments**

par	Initial values for the parameters to be optimized over.
fn	A function to be minimized (or maximized), with first argument the vector of parameters over which minimization is to take place. It should return a scalar result.
gr	A function to return the gradient for the "BFGS", "CG" and "L-BFGS-B" methods. If it is NULL, a finite-difference approximation will be used. For the "SANN" method it specifies a function to generate a new candidate point. If it is NULL a default Gaussian Markov kernel is used.
...	Further arguments to be passed to fn and gr.
method	The method to be used. See 'Details'.
lower, upper	Bounds on the variables for the "L-BFGS-B" method.
control	A list of control parameters. See 'Details'.
hessian	Logical. Should a numerically differentiated Hessian matrix be returned?

**Details**

Note that arguments after . . . must be matched exactly.

By default this function performs minimization, but it will maximize if `control$fnscale` is negative.

The default method is an implementation of that of Nelder and Mead (1965), that uses only function values and is robust but relatively slow. It will work reasonably well for non-differentiable functions.

Method "BFGS" is a quasi-Newton method (also known as a variable metric algorithm), specifically that published simultaneously in 1970 by Broyden, Fletcher, Goldfarb and Shanno. This uses function values and gradients to build up a picture of the surface to be optimized.

Method "CG" is a conjugate gradients method based on that by Fletcher and Reeves (1964) (but with the option of Polak–Ribiere or Beale–Sorenson updates). Conjugate gradient methods will generally be more fragile than the BFGS method, but as they do not store a matrix they may be successful in much larger optimization problems.

Method "L-BFGS-B" is that of Byrd *et al.* (1995) which allows *box constraints*, that is each variable can be given a lower and/or upper bound. The initial value must satisfy the constraints.

This uses a limited-memory modification of the BFGS quasi-Newton method. If non-trivial bounds are supplied, this method will be selected, with a warning.

Nocedal and Wright (1999) is a comprehensive reference for the previous three methods.

Method "SANN" is by default a variant of simulated annealing given in Belisle (1992). Simulated-annealing belongs to the class of stochastic global optimization methods. It uses only function values but is relatively slow. It will also work for non-differentiable functions. This implementation uses the Metropolis function for the acceptance probability. By default the next candidate point is generated from a Gaussian Markov kernel with scale proportional to the actual temperature. If a function to generate a new candidate point is given, method "SANN" can also be used to solve combinatorial optimization problems. Temperatures are decreased according to the logarithmic cooling schedule as given in Belisle (1992, p. 890); specifically, the temperature is set to  $\text{temp} / \log(((t-1) \% \% \text{tmax}) * \text{tmax} + \exp(1))$ , where  $t$  is the current iteration step and  $\text{temp}$  and  $\text{tmax}$  are specifiable via `control`, see below. Note that the "SANN" method depends critically on the settings of the control parameters. It is not a general-purpose method but can be very useful in getting to a good value on a very rough surface.

Function `fn` can return `NA` or `Inf` if the function cannot be evaluated at the supplied value, but the initial value must have a computable finite value of `fn`. (Except for method "L-BFGS-B" where the values should always be finite.)

`optim` can be used recursively, and for a single parameter as well as many. It also accepts a zero-length `par`, and just evaluates the function with that argument.

The `control` argument is a list that can supply any of the following components:

`trace` Non-negative integer. If positive, tracing information on the progress of the optimization is produced. Higher values may produce more tracing information: for method "L-BFGS-B" there are six levels of tracing. (To understand exactly what these do see the source code: higher levels give more detail.)

`fnscale` An overall scaling to be applied to the value of `fn` and `gr` during optimization. If negative, turns the problem into a maximization problem. Optimization is performed on `fn(par)/fnscale`.

`parscale` A vector of scaling values for the parameters. Optimization is performed on `par/parscale` and these should be comparable in the sense that a unit change in any element produces about a unit change in the scaled value.

`ndeps` A vector of step sizes for the finite-difference approximation to the gradient, on `par/parscale` scale. Defaults to  $1e-3$ .

`maxit` The maximum number of iterations. Defaults to 100 for the derivative-based methods, and 500 for "Nelder-Mead".

For "SANN" `maxit` gives the total number of function evaluations: there is no other stopping criterion. Defaults to 10000.

`abstol` The absolute convergence tolerance. Only useful for non-negative functions, as a tolerance for reaching zero.

`reltol` Relative convergence tolerance. The algorithm stops if it is unable to reduce the value by a factor of `reltol * (abs(val) + reltol)` at a step. Defaults to `sqrt(.Machine$double.eps)`, typically about  $1e-8$ .

`alpha`, `beta`, `gamma` Scaling parameters for the "Nelder-Mead" method. `alpha` is the reflection factor (default 1.0), `beta` the contraction factor (0.5) and `gamma` the expansion factor (2.0).

`REPORT` The frequency of reports for the "BFGS", "L-BFGS-B" and "SANN" methods if `control$trace` is positive. Defaults to every 10 iterations for "BFGS" and "L-BFGS-B", or every 100 temperatures for "SANN".

`type` for the conjugate-gradients method. Takes value 1 for the Fletcher–Reeves update, 2 for Polak–Ribiere and 3 for Beale–Sorenson.

`lmm` is an integer giving the number of BFGS updates retained in the "L-BFGS-B" method. It defaults to 5.

`factr` controls the convergence of the "L-BFGS-B" method. Convergence occurs when the reduction in the objective is within this factor of the machine tolerance. Default is  $1e7$ , that is a tolerance of about  $1e-8$ .

`pgtol` helps control the convergence of the "L-BFGS-B" method. It is a tolerance on the projected gradient in the current search direction. This defaults to zero, when the check is suppressed.

`temp` controls the "SANN" method. It is the starting temperature for the cooling schedule. Defaults to 10.

`tmax` is the number of function evaluations at each temperature for the "SANN" method. Defaults to 10.

Any names given to `par` will be copied to the vectors passed to `fn` and `gr`. Note that no other attributes of `par` are copied over.

## Value

A list with components:

<code>par</code>	The best set of parameters found.
<code>value</code>	The value of <code>fn</code> corresponding to <code>par</code> .
<code>counts</code>	A two-element integer vector giving the number of calls to <code>fn</code> and <code>gr</code> respectively. This excludes those calls needed to compute the Hessian, if requested, and any calls to <code>fn</code> to compute a finite-difference approximation to the gradient.
<code>convergence</code>	An integer code. 0 indicates successful completion (which is always the case for "SANN"). Possible error codes are <ul style="list-style-type: none"> <li>1 indicates that the iteration limit <code>maxit</code> had been reached.</li> <li>10 indicates degeneracy of the Nelder–Mead simplex.</li> <li>51 indicates a warning from the "L-BFGS-B" method; see component <code>message</code> for further details.</li> <li>52 indicates an error from the "L-BFGS-B" method; see component <code>message</code> for further details.</li> </ul>
<code>message</code>	A character string giving any additional information returned by the optimizer, or NULL.
<code>hessian</code>	Only if argument <code>hessian</code> is true. A symmetric matrix giving an estimate of the Hessian at the solution found. Note that this is the Hessian of the unconstrained problem even if the box constraints are active.

## Note

`optim` will work with one-dimensional `pars`, but the default method does not work well (and will warn). Use `optimize` instead.



## Source

The code for methods "Nelder-Mead", "BFGS" and "CG" was based originally on Pascal code in Nash (1990) that was translated by p2c and then hand-optimized. Dr Nash has agreed that the code can be made freely available.

The code for method "L-BFGS-B" is based on Fortran code by Zhu, Byrd, Lu-Chen and Nocedal obtained from Netlib (file 'opt/lbfgs\_bcm.shar': another version is in 'toms/778').

The code for method "SANN" was contributed by A. Trapletti.

## References

- Belisle, C. J. P. (1992) Convergence theorems for a class of simulated annealing algorithms on  $R^d$ . *J Applied Probability*, **29**, 885–895.
- Byrd, R. H., Lu, P., Nocedal, J. and Zhu, C. (1995) A limited memory algorithm for bound constrained optimization. *SIAM J. Scientific Computing*, **16**, 1190–1208.
- Fletcher, R. and Reeves, C. M. (1964) Function minimization by conjugate gradients. *Computer Journal* **7**, 148–154.
- Nash, J. C. (1990) *Compact Numerical Methods for Computers. Linear Algebra and Function Minimisation*. Adam Hilger.
- Nelder, J. A. and Mead, R. (1965) A simplex algorithm for function minimization. *Computer Journal* **7**, 308–313.
- Nocedal, J. and Wright, S. J. (1999) *Numerical Optimization*. Springer.

## See Also

[nlm](#), [nlminb](#).

[optimize](#) for one-dimensional minimization and [constrOptim](#) for constrained optimization.

## Examples

```
require(graphics)

fr <- function(x) { ## Rosenbrock Banana function
  x1 <- x[1]
  x2 <- x[2]
  100 * (x2 - x1 * x1)^2 + (1 - x1)^2
}

grr <- function(x) { ## Gradient of 'fr'
  x1 <- x[1]
  x2 <- x[2]
  c(-400 * x1 * (x2 - x1 * x1) - 2 * (1 - x1),
    200 * (x2 - x1 * x1))
}

optim(c(-1.2,1), fr)
optim(c(-1.2,1), fr, grr, method = "BFGS")
optim(c(-1.2,1), fr, NULL, method = "BFGS", hessian = TRUE)
optim(c(-1.2,1), fr, grr, method = "CG")
optim(c(-1.2,1), fr, grr, method = "CG", control=list(type=2))
optim(c(-1.2,1), fr, grr, method = "L-BFGS-B")

flb <- function(x)
  { p <- length(x); sum(c(1, rep(4, p-1)) * (x - c(1, x[-p]))^2)^2 }
## 25-dimensional box constrained
```

```

optim(rep(3, 25), flb, NULL, method = "L-BFGS-B",
      lower=rep(2, 25), upper=rep(4, 25)) # par[24] is *not* at boundary

## "wild" function , global minimum at about -15.81515
fw <- function (x)
  10*sin(0.3*x)*sin(1.3*x^2) + 0.00001*x^4 + 0.2*x+80
plot(fw, -50, 50, n=1000, main = "optim() minimising 'wild function'")

res <- optim(50, fw, method="SANN",
            control=list(maxit=20000, temp=20, parscale=20))
res
## Now improve locally (typically only by a small bit):
(r2 <- optim(res$par, fw, method="BFGS"))
points(r2$par, r2$value, pch = 8, col = "red", cex = 2)

## Combinatorial optimization: Traveling salesman problem
library(stats) # normally loaded

eurodistmat <- as.matrix(eurodist)

distance <- function(sq) { # Target function
  sq2 <- embed(sq, 2)
  return(sum(eurodistmat[cbind(sq2[,2],sq2[,1])]))
}

genseq <- function(sq) { # Generate new candidate sequence
  idx <- seq(2, NROW(eurodistmat)-1, by=1)
  changepoints <- sample(idx, size=2, replace=FALSE)
  tmp <- sq[changepoints[1]]
  sq[changepoints[1]] <- sq[changepoints[2]]
  sq[changepoints[2]] <- tmp
  return(sq)
}

sq <- c(1,2:NROW(eurodistmat),1) # Initial sequence
distance(sq)

set.seed(123) # chosen to get a good soln relatively quickly
res <- optim(sq, distance, genseq, method="SANN",
            control = list(maxit=30000, temp=2000, trace=TRUE, REPORT=500))
res # Near optimum distance around 12842

loc <- cmdscale(eurodist)
rx <- range(x <- loc[,1])
ry <- range(y <- -loc[,2])
tspinit <- loc[sq,]
tspres <- loc[res$par,]
s <- seq(NROW(tspres)-1)

plot(x, y, type="n", asp=1, xlab="", ylab="",
     main="initial solution of traveling salesman problem")
arrows(tspinit[s,1], -tspinit[s,2], tspinit[s+1,1], -tspinit[s+1,2],
       angle=10, col="green")
text(x, y, labels(eurodist), cex=0.8)

plot(x, y, type="n", asp=1, xlab="", ylab="",
     main="optim() 'solving' traveling salesman problem")

```

```
arrows(tspres[s,1], -tspres[s,2], tspres[s+1,1], -tspres[s+1,2],
       angle=10, col="red")
text(x, y, labels(eurodist), cex=0.8)
```

optimize

*One Dimensional Optimization***Description**

The function `optimize` searches the interval from `lower` to `upper` for a minimum or maximum of the function `f` with respect to its first argument.

`optimise` is an alias for `optimize`.

**Usage**

```
optimize(f = , interval = , ..., lower = min(interval),
        upper = max(interval), maximum = FALSE,
        tol = .Machine$double.eps^0.25)
optimise(f = , interval = , ..., lower = min(interval),
        upper = max(interval), maximum = FALSE,
        tol = .Machine$double.eps^0.25)
```

**Arguments**

<code>f</code>	the function to be optimized. The function is either minimized or maximized over its first argument depending on the value of <code>maximum</code> .
<code>interval</code>	a vector containing the end-points of the interval to be searched for the minimum.
<code>...</code>	additional named or unnamed arguments to be passed to <code>f</code> .
<code>lower</code>	the lower end point of the interval to be searched.
<code>upper</code>	the upper end point of the interval to be searched.
<code>maximum</code>	logical. Should we maximize or minimize (the default)?
<code>tol</code>	the desired accuracy.

**Details**

Note that arguments after `...` must be matched exactly.

The method used is a combination of golden section search and successive parabolic interpolation, and was designed for use with continuous functions. Convergence is never much slower than that for a Fibonacci search. If `f` has a continuous second derivative which is positive at the minimum (which is not at `lower` or `upper`), then convergence is superlinear, and usually of the order of about 1.324.

The function `f` is never evaluated at two points closer together than  $\epsilon|x_0| + (tol/3)$ , where  $\epsilon$  is approximately  $\sqrt{.Machine$double.eps}$  and  $x_0$  is the final abscissa `optimize()$minimum`.

If `f` is a unimodal function and the computed values of `f` are always unimodal when separated by at least  $\epsilon|x| + (tol/3)$ , then  $x_0$  approximates the abscissa of the global minimum of `f` on the interval `lower, upper` with an error less than  $\epsilon|x_0| + tol$ .

If  $f$  is not unimodal, then `optimize()` may approximate a local, but perhaps non-global, minimum to the same accuracy.

The first evaluation of  $f$  is always at  $x_1 = a + (1 - \phi)(b - a)$  where  $(a, b) = (\text{lower}, \text{upper})$  and  $\phi = (\sqrt{5} - 1)/2 = 0.61803\dots$  is the golden section ratio. Almost always, the second evaluation is at  $x_2 = a + \phi(b - a)$ . Note that a local minimum inside  $[x_1, x_2]$  will be found as solution, even when  $f$  is constant in there, see the last example.

$f$  will be called as  $f(x, \dots)$  for a numeric value of  $x$ .

### Value

A list with components `minimum` (or `maximum`) and `objective` which give the location of the minimum (or maximum) and the value of the function at that point.

### Source

A C translation of Fortran code <http://www.netlib.org/fmm/fmin.f> based on the Algol 60 procedure `localmin` given in the reference.

### References

Brent, R. (1973) *Algorithms for Minimization without Derivatives*. Englewood Cliffs N.J.: Prentice-Hall.

### See Also

`nlm`, `uniroot`.

### Examples

```
require(graphics)

f <- function(x,a) (x-a)^2
xmin <- optimize(f, c(0, 1), tol = 0.0001, a = 1/3)
xmin

## See where the function is evaluated:
optimize(function(x) x^2*(print(x)-1), lower=0, upper=10)

## "wrong" solution with unlucky interval and piecewise constant f():
f <- function(x) ifelse(x > -1, ifelse(x < 4, exp(-1/abs(x - 1)), 10), 10)
fp <- function(x) { print(x); f(x) }

plot(f, -2,5, ylim = 0:1, col = 2)
optimize(fp, c(-4, 20))# doesn't see the minimum
optimize(fp, c(-7, 20))# ok
```

---

order.dendrogram    *Ordering or Labels of the Leaves in a Dendrogram*

---

### Description

These functions return the order (index) or the "label" attribute for the leaves in a dendrogram. These indices can then be used to access the appropriate components of any additional data.

### Usage

```
order.dendrogram(x)

## S3 method for class 'dendrogram':
labels(object, ...)
```

### Arguments

`x`, `object`    a dendrogram (see [as.dendrogram](#)).

`...`            additional arguments

### Details

The indices or labels for the leaves in left to right order are retrieved.

### Value

A vector with length equal to the number of leaves in the dendrogram is returned. From `r <- order.dendrogram()`, each element is the index into the original data (from which the dendrogram was computed).

### Author(s)

R. Gentleman (`order.dendrogram`) and Martin Maechler (`labels.dendrogram`).

### See Also

[reorder.dendrogram](#).

### Examples

```
set.seed(123)
x <- rnorm(10)
hc <- hclust(dist(x))
hc$order
dd <- as.dendrogram(hc)
order.dendrogram(dd) ## the same :
stopifnot(hc$order == order.dendrogram(dd))

d2 <- as.dendrogram(hclust(dist(USArrests)))
labels(d2) ## in this case the same as
stopifnot(labels(d2) == rownames(USArrests)[order.dendrogram(d2)])
```

---

p.adjust

*Adjust P-values for Multiple Comparisons*

---

### Description

Given a set of p-values, returns p-values adjusted using one of several methods.

### Usage

```
p.adjust(p, method = p.adjust.methods, n = length(p))

p.adjust.methods
# c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY",
#   "fdr", "none")
```

### Arguments

p	vector of p-values (possibly with NAs).
method	correction method
n	number of comparisons, must be at least <code>length(p)</code> ; only set this (to non-default) when you know what you are doing!

### Details

The adjustment methods include the Bonferroni correction ("bonferroni") in which the p-values are multiplied by the number of comparisons. Less conservative corrections are also included by Holm (1979) ("holm"), Hochberg (1988) ("hochberg"), Hommel (1988) ("hommel"), Benjamini & Hochberg (1995) ("BH" or its alias "fdr"), and Benjamini & Yekutieli (2001) ("BY"), respectively. A pass-through option ("none") is also included. The set of methods are contained in the `p.adjust.methods` vector for the benefit of methods that need to have the method as an option and pass it on to `p.adjust`.

The first four methods are designed to give strong control of the family wise error rate. There seems no reason to use the unmodified Bonferroni correction because it is dominated by Holm's method, which is also valid under arbitrary assumptions.

Hochberg's and Hommel's methods are valid when the hypothesis tests are independent or when they are non-negatively associated (Sarkar, 1998; Sarkar and Chang, 1997). Hommel's method is more powerful than Hochberg's, but the difference is usually small and the Hochberg p-values are faster to compute.

The "BH" (aka "fdr") and "BY" method of Benjamini, Hochberg, and Yekutieli control the false discovery rate, the expected proportion of false discoveries amongst the rejected hypotheses. The false discovery rate is a less stringent condition than the family wise error rate, so these methods are more powerful than the others.

Note that you can set `n` larger than `length(p)` which means the unobserved p-values are assumed to be greater than all the observed p for "bonferroni" and "holm" methods and equal to 1 for the other methods.

### Value

A vector of corrected p-values (same length as `p`).

## References

- Benjamini, Y., and Hochberg, Y. (1995). Controlling the false discovery rate: a practical and powerful approach to multiple testing. *Journal of the Royal Statistical Society Series B*, **57**, 289–300.
- Benjamini, Y., and Yekutieli, D. (2001). The control of the false discovery rate in multiple testing under dependency. *Annals of Statistics* **29**, 1165–1188.
- Holm, S. (1979). A simple sequentially rejective multiple test procedure. *Scandinavian Journal of Statistics*, **6**, 65–70.
- Hommel, G. (1988). A stagewise rejective multiple test procedure based on a modified Bonferroni test. *Biometrika*, **75**, 383–386.
- Hochberg, Y. (1988). A sharper Bonferroni procedure for multiple tests of significance. *Biometrika*, **75**, 800–803.
- Shaffer, J. P. (1995). Multiple hypothesis testing. *Annual Review of Psychology*, **46**, 561–576. (An excellent review of the area.)
- Sarkar, S. (1998). Some probability inequalities for ordered MTP2 random variables: a proof of Simes conjecture. *Annals of Statistics*, **26**, 494–504.
- Sarkar, S., and Chang, C. K. (1997). Simes' method for multiple hypothesis testing with positively dependent test statistics. *Journal of the American Statistical Association*, **92**, 1601–1608.
- Wright, S. P. (1992). Adjusted P-values for simultaneous inference. *Biometrics*, **48**, 1005–1013. (Explains the adjusted P-value approach.)

## See Also

pairwise.\* functions such as [pairwise.t.test](#).

## Examples

```
require(graphics)

set.seed(123)
x <- rnorm(50, mean=c(rep(0,25),rep(3,25)))
p <- 2*pnorm( sort(-abs(x)))

round(p, 3)
round(p.adjust(p), 3)
round(p.adjust(p,"BH"), 3)

## or all of them at once (dropping the "fdr" alias):
p.adjust.M <- p.adjust.methods[p.adjust.methods != "fdr"]
p.adj <- sapply(p.adjust.M, function(meth) p.adjust(p, meth))
p.adj.60 <- sapply(p.adjust.M, function(meth) p.adjust(p, meth, n = 60))
stopifnot(identical(p.adj[, "none"], p), p.adj <= p.adj.60)
round(p.adj, 3)
## or a bit nicer:
noquote(apply(p.adj, 2, format.pval, digits = 3))

## and a graphic:
matplot(p, p.adj, ylab="p.adjust(p, meth)", type = "l", asp=1, lty=1:6,
        main = "P-value adjustments")
legend(.7,.6, p.adjust.M, col=1:6, lty=1:6)

## Can work with NA's:
```

```
pN <- p; iN <- c(46,47); pN[iN] <- NA
pN.a <- sapply(p.adjust.M, function(meth) p.adjust(pN, meth))
## The smallest 20 P-values all affected by the NA's :
round((pN.a / p.adj)[1:20, ] , 4)
```

---

pairwise.prop.test *Pairwise comparisons for proportions*

---

### Description

Calculate pairwise comparisons between pairs of proportions with correction for multiple testing

### Usage

```
pairwise.prop.test(x, n, p.adjust.method = p.adjust.methods, ...)
```

### Arguments

x	Vector of counts of successes or a matrix with 2 columns giving the counts of successes and failures, respectively.
n	Vector of counts of trials; ignored if x is a matrix.
p.adjust.method	Method for adjusting p values (see <a href="#">p.adjust</a> )
...	Additional arguments to pass to <code>prop.test</code>

### Value

Object of class "pairwise.htest"

### See Also

[prop.test](#), [p.adjust](#)

### Examples

```
smokers <- c( 83, 90, 129, 70 )
patients <- c( 86, 93, 136, 82 )
pairwise.prop.test(smokers, patients)
```



---

pairwise.t.test      *Pairwise t tests*

---

### Description

Calculate pairwise comparisons between group levels with corrections for multiple testing

### Usage

```
pairwise.t.test(x, g, p.adjust.method = p.adjust.methods,
               pool.sd = !paired, paired = FALSE,
               alternative = c("two.sided", "less", "greater"), ...)
```

### Arguments

x	response vector.
g	grouping vector or factor.
p.adjust.method	Method for adjusting p values (see <a href="#">p.adjust</a> ).
pool.sd	switch to allow/disallow the use of a pooled SD
paired	a logical indicating whether you want paired t-tests.
alternative	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less".
...	additional arguments to pass to <code>t.test</code> .

### Details

The `pool.sd` switch calculates a common SD for all groups and used that for all comparisons (this can be useful if some groups are small). This method does not actually call `t.test`, so extra arguments are ignored. Pooling does not generalize to paired tests so `pool.sd` and `paired` cannot both be TRUE.

Only the lower triangle of the matrix of possible comparisons is being calculated, so setting `alternative` to anything other than "two.sided" requires that the levels of `g` are ordered sensibly.

### Value

Object of class "pairwise.htest"

### See Also

[t.test](#), [p.adjust](#)

### Examples

```
attach(airquality)
Month <- factor(Month, labels = month.abb[5:9])
pairwise.t.test(Ozone, Month)
pairwise.t.test(Ozone, Month, p.adj = "bonf")
pairwise.t.test(Ozone, Month, pool.sd = FALSE)
detach()
```

---

pairwise.table	<i>Tabulate p values for pairwise comparisons</i>
----------------	---

---

**Description**

Creates table of p values for pairwise comparisons with corrections for multiple testing.

**Usage**

```
pairwise.table(compare.levels, level.names, p.adjust.method)
```

**Arguments**

`compare.levels`                   Function to compute (raw) p value given indices *i* and *j*  
`level.names`           Names of the group levels  
`p.adjust.method`       Method for multiple testing adjustment

**Details**

Functions that do multiple group comparisons create separate `compare.levels` functions (assumed to be symmetrical in *i* and *j*) and passes them to this function.

**Value**

Table of p values in lower triangular form.

**See Also**

[pairwise.t.test](#), et al.

---

pairwise.wilcox.test	<i>Pairwise Wilcoxon Rank Sum Tests</i>
----------------------	---

---

**Description**

Calculate pairwise comparisons between group levels with corrections for multiple testing.

**Usage**

```
pairwise.wilcox.test(x, g, p.adjust.method = p.adjust.methods,  
                    paired=FALSE, ...)
```

**Arguments**

<code>x</code>	response vector.
<code>g</code>	grouping vector or factor.
<code>p.adjust.method</code>	method for adjusting p values (see <code>p.adjust</code> ).
<code>paired</code>	a logical indicating whether you want a paired test.
<code>...</code>	additional arguments to pass to <code>wilcox.test</code> .

**Details**

Extra arguments that are passed on to `wilcox.test` may or may not be sensible in this context. In particular, only the lower triangle of the matrix of possible comparisons is being calculated, so setting `alternative` to anything other than `"two.sided"` requires that the levels of `g` are ordered sensibly.

**Value**

Object of class `"pairwise.htest"`

**See Also**

`wilcox.test`, `p.adjust`

**Examples**

```
attach(airquality)
Month <- factor(Month, labels = month.abb[5:9])
## These give warnings because of ties :
pairwise.wilcox.test(Ozone, Month)
pairwise.wilcox.test(Ozone, Month, p.adj = "bonf")
detach()
```

---

plot.acf

*Plot Autocovariance and Autocorrelation Functions*

---

**Description**

Plot method for objects of class `"acf"`.

**Usage**

```
## S3 method for class 'acf':
plot(x, ci = 0.95, type = "h", xlab = "Lag", ylab = NULL,
      ylim = NULL, main = NULL,
      ci.col = "blue", ci.type = c("white", "ma"),
      max.mfrow = 6, ask = Npgs > 1 && dev.interactive(),
      mar = if(nser > 2) c(3,2,2,0.8) else par("mar"),
      oma = if(nser > 2) c(1,1.2,1,1) else par("oma"),
      mgp = if(nser > 2) c(1.5,0.6,0) else par("mgp"),
      xpd = par("xpd"),
      cex.main = if(nser > 2) 1 else par("cex.main"),
      verbose = getOption("verbose"),
      ...)
```

**Arguments**

<code>x</code>	an object of class "acf".
<code>ci</code>	coverage probability for confidence interval. Plotting of the confidence interval is suppressed if <code>ci</code> is zero or negative.
<code>type</code>	the type of plot to be drawn, default to histogram like vertical lines.
<code>xlab</code>	the x label of the plot.
<code>ylab</code>	the y label of the plot.
<code>ylim</code>	numeric of length 2 giving the y limits for the plot.
<code>main</code>	overall title for the plot.
<code>ci.col</code>	colour to plot the confidence interval lines.
<code>ci.type</code>	should the confidence limits assume a white noise input or for lag $k$ an $MA(k-1)$ input?
<code>max.mfrow</code>	positive integer; for multivariate <code>x</code> indicating how many rows and columns of plots should be put on one page, using <code>par(mfrow = c(m, m))</code> .
<code>ask</code>	logical; if TRUE, the user is asked before a new page is started.
<code>mar, oma, mgp, xpd, cex.main</code>	graphics parameters as in <code>par(*)</code> , by default adjusted to use smaller than default margins for multivariate <code>x</code> only.
<code>verbose</code>	logical. Should R report extra information on progress?
<code>...</code>	graphics parameters to be passed to the plotting routines.

**Note**

The confidence interval plotted in `plot.acf` is based on an *uncorrelated* series and should be treated with appropriate caution. Using `ci.type = "ma"` may be less potentially misleading.

**See Also**

`acf` which calls `plot.acf` by default.

**Examples**

```
require(graphics)

z4 <- ts(matrix(rnorm(400), 100, 4), start=c(1961, 1), frequency=12)
z7 <- ts(matrix(rnorm(700), 100, 7), start=c(1961, 1), frequency=12)
acf(z4)
acf(z7, max.mfrow = 7) # squeeze on 1 page
acf(z7) # multi-page
```

---

plot.density      *Plot Method for Kernel Density Estimation*

---

### Description

The plot method for density objects.

### Usage

```
## S3 method for class 'density':
plot(x, main = NULL, xlab = NULL, ylab = "Density", type = "l",
     zero.line = TRUE, ...)
```

### Arguments

x                    a "density" object.  
 main, xlab, ylab, type      plotting parameters with useful defaults.  
 ...                    further plotting parameters.  
 zero.line            logical; if TRUE, add a base line at  $y = 0$

### Value

None.

### See Also

[density](#).

---

plot.HoltWinters      *Plot function for HoltWinters objects*

---

### Description

Produces a chart of the original time series along with the fitted values. Optionally, predicted values (and their confidence bounds) can also be plotted.

### Usage

```
## S3 method for class 'HoltWinters':
plot(x, predicted.values = NA, intervals = TRUE,
     separator = TRUE, col = 1, col.predicted = 2,
     col.intervals = 4, col.separator = 1, lty = 1,
     lty.predicted = 1, lty.intervals = 1, lty.separator = 3,
     ylab = "Observed / Fitted",
     main = "Holt-Winters filtering",
     ylim = NULL, ...)
```

**Arguments**

<code>x</code>	Object of class "HoltWinters"
<code>predicted.values</code>	Predicted values as returned by <code>predict.HoltWinters</code>
<code>intervals</code>	If TRUE, the prediction intervals are plotted (default).
<code>separator</code>	If TRUE, a separating line between fitted and predicted values is plotted (default).
<code>col, lty</code>	Color/line type of original data (default: black solid).
<code>col.predicted, lty.predicted</code>	Color/line type of fitted and predicted values (default: red solid).
<code>col.intervals, lty.intervals</code>	Color/line type of prediction intervals (default: blue solid).
<code>col.separator, lty.separator</code>	Color/line type of observed/predicted values separator (default: black dashed).
<code>ylab</code>	Label of the y-axis.
<code>main</code>	Main title.
<code>ylim</code>	Limits of the y-axis. If NULL, the range is chosen such that the plot contains the original series, the fitted values, and the predicted values if any.
<code>...</code>	Other graphics parameters.

**Author(s)**

David Meyer <David.Meyer@wu-wien.ac.at>

**References**

- C. C. Holt (1957) Forecasting trends and seasonals by exponentially weighted moving averages, *ONR Research Memorandum, Carnegie Institute of Technology* **52**.
- P. R. Winters (1960) Forecasting sales by exponentially weighted moving averages, *Management Science* **6**, 324–342.

**See Also**

[HoltWinters](#), [predict.HoltWinters](#)

---

plot.isoreg

*Plot Method for isoreg Objects*

---

**Description**

The `plot` and `lines` method for R objects of class `isoreg`.

**Usage**

```
## S3 method for class 'isoreg':
plot(x, plot.type = c("single", "row.wise", "col.wise"),
     main = paste("Isotonic regression", deparse(x$call)),
     main2 = "Cumulative Data and Convex Minorant",
     xlab = "x0", ylab = "x$y",
     par.fit = list(col = "red", cex = 1.5, pch = 13, lwd = 1.5),
     mar = if (both) 0.1 + c(3.5, 2.5, 1, 1) else par("mar"),
     mgp = if (both) c(1.6, 0.7, 0) else par("mgp"),
     grid = length(x$x) < 12, ...)

## S3 method for class 'isoreg':
lines(x, col = "red", lwd = 1.5,
      do.points = FALSE, cex = 1.5, pch = 13, ...)
```

**Arguments**

<code>x</code>	an <a href="#">isoreg</a> object.
<code>plot.type</code>	character indicating which type of plot is desired. The first (default) only draws the data and the fit, where the others add a plot of the cumulative data and fit.
<code>main</code>	main title of plot, see <a href="#">title</a> .
<code>main2</code>	title for second (cumulative) plot.
<code>xlab, ylab</code>	x- and y- axis annotation.
<code>par.fit</code>	a <a href="#">list</a> of arguments (for <a href="#">points</a> and <a href="#">lines</a> ) for drawing the fit.
<code>mar, mgp</code>	graphical parameters, see <a href="#">par</a> , mainly for the case of two plots.
<code>grid</code>	logical indicating if grid lines should be drawn. If true, <a href="#">grid()</a> is used for the first plot, where as vertical lines are drawn at ‘touching’ points for the cumulative plot.
<code>do.points</code>	for <a href="#">lines()</a> : logical indicating if the step points should be drawn as well (and as they are drawn in <a href="#">plot()</a> ).
<code>col, lwd, cex, pch</code>	graphical arguments for <a href="#">lines()</a> , where <code>cex</code> and <code>pch</code> are only used when <code>do.points</code> is TRUE.
<code>...</code>	further arguments passed to and from methods.

**See Also**

[isoreg](#) for computation of `isoreg` objects.

**Examples**

```
require(graphics)

utils::example(isoreg) # for the examples there

plot(y3, main = "simple plot(.) + lines(<isoreg>)")
lines(ir3)

## 'same' plot as above, "proving" that only ranks of 'x' are important
plot(isoreg(2^(1:9), c(1,0,4,3,3,5,4,2,0)), plot.type = "row", log = "x")
```

```

plot(ir3, plot.type = "row", ylab = "y3")
plot(isoreg(y3 - 4), plot.t="r", ylab = "y3 - 4")
plot(ir4, plot.type = "ro", ylab = "y4", xlab = "x = 1:n")

## experiment a bit with these (C-c C-j):
plot(isoreg(sample(9), y3), plot.type="row")
plot(isoreg(sample(9), y3), plot.type="col.wise")

plot(ir <- isoreg(sample(10), sample(10, replace = TRUE)),
      plot.type = "r")

```

plot.lm

*Plot Diagnostics for an lm Object***Description**

Six plots (selectable by `which`) are currently available: a plot of residuals against fitted values, a Scale-Location plot of  $\sqrt{|residuals|}$  against fitted values, a Normal Q-Q plot, a plot of Cook's distances versus row labels, a plot of residuals against leverages, and a plot of Cook's distances against leverage/(1-leverage). By default, the first three and 5 are provided.

**Usage**

```

## S3 method for class 'lm':
plot(x, which = c(1:3,5),
      caption = list("Residuals vs Fitted", "Normal Q-Q",
                    "Scale-Location", "Cook's distance",
                    "Residuals vs Leverage",
                    expression("Cook's dist vs Leverage " * h[ii] / (1 - h[ii]))),
      panel = if(add.smooth) panel.smooth else points,
      sub.caption = NULL, main = "",
      ask = prod(par("mfcol")) < length(which) && dev.interactive(),
      ...,
      id.n = 3, labels.id = names(residuals(x)), cex.id = 0.75,
      qqline = TRUE, cook.levels = c(0.5, 1.0),
      add.smooth = getOption("add.smooth"), label.pos = c(4,2),
      cex.caption = 1)

```

**Arguments**

<code>x</code>	lm object, typically result of <code>lm</code> or <code>glm</code> .
<code>which</code>	if a subset of the plots is required, specify a subset of the numbers 1:6.
<code>caption</code>	captions to appear above the plots; <code>character</code> vector or <code>list</code> of valid graphics annotations, see <code>as.graphicsAnnot</code> . Can be set to "" or NA to suppress all captions.
<code>panel</code>	panel function. The useful alternative to <code>points</code> , <code>panel.smooth</code> can be chosen by <code>add.smooth = TRUE</code> .
<code>sub.caption</code>	common title—above the figures if there are more than one; used as <code>sub</code> ( <code>s.title</code> ) otherwise. If NULL, as by default, a possible abbreviated version of <code>deparse(x\$call)</code> is used.



<code>main</code>	title to each plot—in addition to <code>caption</code> .
<code>ask</code>	logical; if TRUE, the user is <i>asked</i> before each plot, see <code>par(ask=.)</code> .
<code>...</code>	other parameters to be passed through to plotting functions.
<code>id.n</code>	number of points to be labelled in each plot, starting with the most extreme.
<code>labels.id</code>	vector of labels, from which the labels for extreme points will be chosen. NULL uses observation numbers.
<code>cex.id</code>	magnification of point labels.
<code>qqline</code>	logical indicating if a <code>qqline()</code> should be added to the normal Q-Q plot.
<code>cook.levels</code>	levels of Cook's distance at which to draw contours.
<code>add.smooth</code>	logical indicating if a smoother should be added to most plots; see also <code>panel</code> above.
<code>label.pos</code>	positioning of labels, for the left half and right half of the graph respectively, for plots 1-3.
<code>cex.caption</code>	controls the size of <code>caption</code> .

### Details

`sub.caption`—by default the function call—is shown as a subtitle (under the x-axis title) on each plot when plots are on separate pages, or as a subtitle in the outer margin (if any) when there are multiple plots per page.

The 'Scale-Location' plot, also called 'Spread-Location' or 'S-L' plot, takes the square root of the absolute residuals in order to diminish skewness ( $\sqrt{|E|}$ ) is much less skewed than  $|E|$  for Gaussian zero-mean  $E$ ).

The 'S-L', the Q-Q, and the Residual-Leverage plot, use *standardized* residuals which have identical variance (under the hypothesis). They are given as  $R_i / (s \times \sqrt{1 - h_{ii}})$  where  $h_{ii}$  are the diagonal entries of the hat matrix, `influence()`  $\hat{s}$  (see also `hat`), and where the Residual-Leverage plot uses standardized Pearson residuals (`residuals.glm(type = "pearson")`) for  $R[i]$ .

The Residual-Leverage plot shows contours of equal Cook's distance, for values of `cook.levels` (by default 0.5 and 1) and omits cases with leverage one with a warning. If the leverages are constant (as is typically the case in a balanced `av` situation) the plot uses factor level combinations instead of the leverages for the x-axis. (The factor levels are ordered by mean fitted value.)

In the Cook's distance vs leverage/(1-leverage) plot, contours of standardized residuals that are equal in magnitude are lines through the origin. The contour lines are labelled with the magnitudes.

### Author(s)

John Maindonald and Martin Maechler.

### References

- Belsley, D. A., Kuh, E. and Welsch, R. E. (1980) *Regression Diagnostics*. New York: Wiley.
- Cook, R. D. and Weisberg, S. (1982) *Residuals and Influence in Regression*. London: Chapman and Hall.
- Firth, D. (1991) Generalized Linear Models. In Hinkley, D. V. and Reid, N. and Snell, E. J., eds: Pp. 55-82 in *Statistical Theory and Modelling*. In Honour of Sir David Cox, FRS. London: Chapman and Hall.
- Hinkley, D. V. (1975) On power transformations to symmetry. *Biometrika* **62**, 101–111.
- McCullagh, P. and Nelder, J. A. (1989) *Generalized Linear Models*. London: Chapman and Hall.

**See Also**

[termplot](#), [lm.influence](#), [cooks.distance](#), [hatvalues](#).

**Examples**

```
require(graphics)

## Analysis of the life-cycle savings data
## given in Belsley, Kuh and Welsch.
plot(lm.SR <- lm(sr ~ pop15 + pop75 + dpi + ddpi, data = LifeCycleSavings))

## 4 plots on 1 page;
## allow room for printing model formula in outer margin:
par(mfrow = c(2, 2), oma = c(0, 0, 2, 0))
plot(lm.SR)
plot(lm.SR, id.n = NULL)           # no id's
plot(lm.SR, id.n = 5, labels.id = NULL) # 5 id numbers

## Was default in R <= 2.1.x:
## Cook's distances instead of Residual-Leverage plot
plot(lm.SR, which = 1:4)

## Fit a smooth curve, where applicable:
plot(lm.SR, panel = panel.smooth)
## Gives a smoother curve
plot(lm.SR, panel = function(x,y) panel.smooth(x, y, span = 1))

par(mfrow=c(2,1)) # same oma as above
plot(lm.SR, which = 1:2, sub.caption = "Saving Rates, n=50, p=5")
```

---

plot.ppr

---

*Plot Ridge Functions for Projection Pursuit Regression Fit*


---

**Description**

Plot ridge functions for projection pursuit regression fit.

**Usage**

```
## S3 method for class 'ppr':
plot(x, ask, type = "o", ...)
```

**Arguments**

x	A fit of class "ppr" as produced by a call to ppr.
ask	the graphics parameter ask: see par for details. If set to TRUE will ask between the plot of each cross-section.
type	the type of line to draw
...	further graphical parameters

**Value**

None

**Side Effects**

A series of plots are drawn on the current graphical device, one for each term in the fit.

**See Also**

[ppr](#), [par](#)

**Examples**

```
require(graphics)

with(rock, {
  areal <- area/10000; peril <- peri/10000
  par(mfrow=c(3,2))# maybe: , pty="s")
  rock.ppr <- ppr(log(perm) ~ areal + peril + shape,
                 data = rock, nterms = 2, max.terms = 5)
  plot(rock.ppr, main="ppr(log(perm) ~ ., nterms=2, max.terms=5)")
  plot(update(rock.ppr, bass=5), main = "update(..., bass = 5)")
  plot(update(rock.ppr, sm.method="gcv", gcvpen=2),
       main = "update(..., sm.method=\"gcv\", gcvpen=2)")
})
```

---

plot.profile.nls    *Plot a profile.nls Object*

---

**Description**

Displays a series of plots of the profile  $t$  function and interpolated confidence intervals for the parameters in a nonlinear regression model that has been fit with `nls` and profiled with `profile.nls`.

**Usage**

```
## S3 method for class 'profile.nls':
plot(x, levels, conf= c(99, 95, 90, 80, 50)/100,
     absVal =TRUE, ...)
```

**Arguments**

<code>x</code>	an object of class "profile.nls"
<code>levels</code>	levels, on the scale of the absolute value of a $t$ statistic, at which to interpolate intervals. Usually <code>conf</code> is used instead of giving <code>levels</code> explicitly.
<code>conf</code>	a numeric vector of confidence levels for profile-based confidence intervals on the parameters. Defaults to <code>c(0.99, 0.95, 0.90, 0.80, 0.50)</code> .
<code>absVal</code>	a logical value indicating whether or not the plots should be on the scale of the absolute value of the profile $t$ . Defaults to <code>TRUE</code> .
<code>...</code>	other arguments to the <code>plot</code> function can be passed here.

**Author(s)**

Douglas M. Bates and Saikat DebRoy

**References**

Bates, D.M. and Watts, D.G. (1988), *Nonlinear Regression Analysis and Its Applications*, Wiley (chapter 6)

**See Also**

[nls](#), [profile](#), [profile.nls](#)

**Examples**

```
require(graphics)

# obtain the fitted object
fm1 <- nls(demand ~ SSasymptOrig(Time, A, lrc), data = BOD)
# get the profile for the fitted model
pr1 <- profile(fm1, alpha = 0.05)
opar <- par(mfrow = c(2,2), oma = c(1.1, 0, 1.1, 0), las = 1)
plot(pr1, conf = c(95, 90, 80, 50)/100)
plot(pr1, conf = c(95, 90, 80, 50)/100, absVal = FALSE)
mtext("Confidence intervals based on the profile sum of squares",
      side = 3, outer = TRUE)
mtext("BOD data - confidence levels of 50%, 80%, 90% and 95%",
      side = 1, outer = TRUE)
par(opar)
```

---

plot.spec

*Plotting Spectral Densities*


---

**Description**

Plotting method for objects of class "spec". For multivariate time series it plots the marginal spectra of the series or pairs plots of the coherency and phase of the cross-spectra.

**Usage**

```
## S3 method for class 'spec':
plot(x, add = FALSE, ci = 0.95, log = c("yes", "dB", "no"),
     xlab = "frequency", ylab = NULL, type = "l",
     ci.col = "blue", ci.lty = 3,
     main = NULL, sub = NULL,
     plot.type = c("marginal", "coherency", "phase"),
     ...)

plot.spec.phase(x, ci = 0.95,
               xlab = "frequency", ylab = "phase",
               ylim = c(-pi, pi), type = "l",
               main = NULL, ci.col = "blue", ci.lty = 3, ...)
```

```
plot.spec.coherency(x, ci = 0.95,
                    xlab = "frequency",
                    ylab = "squared coherency",
                    ylim = c(0, 1), type = "l",
                    main = NULL, ci.col = "blue", ci.lty = 3, ...)
```

### Arguments

x	an object of class "spec".
add	logical. If TRUE, add to already existing plot. Only valid for plot.type = "marginal".
ci	coverage probability for confidence interval. Plotting of the confidence bar/limits is omitted unless ci is strictly positive.
log	If "dB", plot on log10 (decibel) scale (as S-PLUS), otherwise use conventional log scale or linear scale. Logical values are also accepted. The default is "yes" unless options(ts.S.compat = TRUE) has been set, when it is "dB". Only valid for plot.type = "marginal".
xlab	the x label of the plot.
ylab	the y label of the plot. If missing a suitable label will be constructed.
type	the type of plot to be drawn, defaults to lines.
ci.col	colour for plotting confidence bar or confidence intervals for coherency and phase.
ci.lty	line type for confidence intervals for coherency and phase.
main	overall title for the plot. If missing, a suitable title is constructed.
sub	a sub title for the plot. Only used for plot.type = "marginal". If missing, a description of the smoothing is used.
plot.type	For multivariate time series, the type of plot required. Only the first character is needed.
ylim, ...	Graphical parameters.

### See Also

[spectrum](#)

---

plot.stepfun

*Plot Step Functions*

---

### Description

Method of the generic `plot` for `stepfun` objects and utility for plotting piecewise constant functions.

**Usage**

```
## S3 method for class 'stepfun':
plot(x, xval, xlim, ylim = range(c(y,Fn.kn)),
     xlab = "x", ylab = "f(x)", main = NULL,
     add = FALSE, verticals = TRUE, do.points = (n < 1000),
     pch = par("pch"), col = par("col"),
     col.points = col, cex.points = par("cex"),
     col.hor = col, col.vert = col,
     lty = par("lty"), lwd = par("lwd"), ...)

## S3 method for class 'stepfun':
lines(x, ...)
```

**Arguments**

x	an R object inheriting from "stepfun".
xval	numeric vector of abscissa values at which to evaluate x. Defaults to <a href="#">knots(x)</a> restricted to xlim.
xlim, ylim	limits for the plot region: see <a href="#">plot.window</a> . Both have sensible defaults if omitted.
xlab, ylab	labels for x and y axis.
main	main title.
add	logical; if TRUE only <i>add</i> to an existing plot.
verticals	logical; if TRUE, draw vertical lines at steps.
do.points	logical; if TRUE, also draw points at the (xlim restricted) knot locations. Default is true, for sample size < 10000.
pch	character; point character if do.points.
col	default color of all points and lines.
col.points	character or integer code; color of points if do.points.
cex.points	numeric; character expansion factor if do.points.
col.hor	color of horizontal lines.
col.vert	color of vertical lines.
lty, lwd	line type and thickness for all lines.
...	further arguments of <a href="#">plot(.)</a> , or if (add) <a href="#">segments(.)</a> .

**Value**

A list with two components

t	abscissa (x) values, including the two outermost ones.
y	y values 'in between' the t[ ].

**Author(s)**

Martin Maechler <maechler@stat.math.ethz.ch>, 1990, 1993; ported to R, 1997.

**See Also**

[ecdf](#) for empirical distribution functions as special step functions, [approxfun](#) and [splinefun](#).

**Examples**

```

require(graphics)

y0 <- c(1,2,4,3)
sfun0 <- stepfun(1:3, y0, f = 0)
sfun.2 <- stepfun(1:3, y0, f = .2)
sfun1 <- stepfun(1:3, y0, right = TRUE)

tt <- seq(0,3, by=0.1)
op <- par(mfrow=c(2,2))
plot(sfun0); plot(sfun0, xval=tt, add=TRUE, col.hor="bisque")
plot(sfun.2);plot(sfun.2,xval=tt, add=TRUE, col = "orange")# all colors
plot(sfun1);lines(sfun1, xval=tt, col.hor="coral")
##-- This is revealing :
plot(sfun0, verticals= FALSE,
      main = "stepfun(x, y0, f=f) for f = 0, .2, 1")
for(i in 1:3)
  lines(list(sfun0,sfun.2,stepfun(1:3,y0,f = 1))[[i]], col=i)
legend(2.5, 1.9, paste("f =", c(0,0.2,1)), col=1:3, lty=1, y.intersp=1)
par(op)

# Extend and/or restrict 'viewport':
plot(sfun0, xlim = c(0,5), ylim = c(0, 3.5),
      main = "plot(stepfun(*), xlim= . , ylim = .)")

##-- this works too (automatic call to ecdf.):
plot.stepfun(rt(50, df=3), col.vert = "gray20")

```

plot.ts

*Plotting Time-Series Objects***Description**

Plotting method for objects inheriting from class "ts".

**Usage**

```

## S3 method for class 'ts':
plot(x, y = NULL, plot.type = c("multiple", "single"),
      xy.labels, xy.lines, panel = lines, nc, yax.flip = FALSE,
      mar.multi = c(0, 5.1, 0, if(yax.flip) 5.1 else 2.1),
      oma.multi = c(6, 0, 5, 0), axes = TRUE, ...)

## S3 method for class 'ts':
lines(x, ...)

```

**Arguments**

*x*, *y*            time series objects, usually inheriting from class "ts".

*plot.type*        for multivariate time series, should the series be plotted separately (with a common time axis) or on a single plot?

<code>xy.labels</code>	logical, indicating if <code>text()</code> labels should be used for an x-y plot, <i>or</i> character, supplying a vector of labels to be used. The default is to label for up to 150 points, and not for more.
<code>xy.lines</code>	logical, indicating if <code>lines</code> should be drawn for an x-y plot. Defaults to the value of <code>xy.labels</code> if that is logical, otherwise to TRUE.
<code>panel</code>	a function( <code>x</code> , <code>col</code> , <code>bg</code> , <code>pch</code> , <code>type</code> , ...) which gives the action to be carried out in each panel of the display for <code>plot.type="multiple"</code> . The default is <code>lines</code> .
<code>nc</code>	the number of columns to use when <code>type="multiple"</code> . Defaults to 1 for up to 4 series, otherwise to 2.
<code>yax.flip</code>	logical indicating if the y-axis (ticks and numbering) should flip from side 2 (left) to 4 (right) from series to series when <code>type="multiple"</code> .
<code>mar.multi</code> , <code>oma.multi</code>	the (default) <code>par</code> settings for <code>plot.type="multiple"</code> . Modify with care!
<code>axes</code>	logical indicating if x- and y- axes should be drawn.
...	additional graphical arguments, see <code>plot</code> , <code>plot.default</code> and <code>par</code> .

### Details

If `y` is missing, this function creates a time series plot, for multivariate series of one of two kinds depending on `plot.type`.

If `y` is present, both `x` and `y` must be univariate, and a scatter plot  $y \sim x$  will be drawn, enhanced by using `text` if `xy.labels` is TRUE or character, and `lines` if `xy.lines` is TRUE.

### See Also

`ts` for basic time series construction and access functionality.

### Examples

```
require(graphics)

## Multivariate
z <- ts(matrix(rt(200 * 8, df = 3), 200, 8),
         start = c(1961, 1), frequency = 12)
plot(z, yax.flip = TRUE)
plot(z, axes = FALSE, ann = FALSE, frame.plot = TRUE,
     mar.multi = c(0,0,0,0), oma.multi = c(1,1,5,1))
title("plot(ts(.)), axes=FALSE, ann=FALSE, frame.plot=TRUE, mar..., oma...")

z <- window(z[,1:3], end = c(1969,12))
plot(z, type = "b")      # multiple
plot(z, plot.type="single", lty=1:3, col=4:2)

## A phase plot:
plot(nhtemp, c(nhtemp[-1], NA), cex = .8, col="blue",
     main = "Lag plot of New Haven temperatures")
## a clearer way to do this would be
## Not run:
plot(nhtemp, lag(nhtemp, 1), cex = .8, col="blue",
     main = "Lag plot of New Haven temperatures")

## End(Not run)
```



```
## xy.lines and xy.labels are FALSE for large series:
plot(lag(sunspots, 1), sunspots, pch = ".")

SMI <- EuStockMarkets[, "SMI"]
plot(lag(SMI, 1), SMI, pch = ".")
plot(lag(SMI, 20), SMI, pch = ".", log = "xy",
      main = "4 weeks lagged SMI stocks -- log scale", xy.lines= TRUE)
```

**Description**

Density, distribution function, quantile function and random generation for the Poisson distribution with parameter `lambda`.

**Usage**

```
dpois(x, lambda, log = FALSE)
ppois(q, lambda, lower.tail = TRUE, log.p = FALSE)
qpois(p, lambda, lower.tail = TRUE, log.p = FALSE)
rpois(n, lambda)
```

**Arguments**

<code>x</code>	vector of (non-negative integer) quantiles.
<code>q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>n</code>	number of random values to return.
<code>lambda</code>	vector of (non-negative) means.
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$ .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .

**Details**

The Poisson distribution has density

$$p(x) = \frac{\lambda^x e^{-\lambda}}{x!}$$

for  $x = 0, 1, 2, \dots$ . The mean and variance are  $E(X) = \text{Var}(X) = \lambda$ .

If an element of `x` is not integer, the result of `dpois` is zero, with a warning.  $p(x)$  is computed using Loader's algorithm, see the reference in `dbinom`.

The quantile is right continuous: `qpois(p, lambda)` is the smallest integer  $x$  such that  $P(X \leq x) \geq p$ .

Setting `lower.tail = FALSE` allows to get much more precise results when the default, `lower.tail = TRUE` would return 1, see the example below.

**Value**

`dpois` gives the (log) density, `ppois` gives the (log) distribution function, `qpois` gives the quantile function, and `rpois` generates random deviates.

Invalid `lambda` will result in return value `NaN`, with a warning.

**Source**

`dpois` uses C code contributed by Catherine Loader (see [dbinom](#)).

`ppois` uses `pgamma`.

`qpois` uses the Cornish–Fisher Expansion to include a skewness correction to a normal approximation, followed by a search.

`rpois` uses

Ahrens, J. H. and Dieter, U. (1982). Computer generation of Poisson deviates from modified normal distributions. *ACM Transactions on Mathematical Software*, **8**, 163–179.

**See Also**

[dbinom](#) for the binomial and [dnbinom](#) for the negative binomial distribution.

**Examples**

```
require(graphics)

-log(dpois(0:7, lambda=1) * gamma(1+ 0:7)) # == 1
Ni <- rpois(50, lambda = 4); table(factor(Ni, 0:max(Ni)))

1 - ppois(10*(15:25), lambda=100) # becomes 0 (cancellation)
  ppois(10*(15:25), lambda=100, lower.tail=FALSE) # no cancellation

par(mfrow = c(2, 1))
x <- seq(-0.01, 5, 0.01)
plot(x, ppois(x, 1), type="s", ylab="F(x)", main="Poisson(1) CDF")
plot(x, pbinom(x, 100, 0.01), type="s", ylab="F(x)",
      main="Binomial(100, 0.01) CDF")
```

---

poisson.test

*Exact Poisson tests*

---

**Description**

Performs an exact test of a simple null hypothesis about the rate parameter in Poisson distribution, or for the ratio between two rate parameters.

**Usage**

```
poisson.test(x, T = 1, r = 1,
             alternative = c("two.sided", "less", "greater"),
             conf.level = 0.95)
```

**Arguments**

<code>x</code>	number of events. A vector of length one or two.
<code>T</code>	time base for event count. A vector of length one or two.
<code>r</code>	hypothesized rate or rate ratio
<code>alternative</code>	indicates the alternative hypothesis and must be one of "two.sided", "greater" or "less". You can specify just the initial letter.
<code>conf.level</code>	confidence level for the returned confidence interval.

**Details**

Confidence intervals are computed similarly to those of `binom.test` in the one-sample case, and using `binom.test` in the two sample case.

**Value**

A list with class "htest" containing the following components:

<code>statistic</code>	the number of events (in the first sample if there are two.)
<code>parameter</code>	the corresponding expected count
<code>p.value</code>	the p-value of the test.
<code>conf.int</code>	a confidence interval for the rate or rate ratio.
<code>estimate</code>	the estimated rate or rate ratio.
<code>null.value</code>	the rate or rate ratio under the null, <code>r</code> .
<code>alternative</code>	a character string describing the alternative hypothesis.
<code>method</code>	the character string "Exact Poisson test" or "Comparison of Poisson rates" as appropriate.
<code>data.name</code>	a character string giving the names of the data.

**Note**

The rate parameter in Poisson data is often given based on a "time on test" or similar quantity (person-years, population size, or expected number of cases from mortality tables). This is the role of the `T` argument.

The one-sample case is effectively the binomial test with a very large `n`. The two sample case is converted to a binomial test by conditioning on the total event count, and the rate ratio is directly related to the odds in that binomial distribution.

**See Also**

`binom.test`

**Examples**

```
### These are paraphrased from data sets in the ISwR package

## SMR, Welsh Nickel workers
poisson.test(137, 24.19893)

## eba1977, compare Fredericia to other three cities for ages 55-59
poisson.test(c(11, 6+8+7), c(800, 1083+1050+878))
```

**Description**

Returns or evaluates orthogonal polynomials of degree 1 to `degree` over the specified set of points `x`. These are all orthogonal to the constant polynomial of degree 0. Alternatively, evaluate raw polynomials.

**Usage**

```
poly(x, ..., degree = 1, coefs = NULL, raw = FALSE)
polym(..., degree = 1, raw = FALSE)

## S3 method for class 'poly':
predict(object, newdata, ...)
```

**Arguments**

<code>x</code> , <code>newdata</code>	a numeric vector at which to evaluate the polynomial. <code>x</code> can also be a matrix. Missing values are not allowed in <code>x</code> .
<code>degree</code>	the degree of the polynomial. Must be less than the number of unique points.
<code>coefs</code>	for prediction, coefficients from a previous fit.
<code>raw</code>	if true, use raw and not orthogonal polynomials.
<code>object</code>	an object inheriting from class "poly", normally the result of a call to <code>poly</code> with a single vector argument.
<code>...</code>	<code>poly</code> , <code>polym</code> : further vectors. <code>predict.poly</code> : arguments to be passed to or from other methods.

**Details**

Although formally `degree` should be named (as it follows `...`), an unnamed second argument of length 1 will be interpreted as the degree.

The orthogonal polynomial is summarized by the coefficients, which can be used to evaluate it via the three-term recursion given in Kennedy & Gentle (1980, pp. 343–4), and used in the `predict` part of the code.

**Value**

For `poly` with a single vector argument:

A matrix with rows corresponding to points in `x` and columns corresponding to the degree, with attributes "degree" specifying the degrees of the columns and (unless `raw = TRUE`) "coefs" which contains the centering and normalization constants used in constructing the orthogonal polynomials. The matrix has given class `c("poly", "matrix")`.

Other cases of `poly` and `polym`, and `predict.poly`: a matrix.

**Note**

This routine is intended for statistical purposes such as `contr.poly`: it does not attempt to orthogonalize to machine accuracy.

**References**

- Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.  
 Kennedy, W. J. Jr and Gentle, J. E. (1980) *Statistical Computing* Marcel Dekker.

**See Also**

[contr.poly](#).  
[cars](#) for an example of polynomial regression.

**Examples**

```
(z <- poly(1:10, 3))
predict(z, seq(2, 4, 0.5))
poly(seq(4, 6, 0.5), 3, coefs = attr(z, "coefs"))

polym(1:4, c(1, 4:6), degree=3) # or just poly()
poly(cbind(1:4, c(1, 4:6)), degree=3)
```

---

 power

---

*Create a Power Link Object*


---

**Description**

Creates a link object based on the link function  $\eta = \mu^\lambda$ .

**Usage**

```
power(lambda = 1)
```

**Arguments**

lambda            a real number.

**Details**

If lambda is non-positive, it is taken as zero, and the log link is obtained. The default lambda = 1 gives the identity link.

**Value**

A list with components `linkfun`, `linkinv`, `mu.eta`, and `valideta`. See [make.link](#) for information on their meaning.

**References**

- Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

**See Also**

[make.link](#), [family](#)  
 To raise a number to a power, see [Arithmetic](#).  
 To calculate the power of a test, see various functions in the **stats** package, e.g., [power.t.test](#).

**Examples**

```
power()
quasi(link=power(1/3))[c("linkfun", "linkinv")]
```

---

power.anova.test     *Power Calculations for Balanced One-Way Analysis of Variance Tests*

---

**Description**

Compute power of test or determine parameters to obtain target power.

**Usage**

```
power.anova.test(groups = NULL, n = NULL,
                 between.var = NULL, within.var = NULL,
                 sig.level = 0.05, power = NULL)
```

**Arguments**

groups	Number of groups
n	Number of observations (per group)
between.var	Between group variance
within.var	Within group variance
sig.level	Significance level (Type I error probability)
power	Power of test (1 minus Type II error probability)

**Details**

Exactly one of the parameters `groups`, `n`, `between.var`, `power`, `within.var`, and `sig.level` must be passed as `NULL`, and that parameter is determined from the others. Notice that `sig.level` has non-`NULL` default so `NULL` must be explicitly passed if you want it computed.

**Value**

Object of class `"power.htest"`, a list of the arguments (including the computed one) augmented with `method` and `note` elements.

**Note**

`uniroot` is used to solve power equation for unknowns, so you may see errors from it, notably about inability to bracket the root when invalid arguments are given.

**Author(s)**

Claus Ekstrøm

**See Also**

[anova](#), [lm](#), [uniroot](#)

**Examples**

```
power.anova.test(groups=4, n=5, between.var=1, within.var=3)
# Power = 0.3535594

power.anova.test(groups=4, between.var=1, within.var=3,
                 power=.80)
# n = 11.92613

## Assume we have prior knowledge of the group means:
groupmeans <- c(120, 130, 140, 150)
power.anova.test(groups = length(groupmeans),
                 between.var=var(groupmeans),
                 within.var=500, power=.90) # n = 15.18834
```

---

power.prop.test      *Power Calculations for Two-Sample Test for Proportions*

---

**Description**

Compute power of test, or determine parameters to obtain target power.

**Usage**

```
power.prop.test(n = NULL, p1 = NULL, p2 = NULL, sig.level = 0.05,
               power = NULL,
               alternative = c("two.sided", "one.sided"),
               strict = FALSE)
```

**Arguments**

n	Number of observations (per group)
p1	probability in one group
p2	probability in other group
sig.level	Significance level (Type I error probability)
power	Power of test (1 minus Type II error probability)
alternative	One- or two-sided test
strict	Use strict interpretation in two-sided case

**Details**

Exactly one of the parameters `n`, `p1`, `p2`, `power`, and `sig.level` must be passed as `NULL`, and that parameter is determined from the others. Notice that `sig.level` has a non-`NULL` default so `NULL` must be explicitly passed if you want it computed.

If `strict = TRUE` is used, the power will include the probability of rejection in the opposite direction of the true effect, in the two-sided case. Without this the power will be half the significance level if the true difference is zero.

**Value**

Object of class "power.htest", a list of the arguments (including the computed one) augmented with method and note elements.

**Note**

uniroot is used to solve power equation for unknowns, so you may see errors from it, notably about inability to bracket the root when invalid arguments are given. If one of them is computed  $p_1 < p_2$  will hold, although this is not enforced when both are specified.

**Author(s)**

Peter Dalgaard. Based on previous work by Claus Ekstrøm

**See Also**

[prop.test](#), [uniroot](#)

**Examples**

```
power.prop.test(n = 50, p1 = .50, p2 = .75)
power.prop.test(p1 = .50, p2 = .75, power = .90)
power.prop.test(n = 50, p1 = .5, power = .90)
```

---

power.t.test

*Power calculations for one and two sample t tests*

---

**Description**

Compute power of test, or determine parameters to obtain target power.

**Usage**

```
power.t.test(n = NULL, delta = NULL, sd = 1, sig.level = 0.05,
             power = NULL,
             type = c("two.sample", "one.sample", "paired"),
             alternative = c("two.sided", "one.sided"),
             strict = FALSE)
```

**Arguments**

n	Number of observations (per group)
delta	True difference in means
sd	Standard deviation
sig.level	Significance level (Type I error probability)
power	Power of test (1 minus Type II error probability)
type	Type of t test
alternative	One- or two-sided test
strict	Use strict interpretation in two-sided case



**Details**

Exactly one of the parameters `n`, `delta`, `power`, `sd`, and `sig.level` must be passed as `NULL`, and that parameter is determined from the others. Notice that the last two have non-`NULL` defaults so `NULL` must be explicitly passed if you want to compute them.

If `strict = TRUE` is used, the power will include the probability of rejection in the opposite direction of the true effect, in the two-sided case. Without this the power will be half the significance level if the true difference is zero.

**Value**

Object of class `"power.htest"`, a list of the arguments (including the computed one) augmented with `method` and `note` elements.

**Note**

`uniroot` is used to solve power equation for unknowns, so you may see errors from it, notably about inability to bracket the root when invalid arguments are given.

**Author(s)**

Peter Dalgaard. Based on previous work by Claus Ekstrøm

**See Also**

[t.test](#), [uniroot](#)

**Examples**

```
power.t.test(n = 20, delta = 1)
power.t.test(power = .90, delta = 1)
power.t.test(power = .90, delta = 1, alternative = "one.sided")
```

---

 PP.test

---

*Phillips-Perron Test for Unit Roots*


---

**Description**

Computes the Phillips-Perron test for the null hypothesis that  $x$  has a unit root against a stationary alternative.

**Usage**

```
PP.test(x, lshort = TRUE)
```

**Arguments**

<code>x</code>	a numeric vector or univariate time series.
<code>lshort</code>	a logical indicating whether the short or long version of the truncation lag parameter is used.

**Details**

The general regression equation which incorporates a constant and a linear trend is used and the corrected t-statistic for a first order autoregressive coefficient equals one is computed. To estimate  $\sigma^2$  the Newey-West estimator is used. If `lshort` is TRUE, then the truncation lag parameter is set to `trunc(4*(n/100)^0.25)`, otherwise `trunc(12*(n/100)^0.25)` is used. The p-values are interpolated from Table 4.2, page 103 of Banerjee *et al.* (1993).

Missing values are not handled.

**Value**

A list with class "htest" containing the following components:

<code>statistic</code>	the value of the test statistic.
<code>parameter</code>	the truncation lag parameter.
<code>p.value</code>	the p-value of the test.
<code>method</code>	a character string indicating what type of test was performed.
<code>data.name</code>	a character string giving the name of the data.

**Author(s)**

A. Trapletti

**References**

A. Banerjee, J. J. Dolado, J. W. Galbraith, and D. F. Hendry (1993) *Cointegration, Error Correction, and the Econometric Analysis of Non-Stationary Data*, Oxford University Press, Oxford.

P. Perron (1988) Trends and random walks in macroeconomic time series. *Journal of Economic Dynamics and Control* **12**, 297–332.

**Examples**

```
x <- rnorm(1000)
PP.test(x)
y <- cumsum(x) # has unit root
PP.test(y)
```

---

ppoints

*Ordinates for Probability Plotting*

---

**Description**

Generates the sequence of probability points  $(1:m - a) / (m + (1-a) - a)$  where  $m$  is either  $n$ , if `length(n) == 1`, or `length(n)`.

**Usage**

```
ppoints(n, a = ifelse(n <= 10, 3/8, 1/2))
```

**Arguments**

`n` either the number of points generated or a vector of observations.  
`a` the offset fraction to be used; typically in (0, 1).

**Details**

If  $0 < a < 1$ , the resulting values are within (0, 1) (excluding boundaries). In any case, the resulting sequence is symmetric in [0, 1], i.e.,  $p + \text{rev}(p) == 1$ .

`ppoints()` is used in `qqplot` and `qqnorm` to generate the set of probabilities at which to evaluate the inverse distribution.

The choice of `a` follows the documentation of the function of the same name in Becker *et al* (1988), and appears to have been motivated by results from Blom (1958) on approximations to expect normal order statistics (see also [quantile](#)).

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Blom, G. (1958) *Statistical Estimates and Transformed Beta Variables*. Wiley

**See Also**

[qqplot](#), [qqnorm](#).

**Examples**

```
ppoints(4) # the same as ppoints(1:4)
ppoints(10)
ppoints(10, a=1/2)
```

---

 ppr

*Projection Pursuit Regression*


---

**Description**

Fit a projection pursuit regression model.

**Usage**

```
ppr(x, ...)

## S3 method for class 'formula':
ppr(formula, data, weights, subset, na.action,
     contrasts = NULL, ..., model = FALSE)

## Default S3 method:
ppr(x, y, weights = rep(1, n),
     ww = rep(1, q), nterms, max.terms = nterms, optlevel = 2,
     sm.method = c("supsmu", "spline", "gcv spline"),
     bass = 0, span = 0, df = 5, gcvpen = 1, ...)
```

**Arguments**

<code>formula</code>	a formula specifying one or more numeric response variables and the explanatory variables.
<code>x</code>	numeric matrix of explanatory variables. Rows represent observations, and columns represent variables. Missing values are not accepted.
<code>y</code>	numeric matrix of response variables. Rows represent observations, and columns represent variables. Missing values are not accepted.
<code>nterms</code>	number of terms to include in the final model.
<code>data</code>	a data frame (or similar: see <code>model.frame</code> ) from which variables specified in <code>formula</code> are preferentially to be taken.
<code>weights</code>	a vector of weights $w_i$ for each <i>case</i> .
<code>ww</code>	a vector of weights for each <i>response</i> , so the fit criterion is the sum over case $i$ and responses $j$ of $w_i ww_j (y_{ij} - fit_{ij})^2$ divided by the sum of $w_i$ .
<code>subset</code>	an index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)
<code>na.action</code>	a function to specify the action to be taken if NAs are found. The default action is given by <code>getOption("na.action")</code> . (NOTE: If given, this argument must be named.)
<code>contrasts</code>	the contrasts to be used when any factor explanatory variables are coded.
<code>max.terms</code>	maximum number of terms to choose from when building the model.
<code>optlevel</code>	integer from 0 to 3 which determines the thoroughness of an optimization routine in the SMART program. See the 'Details' section.
<code>sm.method</code>	the method used for smoothing the ridge functions. The default is to use Friedman's super smoother <code>supsmu</code> . The alternatives are to use the smoothing spline code underlying <code>smooth.spline</code> , either with a specified (equivalent) degrees of freedom for each ridge functions, or to allow the smoothness to be chosen by GCV.
<code>bass</code>	super smoother bass tone control used with automatic span selection (see <code>supsmu</code> ); the range of values is 0 to 10, with larger values resulting in increased smoothing.
<code>span</code>	super smoother span control (see <code>supsmu</code> ). The default, 0, results in automatic span selection by local cross validation. <code>span</code> can also take a value in $(0, 1]$ .
<code>df</code>	if <code>sm.method</code> is "spline" specifies the smoothness of each ridge term via the requested equivalent degrees of freedom.
<code>gcvpen</code>	if <code>sm.method</code> is "gcv spline" this is the penalty used in the GCV selection for each degree of freedom used.
<code>...</code>	arguments to be passed to or from other methods.
<code>model</code>	logical. If true, the model frame is returned.

**Details**

The basic method is given by Friedman (1984), and is essentially the same code used by S-PLUS's `ppreg`. This code is extremely sensitive to the compiler used.

The algorithm first adds up to `max.terms` ridge terms one at a time; it will use less if it is unable to find a term to add that makes sufficient difference. It then removes the least important term at each step until `nterms` terms are left.

The levels of optimization (argument `optlevel`) differ in how thoroughly the models are refitted during this process. At level 0 the existing ridge terms are not refitted. At level 1 the projection directions are not refitted, but the ridge functions and the regression coefficients are.

Levels 2 and 3 refit all the terms and are equivalent for one response; level 3 is more careful to re-balance the contributions from each regressor at each step and so is a little less likely to converge to a saddle point of the sum of squares criterion.

### Value

A list with the following components, many of which are for use by the method functions.

<code>call</code>	the matched call
<code>p</code>	the number of explanatory variables (after any coding)
<code>q</code>	the number of response variables
<code>mu</code>	the argument <code>nterms</code>
<code>ml</code>	the argument <code>max.terms</code>
<code>gof</code>	the overall residual (weighted) sum of squares for the selected model
<code>gofn</code>	the overall residual (weighted) sum of squares against the number of terms, up to <code>max.terms</code> . Will be invalid (and zero) for less than <code>nterms</code> .
<code>df</code>	the argument <code>df</code>
<code>edf</code>	if <code>sm.method</code> is "spline" or "gcv spline" the equivalent number of degrees of freedom for each ridge term used.
<code>xnames</code>	the names of the explanatory variables
<code>yname</code> s	the names of the response variables
<code>alpha</code>	a matrix of the projection directions, with a column for each ridge term
<code>beta</code>	a matrix of the coefficients applied for each response to the ridge terms: the rows are the responses and the columns the ridge terms
<code>yb</code>	the weighted means of each response
<code>ys</code>	the overall scale factor used: internally the responses are divided by <code>ys</code> to have unit total weighted sum of squares.
<code>fitted.values</code>	the fitted values, as a matrix if <code>q &gt; 1</code> .
<code>residuals</code>	the residuals, as a matrix if <code>q &gt; 1</code> .
<code>smod</code>	internal work array, which includes the ridge functions evaluated at the training set points.
<code>model</code>	(only if <code>model=TRUE</code> ) the model frame.

### References

Friedman, J. H. and Stuetzle, W. (1981) Projection pursuit regression. *Journal of the American Statistical Association*, **76**, 817–823.

Friedman, J. H. (1984) SMART User's Guide. Laboratory for Computational Statistics, Stanford University Technical Report No. 1.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Springer.

### See Also

[plot.ppr](#), [supsmu](#), [smooth.spline](#)

**Examples**

```

require(graphics)

# Note: your numerical values may differ
attach(rock)
areal <- area/10000; peril <- peri/10000
rock.ppr <- ppr(log(perm) ~ areal + peril + shape,
               data = rock, nterms = 2, max.terms = 5)

rock.ppr
# Call:
# ppr.formula(formula = log(perm) ~ areal + peril + shape, data = rock,
#             nterms = 2, max.terms = 5)
#
# Goodness of fit:
# 2 terms 3 terms 4 terms 5 terms
# 8.737806 5.289517 4.745799 4.490378

summary(rock.ppr)
# ..... (same as above)
# .....
#
# Projection direction vectors:
#      term 1      term 2
# areal  0.34357179  0.37071027
# peril -0.93781471 -0.61923542
# shape  0.04961846  0.69218595
#
# Coefficients of ridge terms:
#      term 1      term 2
# 1.6079271  0.5460971

par(mfrow=c(3,2))# maybe: , pty="s")
plot(rock.ppr, main="ppr(log(perm)~ ., nterms=2, max.terms=5)")
plot(update(rock.ppr, bass=5), main = "update(..., bass = 5)")
plot(update(rock.ppr, sm.method="gcv", gcvpen=2),
      main = "update(..., sm.method=\"gcv\", gcvpen=2)")
cbind(perm=rock$perm, prediction=round(exp(predict(rock.ppr)), 1))
detach()

```

prcomp

*Principal Components Analysis***Description**

Performs a principal components analysis on the given data matrix and returns the results as an object of class `prcomp`.

**Usage**

```

prcomp(x, ...)

## S3 method for class 'formula':
prcomp(formula, data = NULL, subset, na.action, ...)

```

```
## Default S3 method:
prcomp(x, retx = TRUE, center = TRUE, scale. = FALSE,
       tol = NULL, ...)

## S3 method for class 'prcomp':
predict(object, newdata, ...)
```

### Arguments

<code>formula</code>	a formula with no response variable, referring only to numeric variables.
<code>data</code>	an optional data frame (or similar: see <code>model.frame</code> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>subset</code>	an optional vector used to select rows (observations) of the data matrix <code>x</code> .
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. The default is set by the <code>na.action</code> setting of <code>options</code> , and is <code>na.fail</code> if that is unset. The 'factory-fresh' default is <code>na.omit</code> .
<code>...</code>	arguments passed to or from other methods. If <code>x</code> is a formula one might specify <code>scale.</code> or <code>tol</code> .
<code>x</code>	a numeric or complex matrix (or data frame) which provides the data for the principal components analysis.
<code>retx</code>	a logical value indicating whether the rotated variables should be returned.
<code>center</code>	a logical value indicating whether the variables should be shifted to be zero centered. Alternately, a vector of length equal the number of columns of <code>x</code> can be supplied. The value is passed to <code>scale</code> .
<code>scale.</code>	a logical value indicating whether the variables should be scaled to have unit variance before the analysis takes place. The default is <code>FALSE</code> for consistency with <code>S</code> , but in general scaling is advisable. Alternatively, a vector of length equal the number of columns of <code>x</code> can be supplied. The value is passed to <code>scale</code> .
<code>tol</code>	a value indicating the magnitude below which components should be omitted. (Components are omitted if their standard deviations are less than or equal to <code>tol</code> times the standard deviation of the first component.) With the default null setting, no components are omitted. Other settings for <code>tol</code> could be <code>tol = 0</code> or <code>tol = sqrt(.Machine\$double.eps)</code> , which would omit essentially constant components.
<code>object</code>	Object of class inheriting from "prcomp"
<code>newdata</code>	An optional data frame or matrix in which to look for variables with which to predict. If omitted, the scores are used. If the original fit used a formula or a data frame or a matrix with column names, <code>newdata</code> must contain columns with the same names. Otherwise it must contain the same number of columns, to be used in the same order.

### Details

The calculation is done by a singular value decomposition of the (centered and possibly scaled) data matrix, not by using `eigen` on the covariance matrix. This is generally the preferred method for numerical accuracy. The `print` method for these objects prints the results in a nice format and the `plot` method produces a scree plot.

Unlike `princomp`, variances are computed with the usual divisor  $N - 1$ .

Note that `scale = TRUE` cannot be used if there are zero or constant (for `center = TRUE`) variables.

### Value

`prcomp` returns a list with class "prcomp" containing the following components:

<code>sdev</code>	the standard deviations of the principal components (i.e., the square roots of the eigenvalues of the covariance/correlation matrix, though the calculation is actually done with the singular values of the data matrix).
<code>rotation</code>	the matrix of variable loadings (i.e., a matrix whose columns contain the eigenvectors). The function <code>princomp</code> returns this in the element <code>loadings</code> .
<code>x</code>	if <code>retx</code> is true the value of the rotated data (the centred (and scaled if requested) data multiplied by the <code>rotation</code> matrix) is returned. Hence, <code>cov(x)</code> is the diagonal matrix <code>diag(sdev^2)</code> . For the formula method, <code>napredict()</code> is applied to handle the treatment of values omitted by the <code>na.action</code> .
<code>center, scale</code>	the centering and scaling used, or <code>FALSE</code> .

### Note

The signs of the columns of the rotation matrix are arbitrary, and so may differ between different programs for PCA, and even between different builds of R.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Mardia, K. V., J. T. Kent, and J. M. Bibby (1979) *Multivariate Analysis*, London: Academic Press.

Venables, W. N. and B. D. Ripley (2002) *Modern Applied Statistics with S*, Springer-Verlag.

### See Also

`biplot.prcomp`, `screeplot`, `princomp`, `cor`, `cov`, `svd`, `eigen`.

### Examples

```
require(graphics)

## the variances of the variables in the
## USArrests data vary by orders of magnitude, so scaling is appropriate
prcomp(USArrests) # inappropriate
prcomp(USArrests, scale = TRUE)
prcomp(~ Murder + Assault + Rape, data = USArrests, scale = TRUE)
plot(prcomp(USArrests))
summary(prcomp(USArrests, scale = TRUE))
biplot(prcomp(USArrests, scale = TRUE))
```



---

`predict`*Model Predictions*

---

## Description

`predict` is a generic function for predictions from the results of various model fitting functions. The function invokes particular *methods* which depend on the `class` of the first argument.

## Usage

```
predict (object, ...)
```

## Arguments

<code>object</code>	a model object for which prediction is desired.
<code>...</code>	additional arguments affecting the predictions produced.

## Details

Most prediction methods which are similar to those for linear models have an argument `newdata` specifying the first place to look for explanatory variables to be used for prediction. Some considerable attempts are made to match up the columns in `newdata` to those used for fitting, for example that they are of comparable types and that any factors have the same level set in the same order (or can be transformed to be so).

Time series prediction methods in package **stats** have an argument `n.ahead` specifying how many time steps ahead to predict.

Many methods have a logical argument `se.fit` saying if standard errors are to returned.

## Value

The form of the value returned by `predict` depends on the class of its argument. See the documentation of the particular methods for details of what is produced by that method.

## References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

## See Also

[predict.glm](#), [predict.lm](#), [predict.loess](#), [predict.nls](#), [predict.poly](#), [predict.princomp](#), [predict.smooth.spline](#).

[SafePrediction](#) for prediction from polynomial and spline fits.

For time-series prediction, [predict.ar](#), [predict.Arima](#), [predict.arima0](#), [predict.HoltWinters](#), [predict.StructTS](#).

**Examples**

```
require(utils)

## All the "predict" methods found
## NB most of the methods in the standard packages are hidden.
for(fn in methods("predict"))
  try({
    f <- eval(substitute(getAnywhere(fn)$objs[[1]], list(fn = fn)))
    cat(fn, ":\n\t", deparse(args(f)), "\n")
  }, silent = TRUE)
```

---

predict.Arima	<i>Forecast from ARIMA fits</i>
---------------	---------------------------------

---

**Description**

Forecast from models fitted by [arima](#).

**Usage**

```
## S3 method for class 'Arima':
predict(object, n.ahead = 1, newxreg = NULL,
        se.fit = TRUE, ...)
```

**Arguments**

object	The result of an <code>arima</code> fit.
n.ahead	The number of steps ahead for which prediction is required.
newxreg	New values of <code>xreg</code> to be used for prediction. Must have at least <code>n.ahead</code> rows.
se.fit	Logical: should standard errors of prediction be returned?
...	arguments passed to or from other methods.

**Details**

Finite-history prediction is used, via [KalmanForecast](#). This is only statistically efficient if the MA part of the fit is invertible, so `predict.Arima` will give a warning for non-invertible MA models.

The standard errors of prediction exclude the uncertainty in the estimation of the ARMA model and the regression coefficients. According to Harvey (1993, pp. 58–9) the effect is small.

**Value**

A time series of predictions, or if `se.fit = TRUE`, a list with components `pred`, the predictions, and `se`, the estimated standard errors. Both components are time series.

## References

- Durbin, J. and Koopman, S. J. (2001) *Time Series Analysis by State Space Methods*. Oxford University Press.
- Harvey, A. C. and McKenzie, C. R. (1982) Algorithm AS182. An algorithm for finite sample prediction from ARIMA processes. *Applied Statistics* **31**, 180–187.
- Harvey, A. C. (1993) *Time Series Models*, 2nd Edition, Harvester Wheatsheaf, sections 3.3 and 4.4.

## See Also

[arima](#)

## Examples

```
predict(arima(lh, order = c(3,0,0)), n.ahead = 12)

(fit <- arima(USAccDeaths, order = c(0,1,1),
             seasonal = list(order=c(0,1,1))))
predict(fit, n.ahead = 6)
```

---

predict.glm                      *Predict Method for GLM Fits*

---

## Description

Obtains predictions and optionally estimates standard errors of those predictions from a fitted generalized linear model object.

## Usage

```
## S3 method for class 'glm':
predict(object, newdata = NULL,
        type = c("link", "response", "terms"),
        se.fit = FALSE, dispersion = NULL, terms = NULL,
        na.action = na.pass, ...)
```

## Arguments

object	a fitted object of class inheriting from "glm".
newdata	optionally, a data frame in which to look for variables with which to predict. If omitted, the fitted linear predictors are used.
type	the type of prediction required. The default is on the scale of the linear predictors; the alternative "response" is on the scale of the response variable. Thus for a default binomial model the default predictions are of log-odds (probabilities on logit scale) and type = "response" gives the predicted probabilities. The "terms" option returns a matrix giving the fitted values of each term in the model formula on the linear predictor scale. The value of this argument can be abbreviated.
se.fit	logical switch indicating if standard errors are required.
dispersion	the dispersion of the GLM fit to be assumed in computing the standard errors. If omitted, that returned by <code>summary</code> applied to the object is used.

terms	with <code>type="terms"</code> by default all terms are returned. A character vector specifies which terms are to be returned
na.action	function determining what should be done with missing values in <code>newdata</code> . The default is to predict NA.
...	further arguments passed to or from other methods.

### Details

If `newdata` is omitted the predictions are based on the data used for the fit. In that case how cases with missing values in the original fit is determined by the `na.action` argument of that fit. If `na.action = na.omit` omitted cases will not appear in the residuals, whereas if `na.action = na.exclude` they will appear (in predictions and standard errors), with residual value NA. See also [napredict](#).

### Value

If `se = FALSE`, a vector or matrix of predictions. If `se = TRUE`, a list with components

fit	Predictions
se.fit	Estimated standard errors
residual.scale	A scalar giving the square root of the dispersion used in computing the standard errors.

### Note

Variables are first looked for in `newdata` and then searched for in the usual way (which will include the environment of the formula used in the fit). A warning will be given if the variables found are not of the same length as those in `newdata` if it was supplied.

### See Also

[glm](#), [SafePrediction](#)

### Examples

```
require(graphics)

## example from Venables and Ripley (2002, pp. 190-2.)
ldose <- rep(0:5, 2)
numdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
sex <- factor(rep(c("M", "F"), c(6, 6)))
SF <- cbind(numdead, numalive=20-numdead)
budworm.lg <- glm(SF ~ sex*ldose, family=binomial)
summary(budworm.lg)

plot(c(1,32), c(0,1), type = "n", xlab = "dose",
      ylab = "prob", log = "x")
text(2^ldose, numdead/20, as.character(sex))
ld <- seq(0, 5, 0.1)
lines(2^ld, predict(budworm.lg, data.frame(ldose=ld,
      sex=factor(rep("M", length(ld)), levels=levels(sex))),
      type = "response"))
lines(2^ld, predict(budworm.lg, data.frame(ldose=ld,
      sex=factor(rep("F", length(ld)), levels=levels(sex))),
```

```
type = "response"))
```

---

```
predict.HoltWinters
```

*Prediction Function for Fitted Holt-Winters Models*

---

## Description

Computes predictions and prediction intervals for models fitted by the Holt-Winters method.

## Usage

```
## S3 method for class 'HoltWinters':  
predict(object, n.ahead=1, prediction.interval = FALSE,  
        level = 0.95, ...)
```

## Arguments

object	An object of class <code>HoltWinters</code> .
n.ahead	Number of future periods to predict.
prediction.interval	logical. If <code>TRUE</code> , the lower and upper bounds of the corresponding prediction intervals are computed.
level	Confidence level for the prediction interval.
...	arguments passed to or from other methods.

## Value

A time series of the predicted values. If prediction intervals are requested, a multiple time series is returned with columns `fit`, `lwr` and `upr` for the predicted values and the lower and upper bounds respectively.

## Author(s)

David Meyer <David.Meyer@wu-wien.ac.at>

## References

C. C. Holt (1957) Forecasting trends and seasonals by exponentially weighted moving averages, *ONR Research Memorandum, Carnegie Institute of Technology* **52**.

P. R. Winters (1960) Forecasting sales by exponentially weighted moving averages, *Management Science* **6**, 324–342.

## See Also

[HoltWinters](#)

**Examples**

```
require(graphics)

m <- HoltWinters(co2)
p <- predict(m, 50, prediction.interval = TRUE)
plot(m, p)
```

---

predict.lm

*Predict method for Linear Model Fits*


---

**Description**

Predicted values based on linear model object.

**Usage**

```
## S3 method for class 'lm':
predict(object, newdata, se.fit = FALSE, scale = NULL, df = Inf,
        interval = c("none", "confidence", "prediction"),
        level = 0.95, type = c("response", "terms"),
        terms = NULL, na.action = na.pass,
        pred.var = res.var/weights, weights = 1, ...)
```

**Arguments**

object	Object of class inheriting from "lm"
newdata	An optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
se.fit	A switch indicating if standard errors are required.
scale	Scale parameter for std.err. calculation
df	Degrees of freedom for scale
interval	Type of interval calculation.
level	Tolerance/confidence level
type	Type of prediction (response or model term).
terms	If type="terms", which terms (default is all terms)
na.action	function determining what should be done with missing values in newdata. The default is to predict NA.
pred.var	the variance(s) for future observations to be assumed for prediction intervals. See 'Details'.
weights	variance weights for prediction. This can be a numeric vector or a one-sided model formula. In the latter case, it is interpreted as an expression evaluated in newdata
...	further arguments passed to or from other methods.

## Details

`predict.lm` produces predicted values, obtained by evaluating the regression function in the frame `newdata` (which defaults to `model.frame(object)`). If the logical `se.fit` is `TRUE`, standard errors of the predictions are calculated. If the numeric argument `scale` is set (with optional `df`), it is used as the residual standard deviation in the computation of the standard errors, otherwise this is extracted from the model fit. Setting `intervals` specifies computation of confidence or prediction (tolerance) intervals at the specified `level`, sometimes referred to as narrow vs. wide intervals.

If the fit is rank-deficient, some of the columns of the design matrix will have been dropped. Prediction from such a fit only makes sense if `newdata` is contained in the same subspace as the original data. That cannot be checked accurately, so a warning is issued.

If `newdata` is omitted the predictions are based on the data used for the fit. In that case how cases with missing values in the original fit is determined by the `na.action` argument of that fit. If `na.action = na.omit` omitted cases will not appear in the residuals, whereas if `na.action = na.exclude` they will appear (in predictions, standard errors or interval limits), with residual value `NA`. See also `napredict`.

The prediction intervals are for a single observation at each case in `newdata` (or by default, the data used for the fit) with error variance(s) `pred.var`. This can be a multiple of `res.var`, the estimated value of  $\sigma^2$ : the default is to assume that future observations have the same error variance as those used for fitting. If `weights` is supplied, the inverse of this is used as a scale factor. For a weighted fit, if the prediction is for the original data frame, `weights` defaults to the weights used for the model fit, with a warning since it might not be the intended result. If the fit was weighted and `newdata` is given, the default is to assume constant prediction variance, with a warning.

## Value

`predict.lm` produces a vector of predictions or a matrix of predictions and bounds with column names `fit`, `lwr`, and `upr` if `interval` is set. If `se.fit` is `TRUE`, a list with the following components is returned:

<code>fit</code>	vector or matrix as above
<code>se.fit</code>	standard error of predicted means
<code>residual.scale</code>	residual standard deviations
<code>df</code>	degrees of freedom for residual

## Note

Variables are first looked for in `newdata` and then searched for in the usual way (which will include the environment of the formula used in the fit). A warning will be given if the variables found are not of the same length as those in `newdata` if it was supplied.

Notice that prediction variances and prediction intervals always refer to *future* observations, possibly corresponding to the same predictors as used for the fit. The variance of the *residuals* will be smaller.

Strictly speaking, the formula used for prediction limits assumes that the degrees of freedom for the fit are the same as those for the residual variance. This may not be the case if `res.var` is not obtained from the fit.

**See Also**

The model fitting function [lm](#), [predict](#).

[SafePrediction](#) for prediction from polynomial and spline fits.

**Examples**

```
require(graphics)

## Predictions
x <- rnorm(15)
y <- x + rnorm(15)
predict(lm(y ~ x))
new <- data.frame(x = seq(-3, 3, 0.5))
predict(lm(y ~ x), new, se.fit = TRUE)
pred.w.plim <- predict(lm(y ~ x), new, interval="prediction")
pred.w.clim <- predict(lm(y ~ x), new, interval="confidence")
matplot(new$x, cbind(pred.w.clim, pred.w.plim[, -1]),
        lty=c(1,2,2,3,3), type="l", ylab="predicted y")

## Prediction intervals, special cases
## The first three of these throw warnings
w <- 1 + x^2
fit <- lm(y ~ x)
wfit <- lm(y ~ x, weights = w)
predict(fit, interval = "prediction")
predict(wfit, interval = "prediction")
predict(wfit, new, interval = "prediction")
predict(wfit, new, interval = "prediction", weights = (new$x)^2)
predict(wfit, new, interval = "prediction", weights = ~x^2)
```

---

predict.loess

*Predict Loess Curve or Surface*

---

**Description**

Predictions from a loess fit, optionally with standard errors.

**Usage**

```
## S3 method for class 'loess':
predict(object, newdata = NULL, se = FALSE, ...)
```

**Arguments**

object	an object fitted by loess.
newdata	an optional data frame in which to look for variables with which to predict, or a matrix or vector containing exactly the variables needs for prediction. If missing, the original data points are used.
se	should standard errors be computed?
...	arguments passed to or from other methods.



**Details**

The standard errors calculation is slower than prediction.

When the fit was made using `surface="interpolate"` (the default), `predict.loess` will not extrapolate – so points outside an axis-aligned hypercube enclosing the original data will have missing (NA) predictions and standard errors.

**Value**

If `se = FALSE`, a vector giving the prediction for each row of `newdata` (or the original data). If `se = TRUE`, a list containing components

<code>fit</code>	the predicted values.
<code>se</code>	an estimated standard error for each predicted value.
<code>residual.scale</code>	the estimated scale of the residuals used in computing the standard errors.
<code>df</code>	an estimate of the effective degrees of freedom used in estimating the residual scale, intended for use with t-based confidence intervals.

If `newdata` was the result of a call to `expand.grid`, the predictions (and s.e.'s if requested) will be an array of the appropriate dimensions.

**Note**

Variables are first looked for in `newdata` and then searched for in the usual way (which will include the environment of the formula used in the fit). A warning will be given if the variables found are not of the same length as those in `newdata` if it was supplied.

**Author(s)**

B. D. Ripley, based on the `cloess` package of Cleveland, Grosse and Shyu.

**See Also**

[loess](#)

**Examples**

```
cars.lo <- loess(dist ~ speed, cars)
predict(cars.lo, data.frame(speed=seq(5, 30, 1)), se=TRUE)
# to get extrapolation
cars.lo2 <- loess(dist ~ speed, cars,
  control=loess.control(surface="direct"))
predict(cars.lo2, data.frame(speed=seq(5, 30, 1)), se=TRUE)
```

---

 predict.nls

*Predicting from Nonlinear Least Squares Fits*


---

### Description

predict.nls produces predicted values, obtained by evaluating the regression function in the frame newdata. If the logical se.fit is TRUE, standard errors of the predictions are calculated. If the numeric argument scale is set (with optional df), it is used as the residual standard deviation in the computation of the standard errors, otherwise this is extracted from the model fit. Setting intervals specifies computation of confidence or prediction (tolerance) intervals at the specified level.

At present se.fit and interval are ignored.

### Usage

```
## S3 method for class 'nls':
predict(object, newdata , se.fit = FALSE, scale = NULL, df = Inf,
        interval = c("none", "confidence", "prediction"),
        level = 0.95, ...)
```

### Arguments

object	An object that inherits from class nls.
newdata	A named list or data frame in which to look for variables with which to predict. If newdata is missing the fitted values at the original data points are returned.
se.fit	A logical value indicating if the standard errors of the predictions should be calculated. Defaults to FALSE. At present this argument is ignored.
scale	A numeric scalar. If it is set (with optional df), it is used as the residual standard deviation in the computation of the standard errors, otherwise this information is extracted from the model fit. At present this argument is ignored.
df	A positive numeric scalar giving the number of degrees of freedom for the scale estimate. At present this argument is ignored.
interval	A character string indicating if prediction intervals or a confidence interval on the mean responses are to be calculated. At present this argument is ignored.
level	A numeric scalar between 0 and 1 giving the confidence level for the intervals (if any) to be calculated. At present this argument is ignored.
...	Additional optional arguments. At present no optional arguments are used.

### Value

predict.nls produces a vector of predictions. When implemented, interval will produce a matrix of predictions and bounds with column names fit, lwr, and upr. When implemented, if se.fit is TRUE, a list with the following components will be returned:

fit	vector or matrix as above
se.fit	standard error of predictions
residual.scale	residual standard deviations
df	degrees of freedom for residual

**Note**

Variables are first looked for in `newdata` and then searched for in the usual way (which will include the environment of the formula used in the fit). A warning will be given if the variables found are not of the same length as those in `newdata` if it was supplied.

**See Also**

The model fitting function `nls`, `predict`.

**Examples**

```
require(graphics)

fm <- nls(demand ~ SSasymptOrig(Time, A, lrc), data = BOD)
predict(fm) # fitted values at observed times
## Form data plot and smooth line for the predictions
opar <- par(las = 1)
plot(demand ~ Time, data = BOD, col = 4,
     main = "BOD data and fitted first-order curve",
     xlim = c(0,7), ylim = c(0, 20) )
tt <- seq(0, 8, length = 101)
lines(tt, predict(fm, list(Time = tt)))
par(opar)
```

---

```
predict.smooth.spline
```

*Predict from Smoothing Spline Fit*

---

**Description**

Predict a smoothing spline fit at new points, return the derivative if desired. The predicted fit is linear beyond the original data.

**Usage**

```
## S3 method for class 'smooth.spline':
predict(object, x, deriv = 0, ...)
```

**Arguments**

<code>object</code>	a fit from <code>smooth.spline</code> .
<code>x</code>	the new values of <code>x</code> .
<code>deriv</code>	integer; the order of the derivative required.
<code>...</code>	further arguments passed to or from other methods.

**Value**

A list with components

<code>x</code>	The input <code>x</code> .
<code>y</code>	The fitted values or derivatives at <code>x</code> .

**See Also**[smooth.spline](#)**Examples**

```

require(graphics)

attach(cars)
cars.spl <- smooth.spline(speed, dist, df=6.4)

## "Proof" that the derivatives are okay, by comparing with approximation
diff.quot <- function(x,y) {
  ## Difference quotient (central differences where available)
  n <- length(x); i1 <- 1:2; i2 <- (n-1):n
  c(diff(y[i1]) / diff(x[i1]), (y[-i1] - y[-i2]) / (x[-i1] - x[-i2]),
    diff(y[i2]) / diff(x[i2]))
}

xx <- unique(sort(c(seq(0,30, by = .2), kn <- unique(speed))))
i.kn <- match(kn, xx)# indices of knots within xx
op <- par(mfrow = c(2,2))
plot(speed, dist, xlim = range(xx), main = "Smooth.spline & derivatives")
lines(pp <- predict(cars.spl, xx), col = "red")
points(kn, pp$y[i.kn], pch = 3, col="dark red")
mtext("s(x)", col = "red")
for(d in 1:3){
  n <- length(pp$x)
  plot(pp$x, diff.quot(pp$x,pp$y), type = 'l', xlab="x", ylab="",
    col = "blue", col.main = "red",
    main= paste("s",paste(rep("'",d), collapse=""), "(x)", sep=""))
  mtext("Difference quotient approx.(last)", col = "blue")
  lines(pp <- predict(cars.spl, xx, deriv = d), col = "red")

  points(kn, pp$y[i.kn], pch = 3, col="dark red")
  abline(h=0, lty = 3, col = "gray")
}
detach(); par(op)

```

preplot

*Pre-computations for a Plotting Object***Description**

Compute an object to be used for plots relating to the given model object.

**Usage**

```
preplot(object, ...)
```

**Arguments**

object	a fitted model object.
...	additional arguments for specific methods.

**Details**

Only the generic function is currently provided in base R, but some add-on packages have methods. Principally here for S compatibility.

**Value**

An object set up to make a plot that describes object.

---

 princomp

*Principal Components Analysis*


---

**Description**

princomp performs a principal components analysis on the given numeric data matrix and returns the results as an object of class princomp.

**Usage**

```
princomp(x, ...)

## S3 method for class 'formula':
princomp(formula, data = NULL, subset, na.action, ...)

## Default S3 method:
princomp(x, cor = FALSE, scores = TRUE, covmat = NULL,
         subset = rep(TRUE, nrow(as.matrix(x))), ...)

## S3 method for class 'princomp':
predict(object, newdata, ...)
```

**Arguments**

formula	a formula with no response variable, referring only to numeric variables.
data	an optional data frame (or similar: see <code>model.frame</code> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
subset	an optional vector used to select rows (observations) of the data matrix <code>x</code> .
na.action	a function which indicates what should happen when the data contain NAs. The default is set by the <code>na.action</code> setting of <code>options</code> , and is <code>na.fail</code> if that is unset. The 'factory-fresh' default is <code>na.omit</code> .
x	a numeric matrix or data frame which provides the data for the principal components analysis.
cor	a logical value indicating whether the calculation should use the correlation matrix or the covariance matrix. (The correlation matrix can only be used if there are no constant variables.)
scores	a logical value indicating whether the score on each principal component should be calculated.

<code>covmat</code>	a covariance matrix, or a covariance list as returned by <code>cov.wt</code> (and <code>cov.mve</code> or <code>cov.mcd</code> from package <b>MASS</b> ). If supplied, this is used rather than the covariance matrix of <code>x</code> .
<code>...</code>	arguments passed to or from other methods. If <code>x</code> is a formula one might specify <code>cor</code> or <code>scores</code> .
<code>object</code>	Object of class inheriting from "princomp"
<code>newdata</code>	An optional data frame or matrix in which to look for variables with which to predict. If omitted, the scores are used. If the original fit used a formula or a data frame or a matrix with column names, <code>newdata</code> must contain columns with the same names. Otherwise it must contain the same number of columns, to be used in the same order.

## Details

`princomp` is a generic function with "formula" and "default" methods.

The calculation is done using `eigen` on the correlation or covariance matrix, as determined by `cor`. This is done for compatibility with the S-PLUS result. A preferred method of calculation is to use `svd` on `x`, as is done in `prcomp`.

Note that the default calculation uses divisor `N` for the covariance matrix.

The `print` method for these objects prints the results in a nice format and the `plot` method produces a scree plot (`screeplot`). There is also a `biplot` method.

If `x` is a formula then the standard NA-handling is applied to the scores (if requested): see `napredict`.

`princomp` only handles so-called R-mode PCA, that is feature extraction of variables. If a data matrix is supplied (possibly via a formula) it is required that there are at least as many units as variables. For Q-mode PCA use `prcomp`.

## Value

`princomp` returns a list with class "princomp" containing the following components:

<code>sdev</code>	the standard deviations of the principal components.
<code>loadings</code>	the matrix of variable loadings (i.e., a matrix whose columns contain the eigenvectors). This is of class "loadings": see <code>loadings</code> for its <code>print</code> method.
<code>center</code>	the means that were subtracted.
<code>scale</code>	the scalings applied to each variable.
<code>n.obs</code>	the number of observations.
<code>scores</code>	if <code>scores = TRUE</code> , the scores of the supplied data on the principal components. These are non-null only if <code>x</code> was supplied, and if <code>covmat</code> was also supplied if it was a covariance list. For the formula method, <code>napredict()</code> is applied to handle the treatment of values omitted by the <code>na.action</code> .
<code>call</code>	the matched call.
<code>na.action</code>	If relevant.

## Note

The signs of the columns of the loadings and scores are arbitrary, and so may differ between different programs for PCA, and even between different builds of R.

**References**

- Mardia, K. V., J. T. Kent and J. M. Bibby (1979). *Multivariate Analysis*, London: Academic Press.
- Venables, W. N. and B. D. Ripley (2002). *Modern Applied Statistics with S*, Springer-Verlag.

**See Also**

[summary.princomp](#), [screeplot](#), [biplot.princomp](#), [prcomp](#), [cor](#), [cov](#), [eigen](#).

**Examples**

```
require(graphics)

## The variances of the variables in the
## USArrests data vary by orders of magnitude, so scaling is appropriate
(pc.cr <- princomp(USArrests)) # inappropriate
princomp(USArrests, cor = TRUE) # ^= prcomp(USArrests, scale=TRUE)
## Similar, but different:
## The standard deviations differ by a factor of sqrt(49/50)

summary(pc.cr <- princomp(USArrests, cor = TRUE))
loadings(pc.cr) ## note that blank entries are small but not zero
plot(pc.cr) # shows a screeplot.
biplot(pc.cr)

## Formula interface
princomp(~ ., data = USArrests, cor = TRUE)
# NA-handling
USArrests[1, 2] <- NA
pc.cr <- princomp(~ Murder + Assault + UrbanPop,
                  data = USArrests, na.action=na.exclude, cor = TRUE)
pc.cr$scores
```

---

```
print.power.htest Print method for power calculation object
```

---

**Description**

Print object of class "power.htest" in nice layout.

**Usage**

```
## S3 method for class 'power.htest':
print(x, ...)
```

**Arguments**

x                    Object of class "power.htest".

...                   further arguments to be passed to or from methods.

**Details**

A `power.htest` object is just a named list of numbers and character strings, supplemented with `method` and `note` elements. The `method` is displayed as a title, the `note` as a footnote, and the remaining elements are given in an aligned 'name = value' format.

**Value**

none

**Author(s)**

Peter Dalgaard

**See Also**

[power.t.test](#), [power.prop.test](#)

---

print.ts

*Printing Time-Series Objects*

---

**Description**

Print method for time series objects.

**Usage**

```
## S3 method for class 'ts':  
print(x, calendar, ...)
```

**Arguments**

<code>x</code>	a time series object.
<code>calendar</code>	enable/disable the display of information about month names, quarter names or year when printing. The default is <code>TRUE</code> for a frequency of 4 or 12, <code>FALSE</code> otherwise.
<code>...</code>	additional arguments to <a href="#">print</a> .

**Details**

This is the [print](#) methods for objects inheriting from class "ts".

**See Also**

[print](#), [ts](#).

**Examples**

```
print(ts(1:10, frequency = 7, start = c(12, 2)), calendar = TRUE)
```



---

printCoefmat                      *Print Coefficient Matrices*

---

### Description

Utility function to be used in higher-level `print` methods, such as `print.summary.lm`, `print.summary.glm` and `print.anova`. The goal is to provide a flexible interface with smart defaults such that often, only `x` needs to be specified.

### Usage

```
printCoefmat(x, digits=max(3, getOption("digits") - 2),
             signif.stars = getOption("show.signif.stars"),
             signif.legend = signif.stars,
             dig.tst = max(1, min(5, digits - 1)),
             cs.ind = 1L:k, tst.ind = k + 1L, zap.ind = integer(0),
             P.values = NULL,
             has.Pvalue = nc >= 4L &&
                 substr(colnames(x)[nc], 1L, 3L) == "Pr(",
             eps.Pvalue = .Machine$double.eps,
             na.print = "NA", ...)
```

### Arguments

<code>x</code>	a numeric matrix like object, to be printed.
<code>digits</code>	minimum number of significant digits to be used for most numbers.
<code>signif.stars</code>	logical; if TRUE, P-values are additionally encoded visually as ‘significance stars’ in order to help scanning of long coefficient tables. It defaults to the <code>show.signif.stars</code> slot of <code>options</code> .
<code>signif.legend</code>	logical; if TRUE, a legend for the ‘significance stars’ is printed provided <code>signif.stars=TRUE</code> .
<code>dig.tst</code>	minimum number of significant digits for the test statistics, see <code>tst.ind</code> .
<code>cs.ind</code>	indices (integer) of column numbers which are (like) coefficients and standard errors to be formatted together.
<code>tst.ind</code>	indices (integer) of column numbers for test statistics.
<code>zap.ind</code>	indices (integer) of column numbers which should be formatted by <code>zapsmall</code> , i.e., by ‘zapping’ values close to 0.
<code>P.values</code>	logical or NULL; if TRUE, the last column of <code>x</code> is formatted by <code>format.pval</code> as P values. If <code>P.values = NULL</code> , the default, it is set to TRUE only if <code>options("show.coef.Pvalue")</code> is TRUE <i>and</i> <code>x</code> has at least 4 columns <i>and</i> the last column name of <code>x</code> starts with <code>"Pr("</code> .
<code>has.Pvalue</code>	logical; if TRUE, the last column of <code>x</code> contains P values; in that case, it is printed if and only if <code>P.values</code> (above) is true.
<code>eps.Pvalue</code>	number,..
<code>na.print</code>	a character string to code NA values in printed output.
<code>...</code>	further arguments for <code>print</code> .

**Value**

Invisibly returns its argument, `x`.

**Author(s)**

Martin Maechler

**See Also**

[print.summary.lm](#), [format.pval](#), [format](#).

**Examples**

```
cmat <- cbind(rnorm(3, 10), sqrt(rchisq(3, 12)))
cmat <- cbind(cmat, cmat[,1]/cmat[,2])
cmat <- cbind(cmat, 2*pnorm(-cmat[,3]))
colnames(cmat) <- c("Estimate", "Std.Err", "Z value", "Pr(>z)")
printCoefmat(cmat[,1:3])
printCoefmat(cmat)
options(show.coef.Pvalues = FALSE)
printCoefmat(cmat, digits=2)
printCoefmat(cmat, digits=2, P.values = TRUE)
options(show.coef.Pvalues = TRUE) # revert
```

---

profile

*Generic Function for Profiling Models*

---

**Description**

Investigates behavior of objective function near the solution represented by `fitted`.

See documentation on method functions for further details.

**Usage**

```
profile(fitted, ...)
```

**Arguments**

`fitted`            the original fitted model object.

`...`            additional parameters. See documentation on individual methods.

**Value**

A list with an element for each parameter being profiled. See the individual methods for further details.

**See Also**

[profile.nls](#), [profile.glm](#) in package **MASS**, ...

For profiling R code, see [Rprof](#).

---

 profile.nls

 Method for Profiling nls Objects
 

---

### Description

Investigates the profile log-likelihood function for a fitted model of class "nls".

### Usage

```
## S3 method for class 'nls':
profile(fitted, which = 1:npar, maxpts = 100, alphamax = 0.01,
       delta.t = cutoff/5, ...)
```

### Arguments

fitted	the original fitted model object.
which	the original model parameters which should be profiled. This can be a numeric or character vector. By default, all non-linear parameters are profiled.
maxpts	maximum number of points to be used for profiling each parameter.
alphamax	highest significance level allowed for the profile t-statistics.
delta.t	suggested change on the scale of the profile t-statistics. Default value chosen to allow profiling at about 10 parameter values.
...	further arguments passed to or from other methods.

### Details

The profile t-statistics is defined as the square root of change in sum-of-squares divided by residual standard error with an appropriate sign.

### Value

A list with an element for each parameter being profiled. The elements are data-frames with two variables

par.vals	a matrix of parameter values for each fitted model.
tau	the profile t-statistics.

### Author(s)

Of the original version, Douglas M. Bates and Saikat DebRoy

### References

Bates, D. M. and Watts, D. G. (1988), *Nonlinear Regression Analysis and Its Applications*, Wiley (chapter 6).

### See Also

[nls](#), [profile](#), [plot.profile.nls](#)

**Examples**

```
# obtain the fitted object
fm1 <- nls(demand ~ SSasymOrig(Time, A, lrc), data = BOD)
# get the profile for the fitted model: default level is too extreme
pr1 <- profile(fm1, alpha = 0.05)
# profiled values for the two parameters
pr1$A
pr1$lrc
# see also example(plot.profile.nls)
```

proj

*Projections of Models***Description**

`proj` returns a matrix or list of matrices giving the projections of the data onto the terms of a linear model. It is most frequently used for [aov](#) models.

**Usage**

```
proj(object, ...)
```

```
## S3 method for class 'aov':
proj(object, onedf = FALSE, unweighted.scale = FALSE, ...)
```

```
## S3 method for class 'aovlist':
proj(object, onedf = FALSE, unweighted.scale = FALSE, ...)
```

```
## Default S3 method:
proj(object, onedf = TRUE, ...)
```

```
## S3 method for class 'lm':
proj(object, onedf = FALSE, unweighted.scale = FALSE, ...)
```

**Arguments**

<code>object</code>	An object of class "lm" or a class inheriting from it, or an object with a similar structure including in particular components <code>qr</code> and <code>effects</code> .
<code>onedf</code>	A logical flag. If <code>TRUE</code> , a projection is returned for all the columns of the model matrix. If <code>FALSE</code> , the single-column projections are collapsed by terms of the model (as represented in the analysis of variance table).
<code>unweighted.scale</code>	If the fit producing <code>object</code> used weights, this determines if the projections correspond to weighted or unweighted observations.
<code>...</code>	Swallow and ignore any other arguments.

**Details**

A projection is given for each stratum of the object, so for `aov` models with an `Error` term the result is a list of projections.

**Value**

A projection matrix or (for multi-stratum objects) a list of projection matrices.

Each projection is a matrix with a row for each observations and either a column for each term (`onedf = FALSE`) or for each coefficient (`onedf = TRUE`). Projection matrices from the default method have orthogonal columns representing the projection of the response onto the column space of the Q matrix from the QR decomposition. The fitted values are the sum of the projections, and the sum of squares for each column is the reduction in sum of squares from fitting that column (after those to the left of it).

The methods for `lm` and `aov` models add a column to the projection matrix giving the residuals (the projection of the data onto the orthogonal complement of the model space).

Strictly, when `onedf = FALSE` the result is not a projection, but the columns represent sums of projections onto the columns of the model matrix corresponding to that term. In this case the matrix does not depend on the coding used.

**Author(s)**

The design was inspired by the S function of the same name described in Chambers *et al.* (1992).

**References**

Chambers, J. M., Freeny, A and Heiberger, R. M. (1992) *Analysis of variance; designed experiments*. Chapter 5 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

[aov](#), [lm](#), [model.tables](#)

**Examples**

```
N <- c(0,1,0,1,1,1,0,0,0,1,1,0,1,1,0,0,1,0,1,0,1,0,1,1,0,0)
P <- c(1,1,0,0,0,1,0,1,1,1,0,0,0,1,0,1,1,0,0,1,0,0,1,0,1,1,0)
K <- c(1,0,0,1,0,1,1,0,0,1,0,1,0,1,1,0,0,0,1,1,1,0,1,0,1,0)
yield <- c(49.5,62.8,46.8,57.0,59.8,58.5,55.5,56.0,62.8,55.8,69.5,
55.0, 62.0,48.8,45.5,44.2,52.0,51.5,49.8,48.8,57.2,59.0,53.2,56.0)

npk <- data.frame(block=gl(6,4), N=factor(N), P=factor(P),
                  K=factor(K), yield=yield)
npk.aov <- aov(yield ~ block + N*P*K, npk)
proj(npk.aov)

## as a test, not particularly sensible
options(contrasts=c("contr.helmert", "contr.treatment"))
npk.aovE <- aov(yield ~ N*P*K + Error(block), npk)
proj(npk.aovE)
```

---

prop.test                      *Test of Equal or Given Proportions*

---

### Description

prop.test can be used for testing the null that the proportions (probabilities of success) in several groups are the same, or that they equal certain given values.

### Usage

```
prop.test(x, n, p = NULL,
          alternative = c("two.sided", "less", "greater"),
          conf.level = 0.95, correct = TRUE)
```

### Arguments

x	a vector of counts of successes, a one-dimensional table with two entries, or a two-dimensional table (or matrix) with 2 columns, giving the counts of successes and failures, respectively.
n	a vector of counts of trials; ignored if x is a matrix or a table.
p	a vector of probabilities of success. The length of p must be the same as the number of groups specified by x, and its elements must be greater than 0 and less than 1.
alternative	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter. Only used for testing the null that a single proportion equals a given value, or that two proportions are equal; ignored otherwise.
conf.level	confidence level of the returned confidence interval. Must be a single number between 0 and 1. Only used when testing the null that a single proportion equals a given value, or that two proportions are equal; ignored otherwise.
correct	a logical indicating whether Yates' continuity correction should be applied where possible.

### Details

Only groups with finite numbers of successes and failures are used. Counts of successes and failures must be nonnegative and hence not greater than the corresponding numbers of trials which must be positive. All finite counts should be integers.

If p is NULL and there is more than one group, the null tested is that the proportions in each group are the same. If there are two groups, the alternatives are that the probability of success in the first group is less than, not equal to, or greater than the probability of success in the second group, as specified by alternative. A confidence interval for the difference of proportions with confidence level as specified by conf.level and clipped to  $[-1, 1]$  is returned. Continuity correction is used only if it does not exceed the difference of the sample proportions in absolute value. Otherwise, if there are more than 2 groups, the alternative is always "two.sided", the returned confidence interval is NULL, and continuity correction is never used.

If there is only one group, then the null tested is that the underlying probability of success is p, or .5 if p is not given. The alternative is that the probability of success is less than, not equal to, or greater than p or 0.5, respectively, as specified by alternative. A confidence interval for the

underlying proportion with confidence level as specified by `conf.level` and clipped to  $[0, 1]$  is returned. Continuity correction is used only if it does not exceed the difference between sample and null proportions in absolute value. The confidence interval is computed by inverting the score test.

Finally, if `p` is given and there are more than 2 groups, the null tested is that the underlying probabilities of success are those given by `p`. The alternative is always `"two.sided"`, the returned confidence interval is `NULL`, and continuity correction is never used.

## Value

A list with class `"htest"` containing the following components:

<code>statistic</code>	the value of Pearson's chi-squared test statistic.
<code>parameter</code>	the degrees of freedom of the approximate chi-squared distribution of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>estimate</code>	a vector with the sample proportions $x/n$ .
<code>conf.int</code>	a confidence interval for the true proportion if there is one group, or for the difference in proportions if there are 2 groups and <code>p</code> is not given, or <code>NULL</code> otherwise. In the cases where it is not <code>NULL</code> , the returned confidence interval has an asymptotic confidence level as specified by <code>conf.level</code> , and is appropriate to the specified alternative hypothesis.
<code>null.value</code>	the value of <code>p</code> if specified by the null, or <code>NULL</code> otherwise.
<code>alternative</code>	a character string describing the alternative.
<code>method</code>	a character string indicating the method used, and whether Yates' continuity correction was applied.
<code>data.name</code>	a character string giving the names of the data.

## References

Wilson, E.B. (1927) Probable inference, the law of succession, and statistical inference. *J. Am. Stat. Assoc.*, **22**, 209–212.

Newcombe R.G. (1998) Two-Sided Confidence Intervals for the Single Proportion: Comparison of Seven Methods. *Statistics in Medicine* **17**, 857–872.

Newcombe R.G. (1998) Interval Estimation for the Difference Between Independent Proportions: Comparison of Eleven Methods. *Statistics in Medicine* **17**, 873–890.

## See Also

[binom.test](#) for an *exact* test of a binomial hypothesis.

## Examples

```
heads <- rbinom(1, size=100, prob = .5)
prop.test(heads, 100)           # continuity correction TRUE by default
prop.test(heads, 100, correct = FALSE)

## Data from Fleiss (1981), p. 139.
## H0: The null hypothesis is that the four populations from which
##     the patients were drawn have the same true proportion of smokers.
## A:  The alternative is that this proportion is different in at
##     least one of the populations.
```

```
smokers <- c( 83, 90, 129, 70 )
patients <- c( 86, 93, 136, 82 )
prop.test(smokers, patients)
```

---

prop.trend.test      *Test for trend in proportions*

---

### Description

Performs chi-squared test for trend in proportions, i.e., a test asymptotically optimal for local alternatives where the log odds vary in proportion with `score`. By default, `score` is chosen as the group numbers.

### Usage

```
prop.trend.test(x, n, score = seq_along(x))
```

### Arguments

<code>x</code>	Number of events
<code>n</code>	Number of trials
<code>score</code>	Group score

### Value

An object of class "htest" with title, test statistic, p-value, etc.

### Note

This really should get integrated with `prop.test`

### Author(s)

Peter Dalgaard

### See Also

[prop.test](#)

### Examples

```
smokers <- c( 83, 90, 129, 70 )
patients <- c( 86, 93, 136, 82 )
prop.test(smokers, patients)
prop.trend.test(smokers, patients)
prop.trend.test(smokers, patients, c(0,0,0,1))
```



qqnorm

*Quantile-Quantile Plots***Description**

qqnorm is a generic function the default method of which produces a normal QQ plot of the values in *y*. qqline adds a line to a normal quantile-quantile plot which passes through the first and third quartiles.

qqplot produces a QQ plot of two datasets.

Graphical parameters may be given as arguments to qqnorm, qqplot and qqline.

**Usage**

```
qqnorm(y, ...)
## Default S3 method:
qqnorm(y, ylim, main = "Normal Q-Q Plot",
        xlab = "Theoretical Quantiles", ylab = "Sample Quantiles",
        plot.it = TRUE, datax = FALSE, ...)

qqline(y, datax = FALSE, ...)

qqplot(x, y, plot.it = TRUE, xlab = deparse(substitute(x)),
        ylab = deparse(substitute(y)), ...)
```

**Arguments**

<i>x</i>	The first sample for qqplot.
<i>y</i>	The second or only data sample.
<i>xlab</i> , <i>ylab</i> , <i>main</i>	plot labels. The <i>xlab</i> and <i>ylab</i> refer to the y and x axes respectively if <i>datax</i> = TRUE.
<i>plot.it</i>	logical. Should the result be plotted?
<i>datax</i>	logical. Should data values be on the x-axis?
<i>ylim</i> , ...	graphical parameters.

**Value**

For qqnorm and qqplot, a list with components

<i>x</i>	The x coordinates of the points that were/would be plotted
<i>y</i>	The original <i>y</i> vector, i.e., the corresponding y coordinates <i>including NAs</i> .

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[ppoints](#), used by qqnorm to generate approximations to expected order statistics for a normal distribution.

**Examples**

```
require(graphics)

y <- rt(200, df = 5)
qqnorm(y); qqline(y, col = 2)
qqplot(y, rt(300, df = 5))

qqnorm(precip, ylab = "Precipitation [in/yr] for 70 US cities")
```

quade.test

*Quade Test***Description**

Performs a Quade test with unrepliated blocked data.

**Usage**

```
quade.test(y, ...)

## Default S3 method:
quade.test(y, groups, blocks, ...)

## S3 method for class 'formula':
quade.test(formula, data, subset, na.action, ...)
```

**Arguments**

<code>y</code>	either a numeric vector of data values, or a data matrix.
<code>groups</code>	a vector giving the group for the corresponding elements of <code>y</code> if this is a vector; ignored if <code>y</code> is a matrix. If not a factor object, it is coerced to one.
<code>blocks</code>	a vector giving the block for the corresponding elements of <code>y</code> if this is a vector; ignored if <code>y</code> is a matrix. If not a factor object, it is coerced to one.
<code>formula</code>	a formula of the form $a \sim b \mid c$ , where <code>a</code> , <code>b</code> and <code>c</code> give the data values and corresponding groups and blocks, respectively.
<code>data</code>	an optional matrix or data frame (or similar: see <code>model.frame</code> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>subset</code>	an optional vector specifying a subset of observations to be used.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. Defaults to <code>getOption("na.action")</code> .
<code>...</code>	further arguments to be passed to or from methods.

## Details

`quade.test` can be used for analyzing unreplicated complete block designs (i.e., there is exactly one observation in `y` for each combination of levels of `groups` and `blocks`) where the normality assumption may be violated.

The null hypothesis is that apart from an effect of `blocks`, the location parameter of `y` is the same in each of the `groups`.

If `y` is a matrix, `groups` and `blocks` are obtained from the column and row indices, respectively. NA's are not allowed in `groups` or `blocks`; if `y` contains NA's, corresponding blocks are removed.

## Value

A list with class "htest" containing the following components:

<code>statistic</code>	the value of Quade's F statistic.
<code>parameter</code>	a vector with the numerator and denominator degrees of freedom of the approximate F distribution of the test statistic.
<code>p.value</code>	the p-value of the test.
<code>method</code>	the character string "Quade test".
<code>data.name</code>	a character string giving the names of the data.

## References

D. Quade (1979), Using weighted rankings in the analysis of complete blocks with additive block effects. *Journal of the American Statistical Association*, **74**, 680–683.

William J. Conover (1999), *Practical nonparametric statistics*. New York: John Wiley & Sons. Pages 373–380.

## See Also

[friedman.test](#).

## Examples

```
## Conover (1999, p. 375f):
## Numbers of five brands of a new hand lotion sold in seven stores
## during one week.
y <- matrix(c( 5,  4,  7, 10, 12,
              1,  3,  1,  0,  2,
              16, 12, 22, 22, 35,
              5,  4,  3,  5,  4,
              10,  9,  7, 13, 10,
              19, 18, 28, 37, 58,
              10,  7,  6,  8,  7),
            nrow = 7, byrow = TRUE,
            dimnames =
              list(Store = as.character(1:7),
                  Brand = LETTERS[1:5]))
y
quade.test(y)
```

---

 quantile

*Sample Quantiles*


---

### Description

The generic function `quantile` produces sample quantiles corresponding to the given probabilities. The smallest observation corresponds to a probability of 0 and the largest to a probability of 1.

### Usage

```
quantile(x, ...)

## Default S3 method:
quantile(x, probs = seq(0, 1, 0.25), na.rm = FALSE,
         names = TRUE, type = 7, ...)
```

### Arguments

<code>x</code>	numeric vector whose sample quantiles are wanted, or an object of a class for which a method has been defined (see also ‘details’). <code>NA</code> and <code>NaN</code> values are not allowed in numeric vectors unless <code>na.rm</code> is <code>TRUE</code> .
<code>probs</code>	numeric vector of probabilities with values in $[0, 1]$ . (As from R 2.8.0 values up to ‘2e-14’ outside that range are accepted and moved to the nearby endpoint.)
<code>na.rm</code>	logical; if true, any <code>NA</code> and <code>NaN</code> ’s are removed from <code>x</code> before the quantiles are computed.
<code>names</code>	logical; if true, the result has a <code>names</code> attribute. Set to <code>FALSE</code> for speedup with many <code>probs</code> .
<code>type</code>	an integer between 1 and 9 selecting one of the nine quantile algorithms detailed below to be used.
<code>...</code>	further arguments passed to or from other methods.

### Details

A vector of length `length(probs)` is returned; if `names = TRUE`, it has a `names` attribute.

`NA` and `NaN` values in `probs` are propagated to the result.

The default method works with objects sufficiently like numeric vectors that `sort` and (not needed by types 1 and 3) addition of elements and multiplication by a number work correctly. Note that as this is in a namespace, the copy of `sort` in **base** will be used, not some S4 generic of that name.

There is a method for the date-time classes (see "[POSIXt](#)"). Types 1 and 3 can be used for class "[Date](#)" and for ordered factors.

### Types

`quantile` returns estimates of underlying distribution quantiles based on one or two order statistics from the supplied elements in `x` at probabilities in `probs`. One of the nine quantile algorithms discussed in Hyndman and Fan (1996), selected by `type`, is employed.

All sample quantiles are defined as weighted averages of consecutive order statistics. Sample quantiles of type  $i$  are defined by:

$$Q_i(p) = (1 - \gamma)x_j + \gamma x_{j+1}$$

where  $1 \leq i \leq 9$ ,  $\frac{j-m}{n} \leq p < \frac{j-m+1}{n}$ ,  $x_j$  is the  $j$ th order statistic,  $n$  is the sample size, the value of  $\gamma$  is a function of  $j = \lfloor np + m \rfloor$  and  $g = np + m - j$ , and  $m$  is a constant determined by the sample quantile type.

### Discontinuous sample quantile types 1, 2, and 3

For types 1, 2 and 3,  $Q_i(p)$  is a discontinuous function of  $p$ , with  $m = 0$  when  $i = 1$  and  $i = 2$ , and  $m = -1/2$  when  $i = 3$ .

**Type 1** Inverse of empirical distribution function.  $\gamma = 0$  if  $g = 0$ , and 1 otherwise.

**Type 2** Similar to type 1 but with averaging at discontinuities.  $\gamma = 0.5$  if  $g = 0$ , and 1 otherwise.

**Type 3** SAS definition: nearest even order statistic.  $\gamma = 0$  if  $g = 0$  and  $j$  is even, and 1 otherwise.

### Continuous sample quantile types 4 through 9

For types 4 through 9,  $Q_i(p)$  is a continuous function of  $p$ , with  $\gamma = g$  and  $m$  given below. The sample quantiles can be obtained equivalently by linear interpolation between the points  $(p_k, x_k)$  where  $x_k$  is the  $k$ th order statistic. Specific expressions for  $p_k$  are given below.

**Type 4**  $m = 0$ .  $p_k = \frac{k}{n}$ . That is, linear interpolation of the empirical cdf.

**Type 5**  $m = 1/2$ .  $p_k = \frac{k-0.5}{n}$ . That is a piecewise linear function where the knots are the values midway through the steps of the empirical cdf. This is popular amongst hydrologists.

**Type 6**  $m = p$ .  $p_k = \frac{k}{n+1}$ . Thus  $p_k = E[F(x_k)]$ . This is used by Minitab and by SPSS.

**Type 7**  $m = 1 - p$ .  $p_k = \frac{k-1}{n-1}$ . In this case,  $p_k = \text{mode}[F(x_k)]$ . This is used by S.

**Type 8**  $m = (p + 1)/3$ .  $p_k = \frac{k-1/3}{n+1/3}$ . Then  $p_k \approx \text{median}[F(x_k)]$ . The resulting quantile estimates are approximately median-unbiased regardless of the distribution of  $\mathbf{x}$ .

**Type 9**  $m = p/4 + 3/8$ .  $p_k = \frac{k-3/8}{n+1/4}$ . The resulting quantile estimates are approximately unbiased for the expected order statistics if  $\mathbf{x}$  is normally distributed.

Further details are provided in Hyndman and Fan (1996) who recommended type 8. The default method is type 7, as used by S and by R < 2.0.0.

### Author(s)

of the version used in R  $\geq$  2.0.0, Ivan Frohne and Rob J Hyndman.

### References

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- Hyndman, R. J. and Fan, Y. (1996) Sample quantiles in statistical packages, *American Statistician*, **50**, 361–365.

### See Also

[ecdf](#) for empirical distributions of which `quantile` is an inverse; [boxplot.stats](#) and [fivenum](#) for computing other versions of quartiles, etc.

**Examples**

```

quantile(x <- rnorm(1001)) # Extremes & Quartiles by default
quantile(x, probs = c(0.1, 0.5, 1, 2, 5, 10, 50, NA)/100)

### Compare different types
p <- c(0.1, 0.5, 1, 2, 5, 10, 50)/100
res <- matrix(as.numeric(NA), 9, 7)
for(type in 1:9) res[type, ] <- y <- quantile(x, p, type = type)
dimnames(res) <- list(1:9, names(y))
round(res, 3)

```

r2dtable

*Random 2-way Tables with Given Marginals***Description**

Generate random 2-way tables with given marginals using Patefield's algorithm.

**Usage**

```
r2dtable(n, r, c)
```

**Arguments**

**n** a non-negative numeric giving the number of tables to be drawn.

**r** a non-negative vector of length at least 2 giving the row totals, to be coerced to integer. Must sum to the same as **c**.

**c** a non-negative vector of length at least 2 giving the column totals, to be coerced to integer.

**Value**

A list of length **n** containing the generated tables as its components.

**References**

Patefield, W. M. (1981) Algorithm AS159. An efficient method of generating  $r \times c$  tables with given row and column totals. *Applied Statistics* **30**, 91–97.

**Examples**

```

## Fisher's Tea Drinker data.
TeaTasting <-
matrix(c(3, 1, 1, 3),
       nrow = 2,
       dimnames = list(Guess = c("Milk", "Tea"),
                       Truth = c("Milk", "Tea")))
## Simulate permutation test for independence based on the maximum
## Pearson residuals (rather than their sum).
rowTotals <- rowSums(TeaTasting)
colTotals <- colSums(TeaTasting)
nOfCases <- sum(rowTotals)

```

```

expected <- outer(rowTotals, colTotals, "*") / nOfCases
maxSqResid <- function(x) max((x - expected) ^ 2 / expected)
simMaxSqResid <-
  sapply(r2dtable(1000, rowTotals, colTotals), maxSqResid)
sum(simMaxSqResid >= maxSqResid(TeaTasting)) / 1000
## Fisher's exact test gives p = 0.4857 ...

```

---

read.ftable                      *Manipulate Flat Contingency Tables*

---

### Description

Read, write and coerce ‘flat’ contingency tables.

### Usage

```

read.ftable(file, sep = "", quote = "\"",
            row.var.names, col.vars, skip = 0)

write.ftable(x, file = "", quote = TRUE, append = FALSE,
            digits = getOption("digits"))

## S3 method for class 'ftable':
format(x, quote = TRUE, digits = getOption("digits"), ...)

```

### Arguments

file	either a character string naming a file or a connection which the data are to be read from or written to. "" indicates input from the console for reading and output to the console for writing.
sep	the field separator string. Values on each line of the file are separated by this string.
quote	a character string giving the set of quoting characters for read.ftable; to disable quoting altogether, use quote="". For write.table, a logical indicating whether strings in the data will be surrounded by double quotes.
row.var.names	a character vector with the names of the row variables, in case these cannot be determined automatically.
col.vars	a list giving the names and levels of the column variables, in case these cannot be determined automatically.
skip	the number of lines of the data file to skip before beginning to read data.
x	an object of class "ftable".
append	logical. If TRUE and file is the name of a file (and not a connection or " cmd"), the output from write.ftable is appended to the file. If FALSE, the contents of file will be overwritten.
digits	an integer giving the number of significant digits to use for (the cell entries of) x.
...	further arguments to be passed to or from methods.

## Details

`read.ftable` reads in a flat-like contingency table from a file. If the file contains the written representation of a flat table (more precisely, a header with all information on names and levels of column variables, followed by a line with the names of the row variables), no further arguments are needed. Similarly, flat tables with only one column variable the name of which is the only entry in the first line are handled automatically. Other variants can be dealt with by skipping all header information using `skip`, and providing the names of the row variables and the names and levels of the column variable using `row.var.names` and `col.vars`, respectively. See the examples below.

Note that flat tables are characterized by their ‘ragged’ display of row (and maybe also column) labels. If the full grid of levels of the row variables is given, one should instead use `read.table` to read in the data, and create the contingency table from this using `xtabs`.

`write.ftable` writes a flat table to a file, which is useful for generating ‘pretty’ ASCII representations of contingency tables.

## References

Agresti, A. (1990) *Categorical data analysis*. New York: Wiley.

## See Also

[ftable](#) for more information on flat contingency tables.

## Examples

```
## Agresti (1990), page 157, Table 5.8.
## Not in ftable standard format, but o.k.
file <- tempfile()
cat("          Intercourse\n",
    "Race Gender      Yes No\n",
    "White Male       43 134\n",
    "      Female     26 149\n",
    "Black Male       29  23\n",
    "      Female     22  36\n",
    file = file)
file.show(file)
ft <- read.ftable(file)
ft
unlink(file)

## Agresti (1990), page 297, Table 8.16.
## Almost o.k., but misses the name of the row variable.
file <- tempfile()
cat("          \"Tonsil Size\"\n",
    "          \"Not Enl.\" \"Enl.\" \"Greatly Enl.\"\n",
    "Noncarriers    497    560          269\n",
    "Carriers       19     29          24\n",
    file = file)
file.show(file)
ft <- read.ftable(file, skip = 2,
                  row.var.names = "Status",
                  col.vars = list("Tonsil Size" =
                                c("Not Enl.", "Enl.", "Greatly Enl.")))
ft
```



```

unlink(file)

ft22 <- ftable(Titanic, row.vars = 2:1, col.vars = 4:3)
write.ftable(ft22, quote = FALSE)

```

---

rect.hclust

*Draw Rectangles Around Hierarchical Clusters*


---

### Description

Draws rectangles around the branches of a dendrogram highlighting the corresponding clusters. First the dendrogram is cut at a certain level, then a rectangle is drawn around selected branches.

### Usage

```

rect.hclust(tree, k = NULL, which = NULL, x = NULL, h = NULL,
            border = 2, cluster = NULL)

```

### Arguments

tree	an object of the type produced by <code>hclust</code> .
k, h	Scalar. Cut the dendrogram such that either exactly <code>k</code> clusters are produced or by cutting at height <code>h</code> .
which, x	A vector selecting the clusters around which a rectangle should be drawn. <code>which</code> selects clusters by number (from left to right in the tree), <code>x</code> selects clusters containing the respective horizontal coordinates. Default is <code>which = 1:k</code> .
border	Vector with border colors for the rectangles.
cluster	Optional vector with cluster memberships as returned by <code>cutree(hclust.obj, k = k)</code> , can be specified for efficiency if already computed.

### Value

(Invisibly) returns a list where each element contains a vector of data points contained in the respective cluster.

### See Also

[hclust](#), [identify.hclust](#).

### Examples

```

require(graphics)

hca <- hclust(dist(USArrests))
plot(hca)
rect.hclust(hca, k=3, border="red")
x <- rect.hclust(hca, h=50, which=c(2,7), border=3:4)
x

```

---

relevel *Reorder Levels of Factor*

---

### Description

The levels of a factor are re-ordered so that the level specified by `ref` is first and the others are moved down. This is useful for `contr.treatment` contrasts which take the first level as the reference.

### Usage

```
relevel(x, ref, ...)
```

### Arguments

<code>x</code>	An unordered factor.
<code>ref</code>	The reference level.
<code>...</code>	Additional arguments for future methods.

### Value

A factor of the same length as `x`.

### See Also

[factor](#), [contr.treatment](#), [levels](#), [reorder](#).

### Examples

```
warpbreaks$tension <- relevel(warpbreaks$tension, ref="M")
summary(lm(breaks ~ wool + tension, data=warpbreaks))
```

---

reorder.default *Reorder Levels of a Factor*

---

### Description

`reorder` is a generic function. The "default" method treats its first argument as a categorical variable, and reorders its levels based on the values of a second variable, usually numeric.

### Usage

```
reorder(x, ...)

## Default S3 method:
reorder(x, X, FUN = mean, ...,
        order = is.ordered(x))
```

**Arguments**

<code>x</code>	An atomic vector, usually a factor (possibly ordered). The vector is treated as a categorical variable whose levels will be reordered. If <code>x</code> is not a factor, its unique values will be used as the implicit levels.
<code>X</code>	a vector of the same length as <code>x</code> , whose subset of values for each unique level of <code>x</code> determines the eventual order of that level.
<code>FUN</code>	a function whose first argument is a vector and returns a scalar, to be applied to each subset of <code>X</code> determined by the levels of <code>x</code> .
<code>...</code>	optional: extra arguments supplied to <code>FUN</code>
<code>order</code>	logical, whether return value will be an ordered factor rather than a factor.

**Value**

A factor or an ordered factor (depending on the value of `order`), with the order of the levels determined by `FUN` applied to `X` grouped by `x`. The levels are ordered such that the values returned by `FUN` are in increasing order. Empty levels will be dropped.

Additionally, the values of `FUN` applied to the subsets of `X` (in the original order of the levels of `x`) is returned as the "scores" attribute.

**Author(s)**

Deepayan Sarkar <deepayan.sarkar@r-project.org>

**See Also**

[reorder.dendrogram](#), [levels](#), [relevel](#).

**Examples**

```
require(graphics)

bymedian <- with(InsectSprays, reorder(spray, count, median))
boxplot(count ~ bymedian, data = InsectSprays,
        xlab = "Type of spray", ylab = "Insect count",
        main = "InsectSprays data", varwidth = TRUE,
        col = "lightgray")
```

---

`reorder.dendrogram` *Reorder a Dendrogram*

---

**Description**

A method for the generic function [reorder](#).

There are many different orderings of a dendrogram that are consistent with the structure imposed. This function takes a dendrogram and a vector of values and reorders the dendrogram in the order of the supplied vector, maintaining the constraints on the dendrogram.

**Usage**

```
## S3 method for class 'dendrogram':
reorder(x, wts, agglo.FUN = sum, ...)
```

**Arguments**

<code>x</code>	the (dendrogram) object to be reordered
<code>wts</code>	numeric weights (arbitrary values) for reordering.
<code>agglo.FUN</code>	a function for weights agglomeration, see below.
<code>...</code>	additional arguments

**Details**

Using the weights `wts`, the leaves of the dendrogram are reordered so as to be in an order as consistent as possible with the weights. At each node, the branches are ordered in increasing weights where the weight of a branch is defined as  $f(w_j)$  where  $f$  is `agglo.FUN` and  $w_j$  is the weight of the  $j$ -th sub branch).

**Value**

A dendrogram where each node has a further attribute `value` with its corresponding weight.

**Author(s)**

R. Gentleman and M. Maechler

**See Also**

[reorder](#).

[rev.dendrogram](#) which simply reverses the nodes' order; [heatmap](#), [cophenetic](#).

**Examples**

```
require(graphics)

set.seed(123)
x <- rnorm(10)
hc <- hclust(dist(x))
dd <- as.dendrogram(hc)
dd.reorder <- reorder(dd, 10:1)
plot(dd, main = "random dendrogram 'dd'")

op <- par(mfcol = 1:2)
plot(dd.reorder, main = "reorder(dd, 10:1)")
plot(reorder(dd,10:1, agglo.FUN= mean),
      main = "reorder(dd, 10:1, mean)")
par(op)
```

---

replications

*Number of Replications of Terms*

---

**Description**

Returns a vector or a list of the number of replicates for each term in the formula.

**Usage**

```
replications(formula, data=NULL, na.action)
```

**Arguments**

formula	a formula or a terms object or a data frame.
data	a data frame used to find the objects in formula.
na.action	function for handling missing values. Defaults to a na.action attribute of data, then a setting of the option na.action, or na.fail if that is not set.

**Details**

If formula is a data frame and data is missing, formula is used for data with the formula ~ ..

**Value**

A vector or list with one entry for each term in the formula giving the number(s) of replications for each level. If all levels are balanced (have the same number of replications) the result is a vector, otherwise it is a list with a component for each terms, as a vector, matrix or array as required.

A test for balance is `!is.list(replications(formula, data))`.

**Author(s)**

The design was inspired by the S function of the same name described in Chambers *et al.* (1992).

**References**

Chambers, J. M., Freeny, A and Heiberger, R. M. (1992) *Analysis of variance; designed experiments*. Chapter 5 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

[model.tables](#)

**Examples**

```
## From Venables and Ripley (2002) p.165.
N <- c(0,1,0,1,1,1,0,0,0,1,1,0,1,1,0,0,1,0,1,0,1,1,0,0)
P <- c(1,1,0,0,0,1,0,1,1,1,0,0,0,1,0,1,1,0,0,1,0,1,1,0)
K <- c(1,0,0,1,0,1,1,0,0,1,0,1,0,1,1,0,0,0,1,1,1,0,1,0)
yield <- c(49.5,62.8,46.8,57.0,59.8,58.5,55.5,56.0,62.8,55.8,69.5,
55.0, 62.0,48.8,45.5,44.2,52.0,51.5,49.8,48.8,57.2,59.0,53.2,56.0)

npk <- data.frame(block=gl(6,4), N=factor(N), P=factor(P),
                  K=factor(K), yield=yield)
replications(~ . - yield, npk)
```

---

 reshape

*Reshape Grouped Data*


---

**Description**

This function reshapes a data frame between ‘wide’ format with repeated measurements in separate columns of the same record and ‘long’ format with the repeated measurements in separate records.

**Usage**

```
reshape(data, varying = NULL, v.names = NULL, timevar = "time",
        idvar = "id", ids = 1:NROW(data),
        times = seq_along(varying[[1]]),
        drop = NULL, direction, new.row.names = NULL,
        sep = ".",
        split = if (sep=="") {
          list(regex="[A-Za-z][0-9]", include=TRUE)
        } else {
          list(regex=sep, include= FALSE, fixed=TRUE)
        }
)
```

**Arguments**

<code>data</code>	a data frame
<code>varying</code>	names of sets of variables in the wide format that correspond to single variables in long format (‘time-varying’). This is canonically a list of vectors of variable names, but it can optionally be a matrix of names, or a single vector of names. In each case, the names can be replaced by indices which are interpreted as referring to <code>names(data)</code> . See below for more details and options.
<code>v.names</code>	names of variables in the long format that correspond to multiple variables in the wide format. See below for details.
<code>timevar</code>	the variable in long format that differentiates multiple records from the same group or individual.
<code>idvar</code>	Names of one or more variables in long format that identify multiple records from the same group/individual. These variables may also be present in wide format
<code>ids</code>	the values to use for a newly created <code>idvar</code> variable in long format.
<code>times</code>	the values to use for a newly created <code>timevar</code> variable in long format. See below for details.
<code>drop</code>	a vector of names of variables to drop before reshaping
<code>direction</code>	character string, either "wide" to reshape to wide format, or "long" to reshape to long format.
<code>new.row.names</code>	logical; if TRUE and <code>direction="wide"</code> , create new row names in long format from the values of the <code>id</code> and <code>time</code> variables.

sep	A character vector of length 1, indicating a separating character in the variable names in the wide format. This is used for guessing <code>v.names</code> and <code>times</code> arguments based on the names in <code>varying</code> . If <code>sep=""</code> , the split is just before the first numeral that follows an alphabetic character.
split	A list with three components, <code>regexp</code> , <code>include</code> , and (optionally) <code>fixed</code> . This allows an extended interface to variable name splitting. See below for details.

### Details

The arguments to this function are described in terms of longitudinal data, as that is the application motivating the functions. A ‘wide’ longitudinal dataset will have one record for each individual with some time-constant variables that occupy single columns and some time-varying variables that occupy a column for each time point. In ‘long’ format there will be multiple records for each individual, with some variables being constant across these records and others varying across the records. A ‘long’ format dataset also needs a ‘time’ variable identifying which time point each record comes from and an ‘id’ variable showing which records refer to the same person.

If the data frame resulted from a previous `reshape` then the operation can be reversed simply by `reshape(a)`. The `direction` argument is optional and the other arguments are stored as attributes on the data frame.

If `direction="wide"` and no `varying` or `v.names` arguments are supplied it is assumed that all variables except `idvar` and `timevar` are time-varying. They are all expanded into multiple variables in wide format.

If `direction="long"` the `varying` argument can be a vector of column names (or a corresponding index). The function will attempt to guess the `v.names` and `times` from these names. The default is variable names like `x.1, x.2`, where `sep="."` specifies to split at the dot and drop it from the name. To have alphabetic followed by numeric times use `sep=""`.

Variable name splitting as described above is only attempted in the case where `varying` is an atomic vector, if it is a list or a matrix, `v.names` and `times` will generally need to be specified, although they will default to, respectively, the first variable name in each set, and sequential times.

Also, guessing is not attempted if `v.names` is given explicitly. Notice that the order of variables in `varying` is like `x.1,y.1,x.2,y.2`.

The `split` argument should not usually be necessary. The `split$regexp` component is passed to either `strsplit()` or `regexp()`, where the latter is used if `split$include` is `TRUE`, in which case the splitting occurs after the first character of the matched string. In the `strsplit()` case, the separator is not included in the result, and it is possible to specify fixed-string matching using `split$fixed`.

### Value

The reshaped data frame with added attributes to simplify reshaping back to the original form.

### See Also

[stack](#), [aperm](#); [relist](#) for reshaping the result of [unlist](#).

### Examples

```
summary(Indometh)
wide <- reshape(Indometh, v.names="conc", idvar="Subject",
               timevar="time", direction="wide")
```

```

wide

reshape(wide, direction="long")
reshape(wide, idvar="Subject", varying=list(2:12),
        v.names="conc", direction="long")

## times need not be numeric
df <- data.frame(id=rep(1:4,rep(2,4)),
                 visit=I(rep(c("Before","After"),4)),
                 x=rnorm(4), y=runif(4))

df
reshape(df, timevar="visit", idvar="id", direction="wide")
## warns that y is really varying
reshape(df, timevar="visit", idvar="id", direction="wide", v.names="x")

## unbalanced 'long' data leads to NA fill in 'wide' form
df2 <- df[1:7,]
df2
reshape(df2, timevar="visit", idvar="id", direction="wide")

## Alternative regular expressions for guessing names
df3 <- data.frame(id=1:4, age=c(40,50,60,50), dose1=c(1,2,1,2),
                 dose2=c(2,1,2,1), dose4=c(3,3,3,3))
reshape(df3, direction="long", varying=3:5, sep="")

## an example that isn't longitudinal data
state.x77 <- as.data.frame(state.x77)
long <- reshape(state.x77, idvar="state", ids=row.names(state.x77),
               times=names(state.x77), timevar="Characteristic",
               varying=list(names(state.x77)), direction="long")

reshape(long, direction="wide")

reshape(long, direction="wide", new.row.names=unique(long$state))

## multiple id variables
df3 <- data.frame(school=rep(1:3,each=4), class=rep(9:10,6),
                 time=rep(c(1,1,2,2),3),
                 score=rnorm(12))
wide <- reshape(df3, idvar=c("school","class"), direction="wide")
wide
## transform back
reshape(wide)

```

---

residuals

*Extract Model Residuals*


---

### Description

`residuals` is a generic function which extracts model residuals from objects returned by modeling functions.



The abbreviated form `resid` is an alias for `residuals`. It is intended to encourage users to access object components through an accessor function rather than by directly referencing an object slot.

All object classes which are returned by model fitting functions should provide a `residuals` method. (Note that the method is for `'residuals'` and not `'resid'`.)

Methods can make use of `naresid` methods to compensate for the omission of missing values. The default, `nls` and `smooth.spline` methods do.

### Usage

```
residuals(object, ...)
resid(object, ...)
```

### Arguments

<code>object</code>	an object for which the extraction of model residuals is meaningful.
<code>...</code>	other arguments.

### Value

Residuals extracted from the object `object`.

### References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*. Wadsworth & Brooks/Cole.

### See Also

[coefficients](#), [fitted.values](#), [glm](#), [lm](#).

[influence.measures](#) for standardized (`rstandard`) and studentized (`rstudent`) residuals.

---

runmed

*Running Medians – Robust Scatter Plot Smoothing*

---

### Description

Compute running medians of odd span. This is the ‘most robust’ scatter plot smoothing possible. For efficiency (and historical reason), you can use one of two different algorithms giving identical results.

### Usage

```
runmed(x, k, endrule = c("median", "keep", "constant"),
       algorithm = NULL, print.level = 0)
```

**Arguments**

<code>x</code>	numeric vector, the ‘dependent’ variable to be smoothed.
<code>k</code>	integer width of median window; must be odd. Turlach had a default of $k \leftarrow 1 + 2 * \min((n-1) \% \% 2, \text{ceiling}(0.1*n))$ . Use $k = 3$ for ‘minimal’ robust smoothing eliminating isolated outliers.
<code>endrule</code>	character string indicating how the values at the beginning and the end (of the data) should be treated. <p>"keep" keeps the first and last <math>k_2</math> values at both ends, where <math>k_2</math> is the half-bandwidth <math>k_2 = k \% \% 2</math>, i.e., <math>y[j] = x[j]</math> for <math>j \in \{1, \dots, k_2; n - k_2 + 1, \dots, n\}</math>;</p> <p>"constant" copies <code>median(y[1:k2])</code> to the first values and analogously for the last ones making the smoothed ends <i>constant</i>;</p> <p>"median" the default, smooths the ends by using symmetrical medians of subsequently smaller bandwidth, but for the very first and last value where Tukey’s robust end-point rule is applied, see <a href="#">smoothEnds</a>.</p>
<code>algorithm</code>	character string (partially matching "Turlach" or "Stuetzle") or the default NULL, specifying which algorithm should be applied. The default choice depends on $n = \text{length}(x)$ and $k$ where "Turlach" will be used for larger problems.
<code>print.level</code>	integer, indicating verbosity of algorithm; should rarely be changed by average users.

**Details**

Apart from the end values, the result  $y = \text{runmed}(x, k)$  simply has  $y[j] = \text{median}(x[(j-k2):(j+k2)])$  ( $k = 2*k2+1$ ), computed very efficiently.

The two algorithms are internally entirely different:

"Turlach" is the Härdle–Steiger algorithm (see Ref.) as implemented by Berwin Turlach. A tree algorithm is used, ensuring performance  $O(n \log k)$  where  $n = \text{length}(x)$  which is asymptotically optimal.

"Stuetzle" is the (older) Stuetzle–Friedman implementation which makes use of median *updating* when one observation enters and one leaves the smoothing window. While this performs as  $O(n \times k)$  which is slower asymptotically, it is considerably faster for small  $k$  or  $n$ .

**Value**

vector of smoothed values of the same length as `x` with an `attribute` `k` containing (the ‘oddified’) `k`.

**Author(s)**

Martin Maechler <maechler@stat.math.ethz.ch>, based on Fortran code from Werner Stuetzle and S-PLUS and C code from Berwin Turlach.

**References**

Härdle, W. and Steiger, W. (1995) [Algorithm AS 296] Optimal median smoothing, *Applied Statistics* **44**, 258–264.

Jerome H. Friedman and Werner Stuetzle (1982) *Smoothing of Scatterplots*; Report, Dep. Statistics, Stanford U., Project Orion 003.

Martin Maechler (2003) Fast Running Medians: Finite Sample and Asymptotic Optimality; working paper available from the author.

### See Also

`smoothEnds` which implements Tukey's end point rule and is called by default from `runmed(*, endrule = "median")`. `smooth` uses running medians of 3 for its compound smoothers.

### Examples

```
require(graphics)

utils::example(nhtemp)
myNHT <- as.vector(nhtemp)
myNHT[20] <- 2 * nhtemp[20]
plot(myNHT, type="b", ylim = c(48,60), main = "Running Medians Example")
lines(runmed(myNHT, 7), col = "red")

## special: multiple y values for one x
plot(cars, main = "'cars' data and runmed(dist, 3)")
lines(cars, col = "light gray", type = "c")
with(cars, lines(speed, runmed(dist, k = 3), col = 2))

## nice quadratic with a few outliers
y <- ys <- (-20:20)^2
y [c(1,10,21,41)] <- c(150, 30, 400, 450)
all(y == runmed(y, 1)) # 1-neighbourhood <==> interpolation
plot(y) ## lines(y, lwd=.1, col="light gray")
lines(lowess(seq(y),y, f = .3), col = "brown")
lines(runmed(y, 7), lwd=2, col = "blue")
lines(runmed(y,11), lwd=2, col = "red")

## Lowess is not robust
y <- ys ; y[21] <- 6666 ; x <- seq(y)
col <- c("black", "brown", "blue")
plot(y, col=col[1])
lines(lowess(x,y, f = .3), col = col[2])

lines(runmed(y, 7), lwd=2, col = col[3])
legend(length(y),max(y), c("data", "lowess(y, f = 0.3)", "runmed(y, 7)"),
       xjust = 1, col = col, lty = c(0, 1,1), pch = c(1,NA,NA))
```

---

scatter.smooth

*Scatter Plot with Smooth Curve Fitted by Loess*

---

### Description

Plot and add a smooth curve computed by `loess` to a scatter plot.

## Usage

```
scatter.smooth(x, y = NULL, span = 2/3, degree = 1,
  family = c("symmetric", "gaussian"),
  xlab = NULL, ylab = NULL,
  ylim = range(y, prediction$y, na.rm = TRUE),
  evaluation = 50, ...)

loess.smooth(x, y, span = 2/3, degree = 1,
  family = c("symmetric", "gaussian"), evaluation = 50, ...)
```

## Arguments

<code>x, y</code>	the <code>x</code> and <code>y</code> arguments provide the <code>x</code> and <code>y</code> coordinates for the plot. Any reasonable way of defining the coordinates is acceptable. See the function <a href="#">xy.coords</a> for details.
<code>span</code>	smoothness parameter for <code>loess</code> .
<code>degree</code>	degree of local polynomial used.
<code>family</code>	if <code>"gaussian"</code> fitting is by least-squares, and if <code>family="symmetric"</code> a re-descending M estimator is used.
<code>xlab</code>	label for <code>x</code> axis.
<code>ylab</code>	label for <code>y</code> axis.
<code>ylim</code>	the <code>y</code> limits of the plot.
<code>evaluation</code>	number of points at which to evaluate the smooth curve.
<code>...</code>	graphical parameters.

## Details

`loess.smooth` is an auxiliary function which evaluates the `loess` smooth at `evaluation` equally spaced points covering the range of `x`.

## Value

For `scatter.smooth`, none.

For `loess.smooth`, a list with two components, `x` (the grid of evaluation points) and `y` (the smoothed values at the grid points).

## See Also

[loess](#); [smoothScatter](#) for scatter plots with smoothed *density* color representation.

## Examples

```
require(graphics)

with(cars, scatter.smooth(speed, dist))
```

---

`screeplot`*Screeplots*

---

## Description

`screeplot.default` plots the variances against the number of the principal component. This is also the plot method for classes `"princomp"` and `"prcomp"`.

## Usage

```
## Default S3 method:
screeplot(x, npcs = min(10, length(x$sdev)),
          type = c("barplot", "lines"),
          main = deparse(substitute(x)), ...)
```

## Arguments

`x` an object containing a `sdev` component, such as that returned by `princomp()` and `prcomp()`.

`npcs` the number of components to be plotted.

`type` the type of plot.

`main, ...` graphics parameters.

## References

Mardia, K. V., J. T. Kent and J. M. Bibby (1979). *Multivariate Analysis*, London: Academic Press.

Venables, W. N. and B. D. Ripley (2002). *Modern Applied Statistics with S*, Springer-Verlag.

## See Also

[princomp](#) and [prcomp](#).

## Examples

```
require(graphics)

## The variances of the variables in the
## USArrests data vary by orders of magnitude, so scaling is appropriate
(pc.cr <- princomp(USArrests, cor = TRUE)) # inappropriate
screeplot(pc.cr)

fit <- princomp(covmat=Harman74.cor)
screeplot(fit)
screeplot(fit, npcs=24, type="lines")
```

---

sd *Standard Deviation*

---

### Description

This function computes the standard deviation of the values in `x`. If `na.rm` is `TRUE` then missing values are removed before computation proceeds. If `x` is a matrix or a data frame, a vector of the standard deviation of the columns is returned.

### Usage

```
sd(x, na.rm = FALSE)
```

### Arguments

`x` a numeric vector, matrix or data frame. An object which is not a vector, matrix or data frame is coerced (if possible) by `as.vector`.

`na.rm` logical. Should missing values be removed?

### Details

Like `var` this uses denominator  $n - 1$ .

The standard deviation of a zero-length vector (after removal of NAs if `na.rm = TRUE`) is not defined and gives an error. The standard deviation of a length-one vector is NA.

### See Also

`var` for its square, and `mad`, the most robust alternative.

### Examples

```
sd(1:2) ^ 2
```

---

se.contrast *Standard Errors for Contrasts in Model Terms*

---

### Description

Returns the standard errors for one or more contrasts in an `aov` object.

### Usage

```
se.contrast(object, ...)
## S3 method for class 'aov':
se.contrast(object, contrast.obj,
             coef = contr.helmert(ncol(contrast))[, 1],
             data = NULL, ...)
```

**Arguments**

<code>object</code>	A suitable fit, usually from <code>aov</code> .
<code>contrast.obj</code>	The contrasts for which standard errors are requested. This can be specified via a list or via a matrix. A single contrast can be specified by a list of logical vectors giving the cells to be contrasted. Multiple contrasts should be specified by a matrix, each column of which is a numerical contrast vector (summing to zero).
<code>coef</code>	used when <code>contrast.obj</code> is a list; it should be a vector of the same length as the list with zero sum. The default value is the first Helmert contrast, which contrasts the first and second cell means specified by the list.
<code>data</code>	The data frame used to evaluate <code>contrast.obj</code> .
<code>...</code>	further arguments passed to or from other methods.

**Details**

Contrasts are usually used to test if certain means are significantly different; it can be easier to use `se.contrast` than compute them directly from the coefficients.

In multistratum models, the contrasts can appear in more than one stratum, in which case the standard errors are computed in the lowest stratum and adjusted for efficiencies and comparisons between strata. (See the comments in the note in the help for `aov` about using orthogonal contrasts.) Such standard errors are often conservative.

Suitable matrices for use with `coef` can be found by calling `contrasts` and indexing the columns by a factor.

**Value**

A vector giving the standard errors for each contrast.

**See Also**

[contrasts](#), [model.tables](#)

**Examples**

```
## From Venables and Ripley (2002) p.165.
N <- c(0,1,0,1,1,1,0,0,0,1,1,0,1,1,0,0,1,0,1,0,1,0,1,1,0,0)
P <- c(1,1,0,0,0,1,0,1,1,1,0,0,0,1,0,1,1,0,0,1,0,1,0,1,1,0)
K <- c(1,0,0,1,0,1,1,0,0,1,0,1,0,1,1,0,0,0,1,1,1,0,1,0)
yield <- c(49.5,62.8,46.8,57.0,59.8,58.5,55.5,56.0,62.8,55.8,69.5,
55.0, 62.0,48.8,45.5,44.2,52.0,51.5,49.8,48.8,57.2,59.0,53.2,56.0)

npk <- data.frame(block = gl(6,4), N = factor(N), P = factor(P),
                 K = factor(K), yield = yield)
## Set suitable contrasts.
options(contrasts=c("contr.helmert", "contr.poly"))
npk.aov1 <- aov(yield ~ block + N + K, data=npk)
se.contrast(npk.aov1, list(N == "0", N == "1"), data=npk)
# or via a matrix
cont <- matrix(c(-1,1), 2, 1, dimnames=list(NULL, "N"))
se.contrast(npk.aov1, cont[N, , drop=FALSE]/12, data=npk)

## test a multi-stratum model
npk.aov2 <- aov(yield ~ N + K + Error(block/(N + K)), data=npk)
```

```

se.contrast(npk.aov2, list(N == "0", N == "1"))

## an example looking at an interaction contrast
## Dataset from R.E. Kirk (1995)
## 'Experimental Design: procedures for the behavioral sciences'
score <- c(12, 8,10, 6, 8, 4,10,12, 8, 6,10,14, 9, 7, 9, 5,11,12,
          7,13, 9, 9, 5,11, 8, 7, 3, 8,12,10,13,14,19, 9,16,14)
A <- gl(2, 18, labels=c("a1", "a2"))
B <- rep(gl(3, 6, labels=c("b1", "b2", "b3")), 2)
fit <- aov(score ~ A*B)
cont <- c(1, -1)[A] * c(1, -1, 0)[B]
sum(cont)          # 0
sum(cont*score)   # value of the contrast
se.contrast(fit, as.matrix(cont))
(t.stat <- sum(cont*score)/se.contrast(fit, as.matrix(cont)))
summary(fit, split=list(B=1:2), expand.split = TRUE)
## t.stat^2 is the F value on the A:B: C1 line (with Helmert contrasts)
## Now look at all three interaction contrasts
cont <- c(1, -1)[A] * cbind(c(1, -1, 0), c(1, 0, -1), c(0, 1, -1))[B,]
se.contrast(fit, cont) # same, due to balance.
rm(A,B,score)

## multi-stratum example where efficiencies play a role
utils::example(eff.aovlist)
fit <- aov(Yield ~ A + B * C + Error(Block), data = aovdat)
cont1 <- c(-1, 1)[A]/32 # Helmert contrasts
cont2 <- c(-1, 1)[B] * c(-1, 1)[C]/32
cont <- cbind(A=cont1, BC=cont2)
colSums(cont*Yield) # values of the contrasts
se.contrast(fit, as.matrix(cont))
## Not run: # comparison with lme
library(nlme)
fit2 <- lme(Yield ~ A + B*C, random = ~1 | Block, data = aovdat)
summary(fit2)$tTable # same estimates, similar (but smaller) se's.

## End(Not run)

```

---

selfStart

*Construct Self-starting Nonlinear Models*


---

### Description

Construct self-starting nonlinear models.

### Usage

```
selfStart(model, initial, parameters, template)
```

### Arguments

model            a function object defining a nonlinear model or a nonlinear formula object of the form `~expression`.



<code>initial</code>	a function object, taking three arguments: <code>mCall</code> , <code>data</code> , and <code>LHS</code> , representing, respectively, a matched call to the function <code>model</code> , a data frame in which to interpret the variables in <code>mCall</code> , and the expression from the left-hand side of the model formula in the call to <code>nls</code> . This function should return initial values for the parameters in <code>model</code> .
<code>parameters</code>	a character vector specifying the terms on the right hand side of <code>model</code> for which initial estimates should be calculated. Passed as the <code>namevec</code> argument to the <code>deriv</code> function.
<code>template</code>	an optional prototype for the calling sequence of the returned object, passed as the <code>function.arg</code> argument to the <code>deriv</code> function. By default, a template is generated with the covariates in <code>model</code> coming first and the parameters in <code>model</code> coming last in the calling sequence.

### Details

This function is generic; methods functions can be written to handle specific classes of objects.

### Value

a function object of class "selfStart", for the formula method obtained by applying `deriv` to the right hand side of the model formula. An `initial` attribute (defined by the `initial` argument) is added to the function to calculate starting estimates for the parameters in the model automatically.

### Author(s)

José Pinheiro and Douglas Bates

### See Also

[nls](#)

### Examples

```
## self-starting logistic model

SSlogis <- selfStart(~ Asym/(1 + exp((xmid - x)/scal)),
  function(mCall, data, LHS)
  {
    xy <- sortedXyData(mCall[["x"]], LHS, data)
    if(nrow(xy) < 4) {
      stop("Too few distinct x values to fit a logistic")
    }
    z <- xy[["y"]]
    if (min(z) <= 0) { z <- z + 0.05 * max(z) } # avoid zeroes
    z <- z/(1.05 * max(z)) # scale to within unit height
    xy[["z"]] <- log(z/(1 - z)) # logit transformation
    aux <- coef(lm(x ~ z, xy))
    parameters(xy) <- list(xmid = aux[1], scal = aux[2])
    pars <- as.vector(coef(nls(y ~ 1/(1 + exp((xmid - x)/scal)),
      data = xy, algorithm = "plinear")))
    value <- c(pars[3], pars[1], pars[2])
    names(value) <- mCall[c("Asym", "xmid", "scal")]
    value
  }, c("Asym", "xmid", "scal"))
```

```
# 'first.order.log.model' is a function object defining a first order
# compartment model
# 'first.order.log.initial' is a function object which calculates initial
# values for the parameters in 'first.order.log.model'

# self-starting first order compartment model
## Not run:
SSfol <- selfStart(first.order.log.model, first.order.log.initial)

## End(Not run)
```

---

setNames

*Set the Names in an Object*

---

### Description

This is a convenience function that sets the names on an object and returns the object. It is most useful at the end of a function definition where one is creating the object to be returned and would prefer not to store it under a name just so the names can be assigned.

### Usage

```
setNames(object, nm)
```

### Arguments

object	an object for which a names attribute will be meaningful
nm	a character vector of names to assign to the object

### Value

An object of the same sort as `object` with the new names assigned.

### Author(s)

Douglas M. Bates and Saikat DebRoy

### See Also

[unname](#) for removing names.

### Examples

```
setNames( 1:3, c("foo", "bar", "baz") )
# this is just a short form of
tmp <- 1:3
names(tmp) <- c("foo", "bar", "baz")
tmp
```

---

shapiro.test                      *Shapiro-Wilk Normality Test*

---

### Description

Performs the Shapiro-Wilk test of normality.

### Usage

```
shapiro.test(x)
```

### Arguments

`x`                      a numeric vector of data values. Missing values are allowed, but the number of non-missing values must be between 3 and 5000.

### Value

A list with class "htest" containing the following components:

<code>statistic</code>	the value of the Shapiro-Wilk statistic.
<code>p.value</code>	an approximate p-value for the test. This is said in Royston (1995) to be adequate for <code>p.value &lt; 0.1</code> .
<code>method</code>	the character string "Shapiro-Wilk normality test".
<code>data.name</code>	a character string giving the name(s) of the data.

### Source

The algorithm used is a C translation of the Fortran code described in Royston (1995) and found at <http://lib.stat.cmu.edu/apstat/R94>. The calculation of the p value is exact for  $n = 3$ , otherwise approximations are used, separately for  $4 \leq n \leq 11$  and  $n \geq 12$ .

### References

- Patrick Royston (1982) An extension of Shapiro and Wilk's  $W$  test for normality to large samples. *Applied Statistics*, **31**, 115–124.
- Patrick Royston (1982) Algorithm AS 181: The  $W$  test for Normality. *Applied Statistics*, **31**, 176–180.
- Patrick Royston (1995) Remark AS R94: A remark on Algorithm AS 181: The  $W$  test for normality. *Applied Statistics*, **44**, 547–551.

### See Also

[qqnorm](#) for producing a normal quantile-quantile plot.

### Examples

```
shapiro.test(rnorm(100, mean = 5, sd = 3))
shapiro.test(runif(100, min = 2, max = 4))
```

**Description**

Density, distribution function, quantile function and random generation for the distribution of the Wilcoxon Signed Rank statistic obtained from a sample with size  $n$ .

**Usage**

```
dsignrank(x, n, log = FALSE)
psignrank(q, n, lower.tail = TRUE, log.p = FALSE)
qsignrank(p, n, lower.tail = TRUE, log.p = FALSE)
rsignrank(nn, n)
```

**Arguments**

<code>x, q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>nn</code>	number of observations. If <code>length(nn) &gt; 1</code> , the length is taken to be the number required.
<code>n</code>	number(s) of observations in the sample(s). A positive integer, or a vector of such integers.
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$ .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .

**Details**

This distribution is obtained as follows. Let  $x$  be a sample of size  $n$  from a continuous distribution symmetric about the origin. Then the Wilcoxon signed rank statistic is the sum of the ranks of the absolute values  $x[i]$  for which  $x[i]$  is positive. This statistic takes values between 0 and  $n(n+1)/2$ , and its mean and variance are  $n(n+1)/4$  and  $n(n+1)(2n+1)/24$ , respectively.

If either of the first two arguments is a vector, the recycling rule is used to do the calculations for all combinations of the two up to the length of the longer vector.

**Value**

`dsignrank` gives the density, `psignrank` gives the distribution function, `qsignrank` gives the quantile function, and `rsignrank` generates random deviates.

**Author(s)**

Kurt Hornik; efficiency improvement by Ivo Ugrina.

**See Also**

`wilcox.test` to calculate the statistic from data, find p values and so on.

`dwilcox` etc, for the distribution of *two-sample* Wilcoxon rank sum statistic.

**Examples**

```
require(graphics)

par(mfrow=c(2,2))
for(n in c(4:5,10,40)) {
  x <- seq(0, n*(n+1)/2, length=501)
  plot(x, dsignrank(x,n=n), type='l', main=paste("dsignrank(x,n=",n,""))
}
```

simulate

*Simulate Responses***Description**

Simulate one or more responses from the distribution corresponding to a fitted model object.

**Usage**

```
simulate(object, nsim, seed, ...)
```

**Arguments**

object	an object representing a fitted model.
nsim	number of response vectors to simulate. Defaults to 1.
seed	an object specifying if and how the random number generator should be initialized ('seeded'). For the "lm" method, either NULL or an integer that will be used in a call to <code>set.seed</code> before simulating the response vectors. If set, the value is saved as the "seed" attribute of the returned value. The default, NULL will not change the random generator state, and return <code>.Random.seed</code> as the "seed" attribute, see 'Value'.
...	additional optional arguments.

**Details**

This is a generic function. Consult the individual modeling functions for details on how to use this function.

Package **stats** has a method for "lm" objects which is used for `lm` and `glm` fits. There is a method for fits from `glm.nb` in package **MASS**, and hence the case of negative binomial families is not covered by the "lm" method.

The methods for linear models fitted by `lm` or `glm(family = "gaussian")` assume that any weights which have been supplied are inversely proportional to the error variance. For other GLMs the (optional) `simulate` component of the `family` object is used—there is no appropriate simulation method for 'quasi' models as they are specified only up to two moments.

For binomial and Poisson GLMs the dispersion is fixed at one. Integer prior weights  $w_i$  can be interpreted as meaning that observation  $i$  is an average of  $w_i$  observations, which is natural for binomials specified as proportions but less so for a Poisson, for which prior weights are ignored with a warning.

For a gamma GLM the shape parameter is estimated by maximum likelihood (using function `gamma.shape` in package **MASS**). The interpretation of weights is as multipliers to a basic shape parameter, since dispersion is inversely proportional to shape.

For an inverse gaussian GLM the model assumed is  $IG(\mu_i, \lambda w_i)$  (see [http://en.wikipedia.org/wiki/Inverse\\_Gaussian\\_distribution](http://en.wikipedia.org/wiki/Inverse_Gaussian_distribution)) where  $\lambda$  is estimated by the inverse of the dispersion estimate for the fit. The variance is  $\mu_i^3/(\lambda w_i)$  and hence inversely proportional to the prior weights. The simulation is done by function `rinvgauss` from the **SuppDists** package, which must be installed.

## Value

Typically, a list of length `nsim` of simulated responses. Where appropriate the result can be a data frame (which is a special type of list).

For the "lm" method, the result is a data frame with an attribute "seed" containing the seed argument if not NULL with "kind" attributes the value of `as.list(RNGkind())`, otherwise (the default) the value of `.Random.seed` before the simulation was started.

## See Also

`fitted.values` and `residuals` for related methods; `glm`, `lm` for model fitting.

There are further examples in the 'simulate.R' tests file in the sources for package **stats**.

## Examples

```
x <- 1:5
mod1 <- lm(c(1:3,7,6) ~ x)
S1 <- simulate(mod1, nsim = 4)
## repeat the simulation:
.Random.seed <- attr(S1, "seed")
identical(S1, simulate(mod1, nsim = 4))

S2 <- simulate(mod1, nsim = 200, seed = 101)
rowMeans(S2) # should be about
fitted(mod1)

## repeat identically:
(sseed <- attr(S2, "seed")) # seed; RNGkind as attribute
stopifnot(identical(S2, simulate(mod1, nsim = 200, seed = sseed)))

## To be sure about the proper RNGkind, e.g., after
RNGversion("2.7.0")
## first set the RNG kind, then simulate
do.call(RNGkind, attr(sseed, "kind"))
identical(S2, simulate(mod1, nsim = 200, seed = sseed))

## Binomial GLM examples
yb1 <- matrix(c(4,4,5,7,8,6,6,5,3,2), ncol = 2)
modb1 <- glm(yb1 ~ x, family = binomial)
S3 <- simulate(modb1, nsim = 4)
# each column of S3 is a two-column matrix.

x2 <- sort(runif(100))
yb2 <- rbinom(100, prob = plogis(2*(x2-1)), size = 1)
yb2 <- factor(1 + yb2, labels = c("failure", "success"))
modb2 <- glm(yb2 ~ x2, family = binomial)
```

```
S4 <- simulate(modb2, nsim = 4)
# each column of S4 is a factor
```

smooth

*Tukey's (Running Median) Smoothing***Description**

Tukey's smoothers, *3RS3R*, *3RSS*, *3R*, etc.

**Usage**

```
smooth(x, kind = c("3RS3R", "3RSS", "3RSR", "3R", "3", "S"),
       twiceit = FALSE, endrule = "Tukey", do.ends = FALSE)
```

**Arguments**

<code>x</code>	a vector or time series
<code>kind</code>	a character string indicating the kind of smoother required; defaults to "3RS3R".
<code>twiceit</code>	logical, indicating if the result should be 'twiced'. Twicing a smoother $S(y)$ means $S(y) + S(y - S(y))$ , i.e., adding smoothed residuals to the smoothed values. This decreases bias (increasing variance).
<code>endrule</code>	a character string indicating the rule for smoothing at the boundary. Either "Tukey" (default) or "copy".
<code>do.ends</code>	logical, indicating if the 3-splitting of ties should also happen at the boundaries (ends). This is only used for <code>kind = "S"</code> .

**Details**

3 is Tukey's short notation for running **medians** of length 3,  
 3R stands for **R**epeated 3 until convergence, and  
 S for **S**plitting of horizontal stretches of length 2 or 3.

Hence, 3RS3R is a concatenation of 3R, S and 3R, 3RSS similarly, whereas 3RSR means first 3R and then (S and 3) **R**epeated until convergence – which can be bad.

**Value**

An object of class "tukeysmooth" (which has `print` and `summary` methods) and is a vector or time series containing the smoothed values with additional attributes.

**Note**

S and S-PLUS use a different (somewhat better) Tukey smoother in `smooth(*)`. Note that there are other smoothing methods which provide rather better results. These were designed for hand calculations and may be used mainly for didactical purposes.

Since R version 1.2, `smooth` *does* really implement Tukey's end-point rule correctly (see argument `endrule`).

`kind = "3RSR"` has been the default till R-1.1, but it can have very bad properties, see the examples.

Note that repeated application of `smooth(*)` *does* smooth more, for the "3RS\*" kinds.

## References

Tukey, J. W. (1977). *Exploratory Data Analysis*, Reading Massachusetts: Addison-Wesley.

## See Also

[lowess](#); [loess](#), [supsmu](#) and [smooth.spline](#).

## Examples

```
require(graphics)

## see also    demo(smooth) !

x1 <- c(4, 1, 3, 6, 6, 4, 1, 6, 2, 4, 2) # very artificial
(x3R <- smooth(x1, "3R")) # 2 iterations of "3"
smooth(x3R, kind = "S")

sm.3RS <- function(x, ...)
  smooth(smooth(x, "3R", ...), "S", ...)

y <- c(1,1, 19:1)
plot(y, main = "misbehaviour of \"3RSR\"", col.main = 3)
lines(sm.3RS(y))
lines(smooth(y))
lines(smooth(y, "3RSR"), col = 3, lwd = 2) # the horror

x <- c(8:10,10, 0,0, 9,9)
plot(x, main = "breakdown of 3R and S and hence 3RSS")
matlines(cbind(smooth(x, "3R"), smooth(x, "S"), smooth(x, "3RSS"), smooth(x)))

presidents[is.na(presidents)] <- 0 # silly
summary(sm3 <- smooth(presidents, "3R"))
summary(sm2 <- smooth(presidents, "3RSS"))
summary(sm <- smooth(presidents))

all.equal(c(sm2), c(smooth(smooth(sm3, "S"), "S"))) # 3RSS === 3R S S
all.equal(c(sm), c(smooth(smooth(sm3, "S"), "3R"))) # 3RS3R === 3R S 3R

plot(presidents, main = "smooth(presidents0, *) : 3R and default 3RS3R")
lines(sm3, col = 3, lwd = 1.5)
lines(sm, col = 2, lwd = 1.25)
```

---

smooth.spline

*Fit a Smoothing Spline*

---

## Description

Fits a cubic smoothing spline to the supplied data.

## Usage

```
smooth.spline(x, y = NULL, w = NULL, df, spar = NULL,
              cv = FALSE, all.knots = FALSE, nknots = NULL,
              keep.data = TRUE, df.offset = 0, penalty = 1,
              control.spar = list())
```



**Arguments**

<code>x</code>	a vector giving the values of the predictor variable, or a list or a two-column matrix specifying <code>x</code> and <code>y</code> .
<code>y</code>	responses. If <code>y</code> is missing, the responses are assumed to be specified by <code>x</code> .
<code>w</code>	optional vector of weights of the same length as <code>x</code> ; defaults to all 1.
<code>df</code>	the desired equivalent number of degrees of freedom (trace of the smoother matrix).
<code>spar</code>	smoothing parameter, typically (but not necessarily) in $(0, 1]$ . The coefficient $\lambda$ of the integral of the squared second derivative in the fit (penalized log likelihood) criterion is a monotone function of <code>spar</code> , see the details below.
<code>cv</code>	ordinary (TRUE) or 'generalized' cross-validation (GCV) when FALSE.
<code>all.knots</code>	if TRUE, all distinct points in <code>x</code> are used as knots. If FALSE (default), a subset of <code>x[]</code> is used, specifically <code>x[j]</code> where the <code>nknots</code> indices are evenly spaced in $1:n$ , see also the next argument <code>nknots</code> .
<code>nknots</code>	integer giving the number of knots to use when <code>all.knots=FALSE</code> . Per default, this is less than $n$ , the number of unique <code>x</code> values for $n > 49$ .
<code>keep.data</code>	logical specifying if the input data should be kept in the result. If TRUE (as per default), fitted values and residuals are available from the result.
<code>df.offset</code>	allows the degrees of freedom to be increased by <code>df.offset</code> in the GCV criterion.
<code>penalty</code>	the coefficient of the penalty for degrees of freedom in the GCV criterion.
<code>control.spar</code>	optional list with named components controlling the root finding when the smoothing parameter <code>spar</code> is computed, i.e., missing or NULL, see below. <b>Note</b> that this is partly <i>experimental</i> and may change with general <code>spar</code> computation improvements! <b>low:</b> lower bound for <code>spar</code> ; defaults to -1.5 (used to implicitly default to 0 in R versions earlier than 1.4). <b>high:</b> upper bound for <code>spar</code> ; defaults to +1.5. <b>tol:</b> the absolute precision ( <b>tolerance</b> ) used; defaults to 1e-4 (formerly 1e-3). <b>eps:</b> the relative precision used; defaults to 2e-8 (formerly 0.00244). <b>trace:</b> logical indicating if iterations should be traced. <b>maxit:</b> integer giving the maximal number of iterations; defaults to 500. Note that <code>spar</code> is only searched for in the interval $[low, high]$ .

**Details**

The `x` vector should contain at least four distinct values. *Distinct* here means 'distinct after rounding to 6 significant digits', i.e., `x` will be transformed to `unique(sort(signif(x, 6)))`, and `y` and `w` are pooled accordingly.

The computational  $\lambda$  used (as a function of  $s = spar$ ) is  $\lambda = r * 256^{3s-1}$  where  $r = tr(X'WX)/tr(\Sigma)$ ,  $\Sigma$  is the matrix given by  $\Sigma_{ij} = \int B_i''(t)B_j''(t)dt$ ,  $X$  is given by  $X_{ij} = B_j(x_i)$ ,  $W$  is the diagonal matrix of weights (scaled such that its trace is  $n$ , the original number of observations) and  $B_k(\cdot)$  is the  $k$ -th B-spline.

Note that with these definitions,  $f_i = f(x_i)$ , and the B-spline basis representation  $f = Xc$  (i.e.,  $c$  is the vector of spline coefficients), the penalized log likelihood is  $L = (y - f)'W(y - f) + \lambda c'\Sigma c$ , and hence  $c$  is the solution of the (ridge regression)  $(X'WX + \lambda\Sigma)c = X'Wy$ .

If `spar` is missing or `NULL`, the value of `df` is used to determine the degree of smoothing. If both are missing, leave-one-out cross-validation (ordinary or ‘generalized’ as determined by `cv`) is used to determine  $\lambda$ . Note that from the above relation,

`spar` is  $s = s_0 + 0.0601 * \log \lambda$ , which is intentionally *different* from the S-PLUS implementation of `smooth.spline` (where `spar` is proportional to  $\lambda$ ). In R’s ( $\log \lambda$ ) scale, it makes more sense to vary `spar` linearly.

Note however that currently the results may become very unreliable for `spar` values smaller than about -1 or -2. The same may happen for values larger than 2 or so. Don’t think of setting `spar` or the controls `low` and `high` outside such a safe range, unless you know what you are doing!

The ‘generalized’ cross-validation method will work correctly when there are duplicated points in `x`. However, it is ambiguous what leave-one-out cross-validation means with duplicated points, and the internal code uses an approximation that involves leaving out groups of duplicated points. `cv=TRUE` is best avoided in that case.

### Value

An object of class "smooth.spline" with components

<code>x</code>	the <i>distinct</i> <code>x</code> values in increasing order, see the ‘Details’ above.
<code>y</code>	the fitted values corresponding to <code>x</code> .
<code>w</code>	the weights used at the unique values of <code>x</code> .
<code>yin</code>	the <code>y</code> values used at the unique <code>y</code> values.
<code>data</code>	only if <code>keep.data = TRUE</code> : itself a <code>list</code> with components <code>x</code> , <code>y</code> and <code>w</code> of the same length. These are the original $(x_i, y_i, w_i), i = 1, \dots, n$ , values where <code>data\$x</code> may have repeated values and hence be longer than the above <code>x</code> component; see details.
<code>lev</code>	leverages, the diagonal values of the smoother matrix.
<code>cv.crit</code>	cross-validation score, ‘generalized’ or <code>true</code> , depending on <code>cv</code> .
<code>pen.crit</code>	penalized criterion
<code>crit</code>	the criterion value minimized in the underlying <code>.Fortran</code> routine ‘ <code>sslvrg</code> ’.
<code>df</code>	equivalent degrees of freedom used. Note that (currently) this value may become quite imprecise when the true <code>df</code> is between and 1 and 2.
<code>spar</code>	the value of <code>spar</code> computed or given.
<code>lambda</code>	the value of $\lambda$ corresponding to <code>spar</code> , see the details above.
<code>iparms</code>	named integer(3) vector where <code>..\$ipars["iter"]</code> gives number of <code>spar</code> computing iterations used.
<code>fit</code>	list for use by <code>predict.smooth.spline</code> , with components <b>knot</b> : the knot sequence (including the repeated boundary knots). <b>nk</b> : number of coefficients or number of ‘proper’ knots plus 2. <b>coef</b> : coefficients for the spline basis used. <b>min, range</b> : numbers giving the corresponding quantities of <code>x</code> .
<code>call</code>	the matched call.

### Note

The default `all.knots = FALSE` and `nknots = NULL` entails using only  $O(n^{0.2})$  knots instead of  $n$  for  $n > 49$ . This cuts speed and memory requirements, but not drastically anymore since R version 1.5.1 where it is only  $O(n_k) + O(n)$  where  $n_k$  is the number of knots. In this case where not all unique `x` values are used as knots, the result is not a smoothing spline in the strict sense, but very close unless a small smoothing parameter (or large `df`) is used.

**Author(s)**

R implementation by B. D. Ripley and Martin Maechler (`spar/lambda`, etc).

This function is based on code in the GAMFIT Fortran program by T. Hastie and R. Tibshirani (<http://lib.stat.cmu.edu/general/>), which makes use of spline code by Finbarr O'Sullivan. Its design parallels the `smooth.spline` function of Chambers & Hastie (1992).

**References**

Chambers, J. M. and Hastie, T. J. (1992) *Statistical Models in S*, Wadsworth & Brooks/Cole.

Green, P. J. and Silverman, B. W. (1994) *Nonparametric Regression and Generalized Linear Models: A Roughness Penalty Approach*. Chapman and Hall.

Hastie, T. J. and Tibshirani, R. J. (1990) *Generalized Additive Models*. Chapman and Hall.

**See Also**

[predict.smooth.spline](#) for evaluating the spline and its derivatives.

**Examples**

```
require(graphics)

attach(cars)
plot(speed, dist, main = "data(cars) & smoothing splines")
cars.spl <- smooth.spline(speed, dist)
(cars.spl)
## This example has duplicate points, so avoid cv=TRUE

lines(cars.spl, col = "blue")
lines(smooth.spline(speed, dist, df=10), lty=2, col = "red")
legend(5,120,c(paste("default [C.V.] => df =",round(cars.spl$df,1)),
               "s( * , df = 10)"), col = c("blue","red"), lty = 1:2,
       bg='bisque')
detach()

## Residual (Tukey Anscombe) plot:
plot(residuals(cars.spl) ~ fitted(cars.spl))
abline(h = 0, col="gray")

## consistency check:
stopifnot(all.equal(cars$dist,
                    fitted(cars.spl) + residuals(cars.spl)))

##-- artificial example
y18 <- c(1:3,5,4,7:3,2*(2:5),rep(10,4))
xx <- seq(1,length(y18), len=201)
(s2 <- smooth.spline(y18)) # GCV
(s02 <- smooth.spline(y18, spar = 0.2))
plot(y18, main=deparse(s2$call), col.main=2)
lines(s2, col = "gray"); lines(predict(s2, xx), col = 2)
lines(predict(s02, xx), col = 3); mtext(deparse(s02$call), col = 3)

## The following shows the problematic behavior of 'spar' searching:
(s2 <- smooth.spline(y18, control = list(trace=TRUE,tol=1e-6, low= -1.5))
(s2m <- smooth.spline(y18, cv = TRUE,
```

```
control = list(trace=TRUE,tol=1e-6, low= -1.5))  
## both above do quite similarly (Df = 8.5 +- 0.2)
```

---

smoothEnds

*End Points Smoothing (for Running Medians)*

---

### Description

Smooth end points of a vector *y* using subsequently smaller medians and Tukey's end point rule at the very end. (of odd span),

### Usage

```
smoothEnds(y, k = 3)
```

### Arguments

*y* dependent variable to be smoothed (vector).  
*k* width of largest median window; must be odd.

### Details

`smoothEnds` is used to only do the 'end point smoothing', i.e., change at most the observations closer to the beginning/end than half the window *k*. The first and last value are computed using *Tukey's end point rule*, i.e.,  $sm[1] = \text{median}(y[1], sm[2], 3*sm[2] - 2*sm[3])$ .

### Value

vector of smoothed values, the same length as *y*.

### Author(s)

Martin Maechler

### References

John W. Tukey (1977) *Exploratory Data Analysis*, Addison.

Velleman, P.F., and Hoaglin, D.C. (1981) *ABC of EDA (Applications, Basics, and Computing of Exploratory Data Analysis)*; Duxbury.

### See Also

`runmed(*, endrule = "median")` which calls `smoothEnds()`.

**Examples**

```
require(graphics)

y <- ys <- (-20:20)^2
y [c(1,10,21,41)] <- c(100, 30, 400, 470)
s7k <- runmed(y,7, endrule = "keep")
s7. <- runmed(y,7, endrule = "const")
s7m <- runmed(y,7)
col3 <- c("midnightblue","blue","steelblue")
plot(y, main = "Running Medians -- runmed(*, k=7, end.rule = X)")
lines(ys, col = "light gray")
matlines(cbind(s7k,s7.,s7m), lwd= 1.5, lty = 1, col = col3)
legend(1,470, paste("endrule",c("keep","constant","median"),sep=" = "),
      col = col3, lwd = 1.5, lty = 1)

stopifnot(identical(s7m, smoothEnds(s7k, 7)))
```

sortedXyData

*Create a sortedXyData object***Description**

This is a constructor function for the class of sortedXyData objects. These objects are mostly used in the `initial` function for a self-starting nonlinear regression model, which will be of the `selfStart` class.

**Usage**

```
sortedXyData(x, y, data)
```

**Arguments**

<code>x</code>	a numeric vector or an expression that will evaluate in <code>data</code> to a numeric vector
<code>y</code>	a numeric vector or an expression that will evaluate in <code>data</code> to a numeric vector
<code>data</code>	an optional data frame in which to evaluate expressions for <code>x</code> and <code>y</code> , if they are given as expressions

**Value**

A `sortedXyData` object. This is a data frame with exactly two numeric columns, named `x` and `y`. The rows are sorted so the `x` column is in increasing order. Duplicate `x` values are eliminated by averaging the corresponding `y` values.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

[selfStart](#), [NLSstClosestX](#), [NLSstLfAsymptote](#), [NLSstRtAsymptote](#)

**Examples**

```
DNase.2 <- DNase[ DNase$Run == "2", ]
sortedXyData( expression(log(conc)), expression(density), DNase.2 )
```

spec.ar

*Estimate Spectral Density of a Time Series from AR Fit***Description**

Fits an AR model to `x` (or uses the existing fit) and computes (and by default plots) the spectral density of the fitted model.

**Usage**

```
spec.ar(x, n.freq, order = NULL, plot = TRUE, na.action = na.fail,
        method = "yule-walker", ...)
```

**Arguments**

<code>x</code>	A univariate (not yet:or multivariate) time series or the result of a fit by <a href="#">ar</a> .
<code>n.freq</code>	The number of points at which to plot.
<code>order</code>	The order of the AR model to be fitted. If omitted, the order is chosen by AIC.
<code>plot</code>	Plot the periodogram?
<code>na.action</code>	NA action function.
<code>method</code>	method for ar fit.
<code>...</code>	Graphical arguments passed to <a href="#">plot.spec</a> .

**Value**

An object of class "spec". The result is returned invisibly if `plot` is true.

**Warning**

Some authors, for example Thomson (1990), warn strongly that AR spectra can be misleading.

**Note**

The multivariate case is not yet implemented.

**References**

Thompson, D.J. (1990) Time series analysis of Holocene climate data. *Phil. Trans. Roy. Soc. A* **330**, 601–616.

Venables, W.N. and Ripley, B.D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer. (Especially page 402.)

**See Also**

[ar](#), [spectrum](#).

**Examples**

```
require(graphics)

spec.ar(lh)

spec.ar(ldeaths)
spec.ar(ldeaths, method="burg")
```

---

spec.pgram	<i>Estimate Spectral Density of a Time Series by a Smoothed Periodogram</i>
------------	---

---

**Description**

spec.pgram calculates the periodogram using a fast Fourier transform, and optionally smooths the result with a series of modified Daniell smoothers (moving averages giving half weight to the end values).

**Usage**

```
spec.pgram(x, spans = NULL, kernel, taper = 0.1,
           pad = 0, fast = TRUE, demean = FALSE, detrend = TRUE,
           plot = TRUE, na.action = na.fail, ...)
```

**Arguments**

x	univariate or multivariate time series.
spans	vector of odd integers giving the widths of modified Daniell smoothers to be used to smooth the periodogram.
kernel	alternatively, a kernel smoother of class "tskernel".
taper	specifies the proportion of data to taper. A split cosine bell taper is applied to this proportion of the data at the beginning and end of the series.
pad	proportion of data to pad. Zeros are added to the end of the series to increase its length by the proportion pad.
fast	logical; if TRUE, pad the series to a highly composite length.
demean	logical. If TRUE, subtract the mean of the series.
detrend	logical. If TRUE, remove a linear trend from the series. This will also remove the mean.
plot	plot the periodogram?
na.action	NA action function.
...	graphical arguments passed to plot.spec.

## Details

The raw periodogram is not a consistent estimator of the spectral density, but adjacent values are asymptotically independent. Hence a consistent estimator can be derived by smoothing the raw periodogram, assuming that the spectral density is smooth.

The series will be automatically padded with zeros until the series length is a highly composite number in order to help the Fast Fourier Transform. This is controlled by the `fast` and not the `pad` argument.

The periodogram at zero is in theory zero as the mean of the series is removed (but this may be affected by tapering): it is replaced by an interpolation of adjacent values during smoothing, and no value is returned for that frequency.

## Value

A list object of class "spec" (see [spectrum](#)) with the following additional components:

<code>kernel</code>	The <code>kernel</code> argument, or the kernel constructed from <code>spans</code> .
<code>df</code>	The distribution of the spectral density estimate can be approximated by a (scaled) chi square distribution with <code>df</code> degrees of freedom.
<code>bandwidth</code>	The equivalent bandwidth of the kernel smoother as defined by Bloomfield (1976, page 201).
<code>taper</code>	The value of the <code>taper</code> argument.
<code>pad</code>	The value of the <code>pad</code> argument.
<code>detrend</code>	The value of the <code>detrend</code> argument.
<code>demean</code>	The value of the <code>demean</code> argument.

The result is returned invisibly if `plot` is true.

## Author(s)

Originally Martyn Plummer; kernel smoothing by Adrian Trapletti, synthesis by B.D. Ripley

## References

- Bloomfield, P. (1976) *Fourier Analysis of Time Series: An Introduction*. Wiley.
- Brockwell, P.J. and Davis, R.A. (1991) *Time Series: Theory and Methods*. Second edition. Springer.
- Venables, W.N. and Ripley, B.D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer. (Especially pp. 392–7.)

## See Also

[spectrum](#), [spec.taper](#), [plot.spec](#), [fft](#)

## Examples

```
require(graphics)

## Examples from Venables & Ripley
spectrum(ldeaths)
spectrum(ldeaths, spans = c(3, 5))
spectrum(ldeaths, spans = c(5, 7))
spectrum(mdeaths, spans = c(3, 3))
```



```
spectrum(fdeaths, spans = c(3,3))

## bivariate example
mfdeaths.spc <- spec.pgram(ts.union(mdeaths, fdeaths), spans = c(3,3))
# plots marginal spectra: now plot coherency and phase
plot(mfdeaths.spc, plot.type = "coherency")
plot(mfdeaths.spc, plot.type = "phase")

## now impose a lack of alignment
mfdeaths.spc <- spec.pgram(ts.intersect(mdeaths, lag(fdeaths, 4)),
  spans = c(3,3), plot = FALSE)
plot(mfdeaths.spc, plot.type = "coherency")
plot(mfdeaths.spc, plot.type = "phase")

stocks.spc <- spectrum(EuStockMarkets, kernel("daniell", c(30,50)),
  plot = FALSE)
plot(stocks.spc, plot.type = "marginal") # the default type
plot(stocks.spc, plot.type = "coherency")
plot(stocks.spc, plot.type = "phase")

sales.spc <- spectrum(ts.union(BJsales, BJsales.lead),
  kernel("modified.daniell", c(5,7)))
plot(sales.spc, plot.type = "coherency")
plot(sales.spc, plot.type = "phase")
```

---

spec.taper

*Taper a Time Series by a Cosine Bell*


---

## Description

Apply a cosine-bell taper to a time series.

## Usage

```
spec.taper(x, p = 0.1)
```

## Arguments

<code>x</code>	A univariate or multivariate time series
<code>p</code>	The proportion to be tapered at each end of the series, either a scalar (giving the proportion for all series) or a vector of the length of the number of series (giving the proportion for each series..)

## Details

The cosine-bell taper is applied to the first and last  $p[i]$  observations of time series  $x[, i]$ .

## Value

A new time series object.

## See Also

[spec.pgram](#), [cpgram](#)

spectrum

*Spectral Density Estimation***Description**

The `spectrum` function estimates the spectral density of a time series.

**Usage**

```
spectrum(x, ..., method = c("pgram", "ar"))
```

**Arguments**

<code>x</code>	A univariate or multivariate time series.
<code>method</code>	String specifying the method used to estimate the spectral density. Allowed methods are "pgram" (the default) and "ar".
<code>...</code>	Further arguments to specific spec methods or <code>plot.spec</code> .

**Details**

`spectrum` is a wrapper function which calls the methods `spec.pgram` and `spec.ar`.

The spectrum here is defined with scaling  $1/\text{frequency}(x)$ , following S-PLUS. This makes the spectral density a density over the range  $(-\text{frequency}(x)/2, +\text{frequency}(x)/2]$ , whereas a more common scaling is  $2\pi$  and range  $(-0.5, 0.5]$  (e.g., Bloomfield) or 1 and range  $(-\pi, \pi]$ .

If available, a confidence interval will be plotted by `plot.spec`: this is asymmetric, and the width of the centre mark indicates the equivalent bandwidth.

**Value**

An object of class "spec", which is a list containing at least the following components:

<code>freq</code>	vector of frequencies at which the spectral density is estimated. (Possibly approximate Fourier frequencies.) The units are the reciprocal of cycles per unit time (and not per observation spacing): see 'Details' below.
<code>spec</code>	Vector (for univariate series) or matrix (for multivariate series) of estimates of the spectral density at frequencies corresponding to <code>freq</code> .
<code>coh</code>	NULL for univariate series. For multivariate time series, a matrix containing the <i>squared</i> coherency between different series. Column $i + (j - 1) * (j - 2)/2$ of <code>coh</code> contains the squared coherency between columns $i$ and $j$ of <code>x</code> , where $i < j$ .
<code>phase</code>	NULL for univariate series. For multivariate time series a matrix containing the cross-spectrum phase between different series. The format is the same as <code>coh</code> .
<code>series</code>	The name of the time series.
<code>snames</code>	For multivariate input, the names of the component series.
<code>method</code>	The method used to calculate the spectrum.

The result is returned invisibly if `plot` is true.

**Note**

The default plot for objects of class "spec" is quite complex, including an error bar and default title, subtitle and axis labels. The defaults can all be overridden by supplying the appropriate graphical parameters.

**Author(s)**

Martyn Plummer, B.D. Ripley

**References**

- Bloomfield, P. (1976) *Fourier Analysis of Time Series: An Introduction*. Wiley.
- Brockwell, P. J. and Davis, R. A. (1991) *Time Series: Theory and Methods*. Second edition. Springer.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S-PLUS*. Fourth edition. Springer. (Especially pages 392–7.)

**See Also**

[spec.ar](#), [spec.pgram](#); [plot.spec](#).

**Examples**

```
require(graphics)

## Examples from Venables & Ripley
## spec.pgram
par(mfrow=c(2,2))
spectrum(lh)
spectrum(lh, spans=3)
spectrum(lh, spans=c(3,3))
spectrum(lh, spans=c(3,5))

spectrum(ldeaths)
spectrum(ldeaths, spans=c(3,3))
spectrum(ldeaths, spans=c(3,5))
spectrum(ldeaths, spans=c(5,7))
spectrum(ldeaths, spans=c(5,7), log="dB", ci=0.8)

# for multivariate examples see the help for spec.pgram

## spec.ar
spectrum(lh, method="ar")
spectrum(ldeaths, method="ar")
```

**Description**

Perform cubic (or Hermite) spline interpolation of given data points, returning either a list of points obtained by the interpolation or a *function* performing the interpolation.

**Usage**

```
splinefun(x, y = NULL, method = c("fmm", "periodic", "natural", "monoH.FC"),
          ties = mean)

spline(x, y = NULL, n = 3*length(x), method = "fmm",
        xmin = min(x), xmax = max(x), xout, ties = mean)

splinefunH(x, y, m)
```

**Arguments**

<code>x, y</code>	vectors giving the coordinates of the points to be interpolated. Alternatively a single plotting structure can be specified: see <a href="#">xy.coords</a> .
<code>m</code>	(for <code>splinefunH()</code> ): vector of <i>slopes</i> $m_i$ at the points $(x_i, y_i)$ ; these together determine the Hermite “spline” which is piecewise cubic, (only) <i>once</i> differentiable continuously.
<code>method</code>	specifies the type of spline to be used. Possible values are "fmm", "natural", "periodic" and "monoH.FC".
<code>n</code>	if <code>xout</code> is left unspecified, interpolation takes place at <code>n</code> equally spaced points spanning the interval <code>[xmin, xmax]</code> .
<code>xmin, xmax</code>	left-hand and right-hand endpoint of the interpolation interval (when <code>xout</code> is unspecified).
<code>xout</code>	an optional set of values specifying where interpolation is to take place.
<code>ties</code>	Handling of tied <code>x</code> values. Either a function with a single vector argument returning a single number result or the string "ordered".

**Details**

The inputs can contain missing values which are deleted, so at least one complete  $(x, y)$  pair is required. If `method = "fmm"`, the spline used is that of Forsythe, Malcolm and Moler (an exact cubic is fitted through the four points at each end of the data, and this is used to determine the end conditions). Natural splines are used when `method = "natural"`, and periodic splines when `method = "periodic"`.

The new (R 2.8.0) method "monoH.FC" computes a *monotone* Hermite spline according to the method of Fritsch and Carlson. It does so by determining slopes such that the Hermite spline, determined by  $(x_i, y_i, m_i)$ , is monotone (increasing or decreasing) **iff** the data are.

These interpolation splines can also be used for extrapolation, that is prediction at points outside the range of `x`. Extrapolation makes little sense for `method = "fmm"`; for natural splines it is linear using the slope of the interpolating curve at the nearest data point.

**Value**

`spline` returns a list containing components `x` and `y` which give the ordinates where interpolation took place and the interpolated values.

`splinefun` returns a function with formal arguments `x` and `deriv`, the latter defaulting to zero. This function can be used to evaluate the interpolating cubic spline (`deriv=0`), or its derivatives (`deriv=1,2,3`) at the points `x`, where the spline function interpolates the data points originally specified. This is often more useful than `spline`.

## References

- Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.
- Forsythe, G. E., Malcolm, M. A. and Moler, C. B. (1977) *Computer Methods for Mathematical Computations*.
- Fritsch, F. N. and Carlson, R. E. (1980) Monotone piecewise cubic interpolation, *SIAM Journal on Numerical Analysis* **17**, 238–246.

## See Also

[approx](#) and [approxfun](#) for constant and linear interpolation.

Package **splines**, especially [interpSpline](#) and [periodicSpline](#) for interpolation splines. That package also generates spline bases that can be used for regression splines.

[smooth.spline](#) for smoothing splines.

## Examples

```
require(graphics)

op <- par(mfrow = c(2,1), mgp = c(2,.8,0), mar = .1+c(3,3,3,1))
n <- 9
x <- 1:n
y <- rnorm(n)
plot(x, y, main = paste("spline[fun](.) through", n, "points"))
lines(spline(x, y))
lines(spline(x, y, n = 201), col = 2)

y <- (x-6)^2
plot(x, y, main = "spline(.) -- 3 methods")
lines(spline(x, y, n = 201), col = 2)
lines(spline(x, y, n = 201, method = "natural"), col = 3)
lines(spline(x, y, n = 201, method = "periodic"), col = 4)
legend(6,25, c("fmm","natural","periodic"), col=2:4, lty=1)

y <- sin((x-0.5)*pi)
f <- splinefun(x, y)
ls(envir = environment(f))
splinecoef <- get("z", envir = environment(f))
curve(f(x), 1, 10, col = "green", lwd = 1.5)
points(splinecoef, col = "purple", cex = 2)
curve(f(x, deriv=1), 1, 10, col = 2, lwd = 1.5)
curve(f(x, deriv=2), 1, 10, col = 2, lwd = 1.5, n = 401)
curve(f(x, deriv=3), 1, 10, col = 2, lwd = 1.5, n = 401)
par(op)

## Manual spline evaluation --- demo the coefficients :
.x <- splinecoef$x
u <- seq(3,6, by = 0.25)
(ii <- findInterval(u, .x))
dx <- u - .x[ii]
f.u <- with(splinecoef,
            y[ii] + dx*(b[ii] + dx*(c[ii] + dx* d[ii])))
stopifnot(all.equal(f(u), f.u))
```

```
## An example with ties (non-unique x values):
set.seed(1); x <- round(rnorm(30), 1); y <- sin(pi * x) + rnorm(30)/10
plot(x,y, main="spline(x,y) when x has ties")
lines(spline(x,y, n= 201), col = 2)
## visualizes the non-unique ones:
tx <- table(x); mx <- as.numeric(names(tx[tx > 1]))
ry <- matrix(unlist(tapply(y, match(x,mx), range, simplify=FALSE)),
            ncol=2, byrow=TRUE)
segments(mx, ry[,1], mx, ry[,2], col = "blue", lwd = 2)

## An example of monotone interpolation
n <- 20
set.seed(11)
x. <- sort(runif(n)) ; y. <- cumsum(abs(rnorm(n)))
plot(x.,y.)
curve(splinefun(x.,y.)(x), add=TRUE, col=2, n=1001)
curve(splinefun(x.,y., method="mono")(x), add=TRUE, col=3, n=1001)
legend("topleft", paste("splinefun( \"", c("fmm", "monoH.CS"), "\" )", sep=''),
      col=2:3, lty=1)
```

---

SSasymp

*Self-Starting Nls Asymptotic Regression Model*


---

## Description

This `selfStart` model evaluates the asymptotic regression function and its gradient. It has an `initial` attribute that will evaluate initial estimates of the parameters `Asym`, `R0`, and `lrc` for a given set of data.

## Usage

```
SSasymp(input, Asym, R0, lrc)
```

## Arguments

<code>input</code>	a numeric vector of values at which to evaluate the model.
<code>Asym</code>	a numeric parameter representing the horizontal asymptote on the right side (very large values of <code>input</code> ).
<code>R0</code>	a numeric parameter representing the response when <code>input</code> is zero.
<code>lrc</code>	a numeric parameter representing the natural logarithm of the rate constant.

## Value

a numeric vector of the same length as `input`. It is the value of the expression  $Asym + (R0 - Asym) \cdot \exp(-\exp(lrc) \cdot input)$ . If all of the arguments `Asym`, `R0`, and `lrc` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

## Author(s)

José Pinheiro and Douglas Bates

**See Also**

`nls`, `selfStart`

**Examples**

```
Lob.329 <- Loblolly[ Loblolly$Seed == "329", ]
SSasympt( Lob.329$age, 100, -8.5, -3.2 ) # response only
Asym <- 100
resp0 <- -8.5
lrc <- -3.2
SSasympt( Lob.329$age, Asym, resp0, lrc ) # response and gradient
getInitial(height ~ SSasympt( age, Asym, resp0, lrc), data = Lob.329)
## Initial values are in fact the converged values
fm1 <- nls(height ~ SSasympt( age, Asym, resp0, lrc), data = Lob.329)
summary(fm1)
```

---

SSasymptOff

*Self-Starting Nls Asymptotic Regression Model with an Offset*


---

**Description**

This `selfStart` model evaluates an alternative parametrization of the asymptotic regression function and the gradient with respect to those parameters. It has an `initial` attribute that creates initial estimates of the parameters `Asym`, `lrc`, and `c0`.

**Usage**

```
SSasymptOff(input, Asym, lrc, c0)
```

**Arguments**

<code>input</code>	a numeric vector of values at which to evaluate the model.
<code>Asym</code>	a numeric parameter representing the horizontal asymptote on the right side (very large values of <code>input</code> ).
<code>lrc</code>	a numeric parameter representing the natural logarithm of the rate constant.
<code>c0</code>	a numeric parameter representing the <code>input</code> for which the response is zero.

**Value**

a numeric vector of the same length as `input`. It is the value of the expression  $Asym * (1 - \exp(-\exp(lrc) * (input - c0)))$ . If all of the arguments `Asym`, `lrc`, and `c0` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

`nls`, `selfStart`; `example(SSasymptOff)` gives graph showing the `SSasymptOff` parametrization, where  $\phi_1$  is `Asym`,  $\phi_3$  is `c0`.

**Examples**

```
CO2.Qn1 <- CO2[CO2$Plant == "Qn1", ]
SSasymptOff( CO2.Qn1$conc, 32, -4, 43 ) # response only
Asym <- 32; lrc <- -4; c0 <- 43
SSasymptOff( CO2.Qn1$conc, Asym, lrc, c0 ) # response and gradient
getInitial(uptake ~ SSasymptOff( conc, Asym, lrc, c0), data = CO2.Qn1)
## Initial values are in fact the converged values
fm1 <- nls(uptake ~ SSasymptOff( conc, Asym, lrc, c0), data = CO2.Qn1)
summary(fm1)
```

---

SSasymptOrig

*Self-Starting Nls Asymptotic Regression Model through the Origin*


---

**Description**

This `selfStart` model evaluates the asymptotic regression function through the origin and its gradient. It has an `initial` attribute that will evaluate initial estimates of the parameters `Asym` and `lrc` for a given set of data.

**Usage**

```
SSasymptOrig(input, Asym, lrc)
```

**Arguments**

<code>input</code>	a numeric vector of values at which to evaluate the model.
<code>Asym</code>	a numeric parameter representing the horizontal asymptote.
<code>lrc</code>	a numeric parameter representing the natural logarithm of the rate constant.

**Value**

a numeric vector of the same length as `input`. It is the value of the expression `Asym*(1 - exp(-exp(lrc)*input))`. If all of the arguments `Asym` and `lrc` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

`nls`, `selfStart`



**Examples**

```
Lob.329 <- Loblolly[ Loblolly$Seed == "329", ]
SSasymOrig( Lob.329$age, 100, -3.2 ) # response only
Asym <- 100; lrc <- -3.2
SSasymOrig( Lob.329$age, Asym, lrc ) # response and gradient
getInitial(height ~ SSasymOrig(age, Asym, lrc), data = Lob.329)
## Initial values are in fact the converged values
fml <- nls(height ~ SSasymOrig( age, Asym, lrc), data = Lob.329)
summary(fml)
```

---

SSbiexp

*Self-Starting Nls Biexponential model*


---

**Description**

This `selfStart` model evaluates the biexponential model function and its gradient. It has an `initial` attribute that creates initial estimates of the parameters `A1`, `lrc1`, `A2`, and `lrc2`.

**Usage**

```
SSbiexp(input, A1, lrc1, A2, lrc2)
```

**Arguments**

<code>input</code>	a numeric vector of values at which to evaluate the model.
<code>A1</code>	a numeric parameter representing the multiplier of the first exponential.
<code>lrc1</code>	a numeric parameter representing the natural logarithm of the rate constant of the first exponential.
<code>A2</code>	a numeric parameter representing the multiplier of the second exponential.
<code>lrc2</code>	a numeric parameter representing the natural logarithm of the rate constant of the second exponential.

**Value**

a numeric vector of the same length as `input`. It is the value of the expression  $A1 \cdot \exp(-\exp(lrc1) \cdot \text{input}) + A2 \cdot \exp(-\exp(lrc2) \cdot \text{input})$ . If all of the arguments `A1`, `lrc1`, `A2`, and `lrc2` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

[nls](#), [selfStart](#)

**Examples**

```

Indo.1 <- Indometh[Indometh$Subject == 1, ]
SSbiexp( Indo.1$time, 3, 1, 0.6, -1.3 ) # response only
A1 <- 3; lrc1 <- 1; A2 <- 0.6; lrc2 <- -1.3
SSbiexp( Indo.1$time, A1, lrc1, A2, lrc2 ) # response and gradient
getInitial(conc ~ SSbiexp(time, A1, lrc1, A2, lrc2), data = Indo.1)
## Initial values are in fact the converged values
fml <- nls(conc ~ SSbiexp(time, A1, lrc1, A2, lrc2), data = Indo.1)
summary(fml)

```

---

SSD

*SSD Matrix and Estimated Variance Matrix in Multivariate Models*


---

**Description**

Functions to compute matrix of residual sums of squares and products, or the estimated variance matrix for multivariate linear models.

**Usage**

```

# S3 method for class 'mlm'
SSD(object, ...)

# S3 methods for class 'SSD' and 'mlm'
estVar(object, ...)

```

**Arguments**

object	object of class "mlm", or "SSD" in the case of estVar.
...	Unused

**Value**

SSD() returns a list of class "SSD" containing the following components

SSD	The residual sums of squares and products matrix
df	Degrees of freedom
call	Copied from object

estVar returns a matrix with the estimated variances and covariances.

**See Also**

[mauchly.test](#), [anova.mlm](#)

**Examples**

```
# Lifted from Baron+Li:
# "Notes on the use of R for psychology experiments and questionnaires"
# Maxwell and Delaney, p. 497
reacttime <- matrix(c(
  420, 420, 480, 480, 600, 780,
  420, 480, 480, 360, 480, 600,
  480, 480, 540, 660, 780, 780,
  420, 540, 540, 480, 780, 900,
  540, 660, 540, 480, 660, 720,
  360, 420, 360, 360, 480, 540,
  480, 480, 600, 540, 720, 840,
  480, 600, 660, 540, 720, 900,
  540, 600, 540, 480, 720, 780,
  480, 420, 540, 540, 660, 780),
  ncol = 6, byrow = TRUE,
  dimnames=list(subj=1:10,
                 cond=c("deg0NA", "deg4NA", "deg8NA",
                       "deg0NP", "deg4NP", "deg8NP")))

mlmfit <- lm(reacttime~1)
SSD(mlmfit)
estVar(mlmfit)
```

SSfol

*Self-Starting Nls First-order Compartment Model***Description**

This `selfStart` model evaluates the first-order compartment function and its gradient. It has an `initial` attribute that creates initial estimates of the parameters `lKe`, `lKa`, and `lCl`.

**Usage**

```
SSfol(Dose, input, lKe, lKa, lCl)
```

**Arguments**

<code>Dose</code>	a numeric value representing the initial dose.
<code>input</code>	a numeric vector at which to evaluate the model.
<code>lKe</code>	a numeric parameter representing the natural logarithm of the elimination rate constant.
<code>lKa</code>	a numeric parameter representing the natural logarithm of the absorption rate constant.
<code>lCl</code>	a numeric parameter representing the natural logarithm of the clearance.

**Value**

a numeric vector of the same length as `input`, which is the value of the expression  $Dose * \exp(lKe+lKa-lCl) * (\exp(-\exp(lKe)*input) - \exp(-\exp(lKa)*input)) / (\exp(lKa) - \exp(lKe))$ .

If all of the arguments `lKe`, `lKa`, and `lCl` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

[nls](#), [selfStart](#)

**Examples**

```
Theoph.1 <- Theoph[ Theoph$Subject == 1, ]
SSfol( Theoph.1$Dose, Theoph.1$Time, -2.5, 0.5, -3 ) # response only
lKe <- -2.5; lKa <- 0.5; lCl <- -3
SSfol( Theoph.1$Dose, Theoph.1$Time, lKe, lKa, lCl ) # response and gradient
getInitial(conc ~ SSfol(Dose, Time, lKe, lKa, lCl), data = Theoph.1)
## Initial values are in fact the converged values
fml <- nls(conc ~ SSfol(Dose, Time, lKe, lKa, lCl), data = Theoph.1)
summary(fml)
```

---

SSfpl

*Self-Starting Nls Four-Parameter Logistic Model*


---

**Description**

This `selfStart` model evaluates the four-parameter logistic function and its gradient. It has an `initial` attribute that will evaluate initial estimates of the parameters `A`, `B`, `xmid`, and `scal` for a given set of data.

**Usage**

```
SSfpl(input, A, B, xmid, scal)
```

**Arguments**

<code>input</code>	a numeric vector of values at which to evaluate the model.
<code>A</code>	a numeric parameter representing the horizontal asymptote on the left side (very small values of <code>input</code> ).
<code>B</code>	a numeric parameter representing the horizontal asymptote on the right side (very large values of <code>input</code> ).
<code>xmid</code>	a numeric parameter representing the <code>input</code> value at the inflection point of the curve. The value of <code>SSfpl</code> will be midway between <code>A</code> and <code>B</code> at <code>xmid</code> .
<code>scal</code>	a numeric scale parameter on the <code>input</code> axis.

**Value**

a numeric vector of the same length as `input`. It is the value of the expression  $A + (B - A) / (1 + \exp((xmid - input) / scal))$ . If all of the arguments `A`, `B`, `xmid`, and `scal` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

[nls](#), [selfStart](#)

**Examples**

```
Chick.1 <- ChickWeight[ChickWeight$Chick == 1, ]
SSfpl( Chick.1$Time, 13, 368, 14, 6 ) # response only
A <- 13; B <- 368; xmid <- 14; scal <- 6
SSfpl( Chick.1$Time, A, B, xmid, scal ) # response and gradient
getInitial(weight ~ SSfpl(Time, A, B, xmid, scal), data = Chick.1)
## Initial values are in fact the converged values
fml <- nls(weight ~ SSfpl(Time, A, B, xmid, scal), data = Chick.1)
summary(fml)
```

---

SSgompertz

*Self-Starting Nls Gompertz Growth Model*

---

**Description**

This `selfStart` model evaluates the Gompertz growth model and its gradient. It has an initial attribute that creates initial estimates of the parameters `Asym`, `b2`, and `b3`.

**Usage**

```
SSgompertz(x, Asym, b2, b3)
```

**Arguments**

<code>x</code>	a numeric vector of values at which to evaluate the model.
<code>Asym</code>	a numeric parameter representing the asymptote.
<code>b2</code>	a numeric parameter related to the value of the function at $x = 0$
<code>b3</code>	a numeric parameter related to the scale the $x$ axis.

**Value**

a numeric vector of the same length as `input`. It is the value of the expression  $Asym * \exp(-b2 * b3^x)$ . If all of the arguments `Asym`, `b2`, and `b3` are names of objects the gradient matrix with respect to these names is attached as an attribute named `gradient`.

**Author(s)**

Douglas Bates

**See Also**

[nls](#), [selfStart](#)

**Examples**

```

DNase.1 <- subset(DNase, Run == 1)
SSlogis(log(DNase.1$conc), 4.5, 2.3, 0.7) # response only
Asym <- 4.5; b2 <- 2.3; b3 <- 0.7
SSgompertz(log(DNase.1$conc), Asym, b2, b3 ) # response and gradient
getInitial(density ~ SSgompertz(log(conc), Asym, b2, b3),
           data = DNase.1)
## Initial values are in fact the converged values
fml <- nls(density ~ SSgompertz(log(conc), Asym, b2, b3),
          data = DNase.1)
summary(fml)

```

---

SSlogis

*Self-Starting Nls Logistic Model*


---

**Description**

This `selfStart` model evaluates the logistic function and its gradient. It has an `initial` attribute that creates initial estimates of the parameters `Asym`, `xmid`, and `scal`.

**Usage**

```
SSlogis(input, Asym, xmid, scal)
```

**Arguments**

<code>input</code>	a numeric vector of values at which to evaluate the model.
<code>Asym</code>	a numeric parameter representing the asymptote.
<code>xmid</code>	a numeric parameter representing the $x$ value at the inflection point of the curve. The value of <code>SSlogis</code> will be <code>Asym/2</code> at <code>xmid</code> .
<code>scal</code>	a numeric scale parameter on the <code>input</code> axis.

**Value**

a numeric vector of the same length as `input`. It is the value of the expression  $\text{Asym}/(1+\exp((\text{xmid}-\text{input})/\text{scal}))$ . If all of the arguments `Asym`, `xmid`, and `scal` are names of objects the gradient matrix with respect to these names is attached as an attribute named `gradient`.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

[nls](#), [selfStart](#)

**Examples**

```

Chick.1 <- ChickWeight[ChickWeight$Chick == 1, ]
SSlogis( Chick.1$Time, 368, 14, 6 ) # response only
Asym <- 368; xmid <- 14; scal <- 6
SSlogis( Chick.1$Time, Asym, xmid, scal ) # response and gradient
getInitial(weight ~ SSlogis(Time, Asym, xmid, scal), data = Chick.1)
## Initial values are in fact the converged values
fml <- nls(weight ~ SSlogis(Time, Asym, xmid, scal), data = Chick.1)
summary(fml)

```

---

SSmicmen

*Self-Starting Nls Michaelis-Menten Model*


---

**Description**

This `selfStart` model evaluates the Michaelis-Menten model and its gradient. It has an `initial` attribute that will evaluate initial estimates of the parameters  $V_m$  and  $K$ .

**Usage**

```
SSmicmen(input, Vm, K)
```

**Arguments**

<code>input</code>	a numeric vector of values at which to evaluate the model.
<code>Vm</code>	a numeric parameter representing the maximum value of the response.
<code>K</code>	a numeric parameter representing the <code>input</code> value at which half the maximum response is attained. In the field of enzyme kinetics this is called the Michaelis parameter.

**Value**

a numeric vector of the same length as `input`. It is the value of the expression  $V_m \cdot \text{input} / (K + \text{input})$ . If both the arguments `Vm` and `K` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

**Author(s)**

José Pinheiro and Douglas Bates

**See Also**

[nls](#), [selfStart](#)

**Examples**

```

PurTrt <- Puromycin[ Puromycin$state == "treated", ]
SSmicmen( PurTrt$conc, 200, 0.05 ) # response only
Vm <- 200; K <- 0.05
SSmicmen( PurTrt$conc, Vm, K ) # response and gradient
getInitial(rate ~ SSmicmen(conc, Vm, K), data = PurTrt)
## Initial values are in fact the converged values
fm1 <- nls(rate ~ SSmicmen(conc, Vm, K), data = PurTrt)
summary( fm1 )
## Alternative call using the subset argument
fm2 <- nls(rate ~ SSmicmen(conc, Vm, K), data = Puromycin,
            subset = state == "treated")
summary( fm2)

```

SSweibull

*Self-Starting Nls Weibull Growth Curve Model***Description**

This `selfStart` model evaluates the Weibull model for growth curve data and its gradient. It has an `initial` attribute that will evaluate initial estimates of the parameters `Asym`, `Drop`, `lrc`, and `pwr` for a given set of data.

**Usage**

```
SSweibull(x, Asym, Drop, lrc, pwr)
```

**Arguments**

<code>x</code>	a numeric vector of values at which to evaluate the model.
<code>Asym</code>	a numeric parameter representing the horizontal asymptote on the right side (very small values of <code>x</code> ).
<code>Drop</code>	a numeric parameter representing the change from <code>Asym</code> to the <code>y</code> intercept.
<code>lrc</code>	a numeric parameter representing the natural logarithm of the rate constant.
<code>pwr</code>	a numeric parameter representing the power to which <code>x</code> is raised.

**Details**

This model is a generalization of the `SSasymp` model in that it reduces to `SSasymp` when `pwr` is unity.

**Value**

a numeric vector of the same length as `x`. It is the value of the expression `Asym-Drop*exp(-exp(lrc)*x^pwr)`. If all of the arguments `Asym`, `Drop`, `lrc`, and `pwr` are names of objects, the gradient matrix with respect to these names is attached as an attribute named `gradient`.

**Author(s)**

Douglas Bates



## References

Ratkowsky, David A. (1983), *Nonlinear Regression Modeling*, Dekker. (section 4.4.5)

## See Also

[nls](#), [selfStart](#), [SSasymp](#)

## Examples

```
Chick.6 <- subset(ChickWeight, (Chick == 6) & (Time > 0))
SSweibull(Chick.6$Time, 160, 115, -5.5, 2.5 ) # response only
Asym <- 160; Drop <- 115; lrc <- -5.5; pwr <- 2.5
SSweibull(Chick.6$Time, Asym, Drop, lrc, pwr) # response and gradient
getInitial(weight ~ SSweibull(Time, Asym, Drop, lrc, pwr), data = Chick.6)
## Initial values are in fact the converged values
fml <- nls(weight ~ SSweibull(Time, Asym, Drop, lrc, pwr), data = Chick.6)
summary(fml)
```

---

start

*Encode the Terminal Times of Time Series*

---

## Description

Extract and encode the times the first and last observations were taken. Provided only for compatibility with S version 2.

## Usage

```
start(x, ...)
end(x, ...)
```

## Arguments

**x** a univariate or multivariate time-series, or a vector or matrix.  
**...** extra arguments for future methods.

## Details

These are generic functions, which will use the `tsp` attribute of `x` if it exists. Their default methods decode the start time from the original time units, so that for a monthly series 1995.5 is represented as `c(1995, 7)`. For a series of frequency `f`, time `n+i/f` is presented as `c(n, i+1)` (even for `i = 0` and `f = 1`).

## Warning

The representation used by `start` and `end` has no meaning unless the frequency is supplied.

## See Also

[ts](#), [time](#), [tsp](#).

---

`stat.anova`*GLM Anova Statistics*

---

### Description

This is a utility function, used in `lm` and `glm` methods for `anova(..., test != NULL)` and should not be used by the average user.

### Usage

```
stat.anova(table, test = c("Chisq", "F", "Cp"), scale, df.scale, n)
```

### Arguments

<code>table</code>	numeric matrix as results from <code>anova.glm(..., test=NULL)</code> .
<code>test</code>	a character string, matching one of "Chisq", "F" or "Cp".
<code>scale</code>	a residual mean square or other scale estimate to be used as the denominator in an F test.
<code>df.scale</code>	degrees of freedom corresponding to <code>scale</code> .
<code>n</code>	number of observations.

### Value

A matrix which is the original `table`, augmented by a column of test statistics, depending on the `test` argument.

### References

Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models*. Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

### See Also

[anova.lm](#), [anova.glm](#).

### Examples

```
##-- Continued from '?glm':

print(ag <- anova(glm.D93))
stat.anova(ag$table, test = "Cp",
           scale = sum(resid(glm.D93, "pearson")^2)/4,
           df.scale = 4, n = 9)
```

---

stats-deprecated     *Deprecated Functions in Stats package*

---

### Description

These functions are provided for compatibility with older versions of R only, and may be defunct as soon as the next release.

### Details

There are currently no deprecated functions in this package.

### See Also

[Deprecated](#)

---

step     *Choose a model by AIC in a Stepwise Algorithm*

---

### Description

Select a formula-based model by AIC.

### Usage

```
step(object, scope, scale = 0,
      direction = c("both", "backward", "forward"),
      trace = 1, keep = NULL, steps = 1000, k = 2, ...)
```

### Arguments

object	an object representing a model of an appropriate class (mainly "lm" and "glm"). This is used as the initial model in the stepwise search.
scope	defines the range of models examined in the stepwise search. This should be either a single formula, or a list containing components <code>upper</code> and <code>lower</code> , both formulae. See the details for how to specify the formulae and how they are used.
scale	used in the definition of the AIC statistic for selecting the models, currently only for <code>lm</code> , <code>ov</code> and <code>glm</code> models. The default value, 0, indicates the scale should be estimated: see <code>extractAIC</code> .
direction	the mode of stepwise search, can be one of "both", "backward", or "forward", with a default of "both". If the <code>scope</code> argument is missing the default for <code>direction</code> is "backward".
trace	if positive, information is printed during the running of <code>step</code> . Larger values may give more detailed information.
keep	a filter function whose input is a fitted model object and the associated AIC statistic, and whose output is arbitrary. Typically <code>keep</code> will select a subset of the components of the object and return them. The default is not to keep anything.

steps	the maximum number of steps to be considered. The default is 1000 (essentially as many as required). It is typically used to stop the process early.
k	the multiple of the number of degrees of freedom used for the penalty. Only $k = 2$ gives the genuine AIC: $k = \log(n)$ is sometimes referred to as BIC or SBC.
...	any additional arguments to <code>extractAIC</code> .

### Details

`step` uses `add1` and `drop1` repeatedly; it will work for any method for which they work, and that is determined by having a valid method for `extractAIC`. When the additive constant can be chosen so that AIC is equal to Mallows'  $C_p$ , this is done and the tables are labelled appropriately.

The set of models searched is determined by the `scope` argument. The right-hand-side of its `lower` component is always included in the model, and right-hand-side of the model is included in the `upper` component. If `scope` is a single formula, it specifies the `upper` component, and the `lower` model is empty. If `scope` is missing, the initial model is used as the `upper` model.

Models specified by `scope` can be templates to update `object` as used by `update.formula`. So using `.` in a `scope` formula means 'what is already there', with `.^2` indicating all interactions of existing terms.

There is a potential problem in using `glm` fits with a variable `scale`, as in that case the deviance is not simply related to the maximized log-likelihood. The "glm" method for function `extractAIC` makes the appropriate adjustment for a `gaussian` family, but may need to be amended for other cases. (The `binomial` and `poisson` families have fixed `scale` by default and do not correspond to a particular maximum-likelihood problem for variable `scale`.)

### Value

the stepwise-selected model is returned, with up to two additional components. There is an "anova" component corresponding to the steps taken in the search, as well as a "keep" component if the `keep=` argument was supplied in the call. The "Resid. Dev" column of the analysis of deviance table refers to a constant minus twice the maximized log likelihood: it will be a deviance only in cases where a saturated model is well-defined (thus excluding `lm`, `aov` and `survreg` fits, for example).

### Warning

The model fitting must apply the models to the same dataset. This may be a problem if there are missing values and R's default of `na.action = na.omit` is used. We suggest you remove the missing values first.

### Note

This function differs considerably from the function in S, which uses a number of approximations and does not in general compute the correct AIC.

This is a minimal implementation. Use `stepAIC` in package **MASS** for a wider range of object classes.

### Author(s)

B. D. Ripley: `step` is a slightly simplified version of `stepAIC` in package **MASS** (Venables & Ripley, 2002 and earlier editions).

The idea of a step function follows that described in Hastie & Pregibon (1992); but the implementation in **R** is more general.

## References

Hastie, T. J. and Pregibon, D. (1992) *Generalized linear models*. Chapter 6 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. New York: Springer (4th ed).

## See Also

[stepAIC](#) in [MASS](#), [add1](#), [drop1](#)

## Examples

```
utils::example(lm)
step(lm.D9)

summary(lm1 <- lm(Fertility ~ ., data = swiss))
slm1 <- step(lm1)
summary(slm1)
slm1$anova
```

---

stepfun

*Step Function Class*

---

## Description

Given the vectors  $(x_1, \dots, x_n)$  and  $(y_0, y_1, \dots, y_n)$  (one value more!), `stepfun(x, y, ...)` returns an interpolating ‘step’ function, say `fn`. I.e.,  $fn(t) = c_i$  (constant) for  $t \in (x_i, x_{i+1})$  and at the abscissa values, if (by default) `right = FALSE`,  $fn(x_i) = y_i$  and for `right = TRUE`,  $fn(x_i) = y_{i-1}$ , for  $i = 1, \dots, n$ .

The value of the constant  $c_i$  above depends on the ‘continuity’ parameter `f`. For the default, `right = FALSE`, `f = 0`, `fn` is a *cadlag* function, i.e., continuous at right, limit (‘the point’) at left. In general,  $c_i$  is interpolated in between the neighbouring  $y$  values,  $c_i = (1-f)y_i + f \cdot y_{i+1}$ . Therefore, for non-0 values of `f`, `fn` may no longer be a proper step function, since it can be discontinuous from both sides, unless `right = TRUE`, `f = 1` which is right-continuous.

## Usage

```
stepfun(x, y, f = as.numeric(right), ties = "ordered",
        right = FALSE)

is.stepfun(x)
knots(Fn, ...)
as.stepfun(x, ...)

## S3 method for class 'stepfun':
print(x, digits = getOption("digits") - 2, ...)

## S3 method for class 'stepfun':
summary(object, ...)
```

**Arguments**

<code>x</code>	numeric vector giving the knots or jump locations of the step function for <code>stepfun()</code> . For the other functions, <code>x</code> is as <code>object</code> below.
<code>y</code>	numeric vector one longer than <code>x</code> , giving the heights of the function values <i>between</i> the <code>x</code> values.
<code>f</code>	a number between 0 and 1, indicating how interpolation outside the given <code>x</code> values should happen. See <a href="#">approxfun</a> .
<code>ties</code>	Handling of tied <code>x</code> values. Either a function or the string "ordered". See <a href="#">approxfun</a> .
<code>right</code>	logical, indicating if the intervals should be closed on the right (and open on the left) or vice versa.
<code>Fn, object</code>	an R object inheriting from "stepfun".
<code>digits</code>	number of significant digits to use, see <a href="#">print</a> .
<code>...</code>	potentially further arguments (required by the generic).

**Value**

A function of class "stepfun", say `fn`.

There are methods available for summarizing (`summary(.)`), representing (`print(.)`) and plotting (`plot(.)`), see [plot.stepfun](#) "stepfun" objects.

The [environment](#) of `fn` contains all the information needed;

<code>"x", "y"</code>	the original arguments
<code>"n"</code>	number of knots (x values)
<code>"f"</code>	continuity parameter
<code>"yleft", "yright"</code>	the function values <i>outside</i> the knots
<code>"method"</code>	(always == "constant", from <a href="#">approxfun(.)</a> ).

The knots are also available via `knots(fn)`.

**Author(s)**

Martin Maechler, <maechler@stat.math.ethz.ch> with some basic code from Thomas Lumley.

**See Also**

[ecdf](#) for empirical distribution functions as special step functions and [plot.stepfun](#) for *plotting* step functions.

[approxfun](#) and [splinefun](#).

**Examples**

```

y0 <- c(1., 2., 4., 3.)
sfun0 <- stepfun(1:3, y0, f = 0)
sfun.2 <- stepfun(1:3, y0, f = .2)
sfun1 <- stepfun(1:3, y0, f = 1)
sfunlc <- stepfun(1:3, y0, right=TRUE)# hence f=1
sfun0

```

```

summary(sfun0)
summary(sfun.2)

## look at the internal structure:
unclass(sfun0)
ls(envir = environment(sfun0))

x0 <- seq(0.5,3.5, by = 0.25)
rbind(x=x0, f.f0 = sfun0(x0), f.f02= sfun.2(x0),
      f.f1 = sfun1(x0), f.f1c = sfun1c(x0))
## Identities :
stopifnot(identical(y0[-1], sfun0(1:3)),# right = FALSE
          identical(y0[-4], sfun1c(1:3))# right = TRUE

```

---

stl

*Seasonal Decomposition of Time Series by Loess*


---

## Description

Decompose a time series into seasonal, trend and irregular components using loess, acronym STL.

## Usage

```

stl(x, s.window, s.degree = 0,
    t.window = NULL, t.degree = 1,
    l.window = nextodd(period), l.degree = t.degree,
    s.jump = ceiling(s.window/10),
    t.jump = ceiling(t.window/10),
    l.jump = ceiling(l.window/10),
    robust = FALSE,
    inner = if(robust) 1 else 2,
    outer = if(robust) 15 else 0,
    na.action = na.fail)

```

## Arguments

x	univariate time series to be decomposed. This should be an object of class "ts" with a frequency greater than one.
s.window	either the character string "periodic" or the span (in lags) of the loess window for seasonal extraction, which should be odd. This has no default.
s.degree	degree of locally-fitted polynomial in seasonal extraction. Should be zero or one.
t.window	the span (in lags) of the loess window for trend extraction, which should be odd. If NULL, the default, $\text{nextodd}(\text{ceiling}((1.5 \cdot \text{period}) / (1 - (1.5 / \text{s.window}))))$ , is taken.
t.degree	degree of locally-fitted polynomial in trend extraction. Should be zero or one.
l.window	the span (in lags) of the loess window of the low-pass filter used for each subseries. Defaults to the smallest odd integer greater than or equal to frequency(x) which is recommended since it prevents competition between the trend and seasonal components. If not an odd integer its given value is increased to the next odd one.

<code>l.degree</code>	degree of locally-fitted polynomial for the subseries low-pass filter. Must be 0 or 1.
<code>s.jump</code> , <code>t.jump</code> , <code>l.jump</code>	integers at least one to increase speed of the respective smoother. Linear interpolation happens between every <code>*.jumpth</code> value.
<code>robust</code>	logical indicating if robust fitting be used in the <code>loess</code> procedure.
<code>inner</code>	integer; the number of ‘inner’ (backfitting) iterations; usually very few (2) iterations suffice.
<code>outer</code>	integer; the number of ‘outer’ robustness iterations.
<code>na.action</code>	action on missing values.

### Details

The seasonal component is found by *loess* smoothing the seasonal sub-series (the series of all January values, ...); if `s.window = "periodic"` smoothing is effectively replaced by taking the mean. The seasonal values are removed, and the remainder smoothed to find the trend. The overall level is removed from the seasonal component and added to the trend component. This process is iterated a few times. The `remainder` component is the residuals from the seasonal plus trend fit.

Several methods for the resulting class "`stl`" objects, see, `plot.stl`.

### Value

`stl` returns an object of class "`stl`" with components

<code>time.series</code>	a multiple time series with columns <code>seasonal</code> , <code>trend</code> and <code>remainder</code> .
<code>weights</code>	the final robust weights (all one if fitting is not done robustly).
<code>call</code>	the matched call.
<code>win</code>	integer (length 3 vector) with the spans used for the " <code>s</code> ", " <code>t</code> ", and " <code>l</code> " smoothers.
<code>deg</code>	integer (length 3) vector with the polynomial degrees for these smoothers.
<code>jump</code>	integer (length 3) vector with the ‘jumps’ (skips) used for these smoothers.
<code>ni</code>	number of inner iterations
<code>no</code>	number of outer robustness iterations

### Note

This is similar to but not identical to the `stl` function in S-PLUS. The `remainder` component given by S-PLUS is the sum of the `trend` and `remainder` series from this function.

### Author(s)

B.D. Ripley; Fortran code by Cleveland *et al.* (1990) from ‘netlib’.

### References

R. B. Cleveland, W. S. Cleveland, J.E. McRae, and I. Terpenning (1990) STL: A Seasonal-Trend Decomposition Procedure Based on Loess. *Journal of Official Statistics*, **6**, 3–73.



**See Also**

[plot.stl](#) for stl methods; [loess](#) in package **stats** (which is not actually used in stl).  
[StructTS](#) for different kind of decomposition.

**Examples**

```
require(graphics)

plot(stl(nottem, "per"))
plot(stl(nottem, s.window = 4, t.window = 50, t.jump = 1))

plot(stllc <- stl(log(co2), s.window=21))
summary(stllc)
## linear trend, strict period.
plot(stl(log(co2), s.window="per", t.window=1000))

## Two STL plotted side by side :
      stmd <- stl(mdeaths, s.window = "per") # non-robust
summary(stmR <- stl(mdeaths, s.window = "per", robust = TRUE))
op <- par(mar = c(0, 4, 0, 3), oma = c(5, 0, 4, 0), mfcol = c(4, 2))
plot(stmd, set.pars=NULL, labels = NULL,
      main = "stl(mdeaths, s.w = \"per\", robust = FALSE / TRUE)")
plot(stmR, set.pars=NULL)
# mark the 'outliers' :
(iO <- which(stmR $ weights < 1e-8)) # 10 were considered outliers
sts <- stmR$time.series
points(time(sts)[iO], 0.8* sts[,"remainder"][iO], pch = 4, col = "red")
par(op)# reset
```

---

stlmethods

*Methods for STL Objects*


---

**Description**

Methods for objects of class `stl`, typically the result of `stl`. The `plot` method does a multiple figure plot with some flexibility.

There are also (non-visible) `print` and `summary` methods.

**Usage**

```
## S3 method for class 'stl':
plot(x, labels = colnames(X),
      set.pars = list(mar = c(0, 6, 0, 6), oma = c(6, 0, 4, 0),
                     tck = -0.01, mfrow = c(nplot, 1)),
      main = NULL, range.bars = TRUE, ..., col.range = "light gray")
```

**Arguments**

`x` `stl` object.  
`labels` character of length 4 giving the names of the component time-series.  
`set.pars` settings for `par(.)` when setting up the plot.

<code>main</code>	plot main title.
<code>range.bars</code>	logical indicating if each plot should have a bar at its right side which are of equal heights in user coordinates.
<code>...</code>	further arguments passed to or from other methods.
<code>col.range</code>	colour to be used for the range bars, if plotted. Note this appears after <code>...</code> and so cannot be abbreviated.

**See Also**

`plot.ts` and `stl`, particularly for examples.

---

StructTS

*Fit Structural Time Series*


---

**Description**

Fit a structural model for a time series by maximum likelihood.

**Usage**

```
StructTS(x, type = c("level", "trend", "BSM"), init = NULL,
         fixed = NULL, optim.control = NULL)
```

**Arguments**

<code>x</code>	a univariate numeric time series. Missing values are allowed.
<code>type</code>	the class of structural model. If omitted, a BSM is used for a time series with $\text{frequency}(x) > 1$ , and a local trend model otherwise.
<code>init</code>	initial values of the variance parameters.
<code>fixed</code>	optional numeric vector of the same length as the total number of parameters. If supplied, only NA entries in <code>fixed</code> will be varied. Probably most useful for setting variances to zero.
<code>optim.control</code>	List of control parameters for <code>optim</code> . Method "L-BFGS-B" is used.

**Details**

*Structural time series* models are (linear Gaussian) state-space models for (univariate) time series based on a decomposition of the series into a number of components. They are specified by a set of error variances, some of which may be zero.

The simplest model is the *local level* model specified by `type = "level"`. This has an underlying level  $\mu_t$  which evolves by

$$\mu_{t+1} = \mu_t + \xi_t, \quad \xi_t \sim N(0, \sigma_\xi^2)$$

The observations are

$$x_t = \mu_t + \epsilon_t, \quad \epsilon_t \sim N(0, \sigma_\epsilon^2)$$

There are two parameters,  $\sigma_\xi^2$  and  $\sigma_\epsilon^2$ . It is an ARIMA(0,1,1) model, but with restrictions on the parameter set.

The *local linear trend model*, `type = "trend"`, has the same measurement equation, but with a time-varying slope in the dynamics for  $\mu_t$ , given by

$$\mu_{t+1} = \mu_t + \nu_t + \xi_t, \quad \xi_t \sim N(0, \sigma_\xi^2)$$

$$\nu_{t+1} = \nu_t + \zeta_t, \quad \zeta_t \sim N(0, \sigma_\zeta^2)$$

with three variance parameters. It is not uncommon to find  $\sigma_\zeta^2 = 0$  (which reduces to the local level model) or  $\sigma_\xi^2 = 0$ , which ensures a smooth trend. This is a restricted ARIMA(0,2,2) model.

The *basic structural model*, `type = "BSM"`, is a local trend model with an additional seasonal component. Thus the measurement equation is

$$x_t = \mu_t + \gamma_t + \epsilon_t, \quad \epsilon_t \sim N(0, \sigma_\epsilon^2)$$

where  $\gamma_t$  is a seasonal component with dynamics

$$\gamma_{t+1} = -\gamma_t + \dots + \gamma_{t-s+2} + \omega_t, \quad \omega_t \sim N(0, \sigma_\omega^2)$$

The boundary case  $\sigma_\omega^2 = 0$  corresponds to a deterministic (but arbitrary) seasonal pattern. (This is sometimes known as the ‘dummy variable’ version of the BSM.)

## Value

A list of class "StructTS" with components:

<code>coef</code>	the estimated variances of the components.
<code>loglik</code>	the maximized log-likelihood. Note that as all these models are non-stationary this includes a diffuse prior for some observations and hence is not comparable with <a href="#">arima</a> nor different types of structural models.
<code>data</code>	the time series <code>x</code> .
<code>residuals</code>	the standardized residuals.
<code>fitted</code>	a multiple time series with one component for the level, slope and seasonal components, estimated contemporaneously (that is at time $t$ and not at the end of the series).
<code>call</code>	the matched call.
<code>series</code>	the name of the series <code>x</code> .
<code>code</code>	the convergence code returned by <a href="#">optim</a> .
<code>model, model0</code>	Lists representing the Kalman Filter used in the fitting. See <a href="#">KalmanLike</a> . <code>model0</code> is the initial state of the filter, <code>model</code> its final state.
<code>xtsp</code>	the <code>tsp</code> attributes of <code>x</code> .

## Note

Optimization of structural models is a lot harder than many of the references admit. For example, the [AirPassengers](#) data are considered in Brockwell & Davis (1996): their solution appears to be a local maximum, but nowhere near as good a fit as that produced by `StructTS`. It is quite common to find fits with one or more variances zero, and this can include  $\sigma_\epsilon^2$ .

## References

- Brockwell, P. J. & Davis, R. A. (1996). *Introduction to Time Series and Forecasting*. Springer, New York. Sections 8.2 and 8.5.
- Durbin, J. and Koopman, S. J. (2001) *Time Series Analysis by State Space Methods*. Oxford University Press.
- Harvey, A. C. (1989) *Forecasting, Structural Time Series Models and the Kalman Filter*. Cambridge University Press.
- Harvey, A. C. (1993) *Time Series Models*. 2nd Edition, Harvester Wheatsheaf.

## See Also

[KalmanLike](#), [tsSmooth](#); [stl](#) for different kind of (seasonal) decomposition.

## Examples

```
## see also JohnsonJohnson, Nile and AirPassengers
require(graphics)

trees <- window(treering, start=0)
(fit <- StructTS(trees, type = "level"))
plot(trees)
lines(fitted(fit), col = "green")
tsdiag(fit)

(fit <- StructTS(log10(UKgas), type = "BSM"))
par(mfrow = c(4, 1))
plot(log10(UKgas))
plot(cbind(fitted(fit), resid=resid(fit)), main = "UK gas consumption")

## keep some parameters fixed; trace optimizer:
StructTS(log10(UKgas), type = "BSM", fixed = c(0.1,0.001,NA,NA),
         optim.control = list(trace=TRUE))
```

---

summary.aov

*Summarize an Analysis of Variance Model*

---

## Description

Summarize an analysis of variance model.

## Usage

```
## S3 method for class 'aov':
summary(object, intercept = FALSE, split,
        expand.split = TRUE, keep.zero.df = TRUE, ...)

## S3 method for class 'aovlist':
summary(object, ...)
```

**Arguments**

<code>object</code>	An object of class "aov" or "aovlist".
<code>intercept</code>	logical: should intercept terms be included?
<code>split</code>	an optional named list, with names corresponding to terms in the model. Each component is itself a list with integer components giving contrasts whose contributions are to be summed.
<code>expand.split</code>	logical: should the split apply also to interactions involving the factor?
<code>keep.zero.df</code>	logical: should terms with no degrees of freedom be included?
<code>...</code>	Arguments to be passed to or from other methods, for <code>summary.aovlist</code> including those for <code>summary.aov</code> .

**Value**

An object of class `c("summary.aov", "listof")` or `"summary.aovlist"` respectively. For fits with a single stratum the result will be a list of ANOVA tables, one for each response (even if there is only one response): the tables are of class `"anova"` inheriting from class `"data.frame"`. They have columns `"Df"`, `"Sum Sq"`, `"Mean Sq"`, as well as `"F value"` and `"Pr(>F)"` if there are non-zero residual degrees of freedom. There is a row for each term in the model, plus one for `"Residuals"` if there are any.

For multistratum fits the return value is a list of such summaries, one for each stratum.

**Note**

The use of `expand.split = TRUE` is little tested: it is always possible to set it to `FALSE` and specify exactly all the splits required.

**See Also**

[aov](#), [summary](#), [model.tables](#), [TukeyHSD](#)

**Examples**

```
## From Venables and Ripley (2002) p.165.
N <- c(0,1,0,1,1,1,0,0,0,1,1,0,1,1,0,0,1,0,1,0,1,0,1,1,0,0)
P <- c(1,1,0,0,0,1,0,1,1,1,0,0,0,1,0,1,1,0,0,1,0,1,0,1,1,0)
K <- c(1,0,0,1,0,1,1,0,0,1,0,1,0,1,1,0,0,0,1,1,1,0,0,1,0)
yield <- c(49.5,62.8,46.8,57.0,59.8,58.5,55.5,56.0,62.8,55.8,69.5,55.0,
          62.0,48.8,45.5,44.2,52.0,51.5,49.8,48.8,57.2,59.0,53.2,56.0)
npk <- data.frame(block=gl(6,4), N=factor(N), P=factor(P),
                 K=factor(K), yield=yield)

( npk.aov <- aov(yield ~ block + N*P*K, npk) )
summary(npk.aov)
coefficients(npk.aov)

# Cochran and Cox (1957, p.164)
# 3x3 factorial with ordered factors, each is average of 12.
CC <- data.frame(
  y = c(449, 413, 326, 409, 358, 291, 341, 278, 312)/12,
  P = ordered(gl(3, 3)), N = ordered(gl(3, 1, 9))
)
CC.aov <- aov(y ~ N * P, data = CC , weights = rep(12, 9))
```

```
summary(CC.aov)

# Split both main effects into linear and quadratic parts.
summary(CC.aov, split = list(N = list(L = 1, Q = 2),
                             P = list(L = 1, Q = 2)))

# Split only the interaction
summary(CC.aov, split = list("N:P" = list(L.L = 1, Q = 2:4)))

# split on just one var
summary(CC.aov, split = list(P = list(lin = 1, quad = 2)))
summary(CC.aov, split = list(P = list(lin = 1, quad = 2)),
        expand.split=FALSE)
```

---

summary.glm

*Summarizing Generalized Linear Model Fits*


---

## Description

These functions are all [methods](#) for class `glm` or `summary.glm` objects.

## Usage

```
## S3 method for class 'glm':
summary(object, dispersion = NULL, correlation = FALSE,
        symbolic.cor = FALSE, ...)

## S3 method for class 'summary.glm':
print(x, digits = max(3, getOption("digits") - 3),
      symbolic.cor = x$symbolic.cor,
      signif.stars = getOption("show.signif.stars"), ...)
```

## Arguments

<code>object</code>	an object of class "glm", usually, a result of a call to <a href="#">glm</a> .
<code>x</code>	an object of class "summary.glm", usually, a result of a call to <code>summary.glm</code> .
<code>dispersion</code>	the dispersion parameter for the family used. Either a single numerical value or NULL (the default), when it is inferred from <code>object</code> (see ‘Details’).
<code>correlation</code>	logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed.
<code>digits</code>	the number of significant digits to use when printing.
<code>symbolic.cor</code>	logical. If TRUE, print the correlations in a symbolic form (see <a href="#">symnum</a> ) rather than as numbers.
<code>signif.stars</code>	logical. If TRUE, ‘significance stars’ are printed for each coefficient.
<code>...</code>	further arguments passed to or from other methods.

## Details

`print.summary.glm` tries to be smart about formatting the coefficients, standard errors, etc. and additionally gives 'significance stars' if `signif.stars` is `TRUE`. The `coefficients` component of the result gives the estimated coefficients and their estimated standard errors, together with their ratio. This third column is labelled `t_ratio` if the dispersion is estimated, and `z_ratio` if the dispersion is known (or fixed by the family). A fourth column gives the two-tailed p-value corresponding to the t or z ratio based on a Student t or Normal reference distribution. (It is possible that the dispersion is not known and there are no residual degrees of freedom from which to estimate it. In that case the estimate is `NaN`.)

Aliased coefficients are omitted in the returned object but restored by the `print` method.

Correlations are printed to two decimal places (or symbolically): to see the actual correlations print `summary(object)$correlation` directly.

The dispersion of a GLM is not used in the fitting process, but it is needed to find standard errors. If `dispersion` is not supplied or `NULL`, the dispersion is taken as 1 for the `binomial` and `Poisson` families, and otherwise estimated by the residual Chisquared statistic (calculated from cases with non-zero weights) divided by the residual degrees of freedom.

`summary` can be used with Gaussian `glm` fits to handle the case of a linear regression with known error variance, something not handled by `summary.lm`.

## Value

`summary.glm` returns an object of class `"summary.glm"`, a list with components

<code>call</code>	the component from <code>object</code> .
<code>family</code>	the component from <code>object</code> .
<code>deviance</code>	the component from <code>object</code> .
<code>contrasts</code>	the component from <code>object</code> .
<code>df.residual</code>	the component from <code>object</code> .
<code>null.deviance</code>	the component from <code>object</code> .
<code>df.null</code>	the component from <code>object</code> .
<code>deviance.resid</code>	the deviance residuals: see <code>residuals.glm</code> .
<code>coefficients</code>	the matrix of coefficients, standard errors, z-values and p-values. Aliased coefficients are omitted.
<code>aliased</code>	named logical vector showing if the original coefficients are aliased.
<code>dispersion</code>	either the supplied argument or the inferred/estimated dispersion if the latter is <code>NULL</code> .
<code>df</code>	a 3-vector of the rank of the model and the number of residual degrees of freedom, plus number of non-aliased coefficients.
<code>cov.unscaled</code>	the unscaled ( <code>dispersion = 1</code> ) estimated covariance matrix of the estimated coefficients.
<code>cov.scaled</code>	ditto, scaled by <code>dispersion</code> .
<code>correlation</code>	(only if <code>correlation</code> is true.) The estimated correlations of the estimated coefficients.
<code>symbolic.cor</code>	(only if <code>correlation</code> is true.) The value of the argument <code>symbolic.cor</code> .

**See Also**

[glm](#), [summary](#).

**Examples**

```
## --- Continuing the Example from '?glm':
summary(glm.D93)
```

---

summary.lm

*Summarizing Linear Model Fits*


---

**Description**

summary method for class "lm".

**Usage**

```
## S3 method for class 'lm':
summary(object, correlation = FALSE, symbolic.cor = FALSE, ...)

## S3 method for class 'summary.lm':
print(x, digits = max(3, getOption("digits") - 3),
      symbolic.cor = x$symbolic.cor,
      signif.stars = getOption("show.signif.stars"), ...)
```

**Arguments**

object	an object of class "lm", usually, a result of a call to <a href="#">lm</a> .
x	an object of class "summary.lm", usually, a result of a call to <code>summary.lm</code> .
correlation	logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed.
digits	the number of significant digits to use when printing.
symbolic.cor	logical. If TRUE, print the correlations in a symbolic form (see <a href="#">symnum</a> ) rather than as numbers.
signif.stars	logical. If TRUE, 'significance stars' are printed for each coefficient.
...	further arguments passed to or from other methods.

**Details**

`print.summary.lm` tries to be smart about formatting the coefficients, standard errors, etc. and additionally gives 'significance stars' if `signif.stars` is TRUE.

Correlations are printed to two decimal places (or symbolically): to see the actual correlations print `summary(object)$correlation` directly.



**Value**

The function `summary.lm` computes and returns a list of summary statistics of the fitted linear model given in `object`, using the components (list elements) `"call"` and `"terms"` from its argument, plus

`residuals` the *weighted* residuals, the usual residuals rescaled by the square root of the weights specified in the call to `lm`.

`coefficients` a  $p \times 4$  matrix with columns for the estimated coefficient, its standard error, t-statistic and corresponding (two-sided) p-value. Aliased coefficients are omitted.

`aliased` named logical vector showing if the original coefficients are aliased.

`sigma` the square root of the estimated variance of the random error

$$\hat{\sigma}^2 = \frac{1}{n-p} \sum_i w_i R_i^2,$$

where  $R_i$  is the  $i$ -th residual, `residuals[i]`.

`df` degrees of freedom, a 3-vector  $(p, n-p, p^*)$ , the last being the number of non-aliased coefficients.

`fstatistic` (for models including non-intercept terms) a 3-vector with the value of the F-statistic with its numerator and denominator degrees of freedom.

`r.squared`  $R^2$ , the ‘fraction of variance explained by the model’,

$$R^2 = 1 - \frac{\sum_i R_i^2}{\sum_i (y_i - y^*)^2},$$

where  $y^*$  is the mean of  $y_i$  if there is an intercept and zero otherwise.

`adj.r.squared`

the above  $R^2$  statistic ‘adjusted’, penalizing for higher  $p$ .

`cov.unscaled` a  $p \times p$  matrix of (unscaled) covariances of the  $\hat{\beta}_j, j = 1, \dots, p$ .

`correlation` the correlation matrix corresponding to the above `cov.unscaled`, if `correlation = TRUE` is specified.

`symbolic.cor` (only if `correlation` is true.) The value of the argument `symbolic.cor`.

`na.action` from `object`, if present there.

**See Also**

The model fitting function `lm`, `summary`.

Function `coef` will extract the matrix of coefficients with standard errors, t-statistics and p-values.

**Examples**

```
##-- Continuing the lm(.) example:
coef(lm.D90) # the bare coefficients
sld90 <- summary(lm.D90 <- lm(weight ~ group -1)) # omitting intercept
sld90
coef(sld90) # much more
```

---

summary.manova      *Summary Method for Multivariate Analysis of Variance*


---

## Description

A summary method for class "manova".

## Usage

```
## S3 method for class 'manova':
summary(object,
        test = c("Pillai", "Wilks", "Hotelling-Lawley", "Roy"),
        intercept = FALSE, tol = 1e-7, ...)
```

## Arguments

object	An object of class "manova" or an aov object with multiple responses.
test	The name of the test statistic to be used. Partial matching is used so the name can be abbreviated.
intercept	logical. If TRUE, the intercept term is included in the table.
tol	tolerance to be used in deciding if the residuals are rank-deficient: see <a href="#">qr</a> .
...	further arguments passed to or from other methods.

## Details

The `summary.manova` method uses a multivariate test statistic for the summary table. Wilks' statistic is most popular in the literature, but the default Pillai-Bartlett statistic is recommended by Hand and Taylor (1987).

The table gives a transformation of the test statistic which has approximately an F distribution. The approximations used follow S-PLUS and SAS (the latter apart from some cases of the Hotelling-Lawley statistic), but many other distributional approximations exist: see Anderson (1984) and Krzanowski and Marriott (1994) for further references. All four approximate F statistics are the same when the term being tested has one degree of freedom, but in other cases that for the Roy statistic is an upper bound.

The tolerance `tol` is applied to the QR decomposition of the residual correlation matrix (unless some response has essentially zero residuals, when it is unscaled). Thus the default value guards against very highly correlated responses: it can be reduced but doing so will allow rather inaccurate results and it will normally be better to transform the responses to remove the high correlation.

## Value

An object of class "summary.manova". If there is a positive residual degrees of freedom, this is a list with components

row.names	The names of the terms, the row names of the <code>stats</code> table if present.
SS	A named list of sums of squares and product matrices.
Eigenvalues	A matrix of eigenvalues.
stats	A matrix of the statistics, approximate F value, degrees of freedom and P value.

otherwise components `row.names`, `SS` and `Df` (degrees of freedom) for the terms (and not the residuals).

**References**

- Anderson, T. W. (1994) *An Introduction to Multivariate Statistical Analysis*. Wiley.
- Hand, D. J. and Taylor, C. C. (1987) *Multivariate Analysis of Variance and Repeated Measures*. Chapman and Hall.
- Krzanowski, W. J. (1988) *Principles of Multivariate Analysis. A User's Perspective*. Oxford.
- Krzanowski, W. J. and Marriott, F. H. C. (1994) *Multivariate Analysis. Part I: Distributions, Ordination and Inference*. Edward Arnold.

**See Also**

[manova](#), [aov](#)

**Examples**

```
## Example on producing plastic film from Krzanowski (1998, p. 381)
tear <- c(6.5, 6.2, 5.8, 6.5, 6.5, 6.9, 7.2, 6.9, 6.1, 6.3,
          6.7, 6.6, 7.2, 7.1, 6.8, 7.1, 7.0, 7.2, 7.5, 7.6)
gloss <- c(9.5, 9.9, 9.6, 9.6, 9.2, 9.1, 10.0, 9.9, 9.5, 9.4,
           9.1, 9.3, 8.3, 8.4, 8.5, 9.2, 8.8, 9.7, 10.1, 9.2)
opacity <- c(4.4, 6.4, 3.0, 4.1, 0.8, 5.7, 2.0, 3.9, 1.9, 5.7,
             2.8, 4.1, 3.8, 1.6, 3.4, 8.4, 5.2, 6.9, 2.7, 1.9)
Y <- cbind(tear, gloss, opacity)
rate <- factor(gl(2,10), labels=c("Low", "High"))
additive <- factor(gl(2, 5, length=20), labels=c("Low", "High"))

fit <- manova(Y ~ rate * additive)
summary.aov(fit)           # univariate ANOVA tables
summary(fit, test="Wilks") # ANOVA table of Wilks' lambda
summary(fit)              # same F statistics as single-df terms
```

---

summary.nls

*Summarizing Non-Linear Least-Squares Model Fits*

---

**Description**

summary method for class "nls".

**Usage**

```
## S3 method for class 'nls':
summary(object, correlation = FALSE, symbolic.cor = FALSE, ...)

## S3 method for class 'summary.nls':
print(x, digits = max(3, getOption("digits") - 3),
      symbolic.cor = x$symbolic.cor,
      signif.stars = getOption("show.signif.stars"), ...)
```

**Arguments**

object	an object of class "nls".
x	an object of class "summary.nls", usually the result of a call to summary.nls.
correlation	logical; if TRUE, the correlation matrix of the estimated parameters is returned and printed.
digits	the number of significant digits to use when printing.
symbolic.cor	logical. If TRUE, print the correlations in a symbolic form (see <a href="#">symnum</a> ) rather than as numbers.
signif.stars	logical. If TRUE, 'significance stars' are printed for each coefficient.
...	further arguments passed to or from other methods.

**Details**

The distribution theory used to find the distribution of the standard errors and of the residual standard error (for t ratios) is based on linearization and is approximate, maybe very approximate.

print.summary.nls tries to be smart about formatting the coefficients, standard errors, etc. and additionally gives 'significance stars' if signif.stars is TRUE.

Correlations are printed to two decimal places (or symbolically): to see the actual correlations print summary(object)\$correlation directly.

**Value**

The function summary.nls computes and returns a list of summary statistics of the fitted model given in object, using the component "formula" from its argument, plus

residuals	the <i>weighted</i> residuals, the usual residuals rescaled by the square root of the weights specified in the call to nls.
coefficients	a $p \times 4$ matrix with columns for the estimated coefficient, its standard error, t-statistic and corresponding (two-sided) p-value.
sigma	the square root of the estimated variance of the random error

$$\hat{\sigma}^2 = \frac{1}{n-p} \sum_i R_i^2,$$

where  $R_i$  is the  $i$ -th weighted residual.

df	degrees of freedom, a 2-vector $(p, n - p)$ . (Here and elsewhere $n$ omits observations with zero weights.)
cov.unscaled	a $p \times p$ matrix of (unscaled) covariances of the parameter estimates.
correlation	the correlation matrix corresponding to the above cov.unscaled, if correlation = TRUE is specified and there are a non-zero number of residual degrees of freedom.
symbolic.cor	(only if correlation is true.) The value of the argument symbolic.cor.

**See Also**

The model fitting function [nls](#), [summary](#).

Function [coef](#) will extract the matrix of coefficients with standard errors, t-statistics and p-values.

summary.princomp     *Summary method for Principal Components Analysis*

---

### Description

The `summary` method for class "princomp".

### Usage

```
## S3 method for class 'princomp':  
summary(object, loadings = FALSE, cutoff = 0.1, ...)
```

```
## S3 method for class 'summary.princomp':  
print(x, digits = 3, loadings = x$print.loadings,  
      cutoff = x$cutoff, ...)
```

### Arguments

<code>object</code>	an object of class "princomp", as from <code>princomp()</code> .
<code>loadings</code>	logical. Should loadings be included?
<code>cutoff</code>	numeric. Loadings below this cutoff in absolute value are shown as blank in the output.
<code>x</code>	an object of class "summary.princomp".
<code>digits</code>	the number of significant digits to be used in listing loadings.
<code>...</code>	arguments to be passed to or from other methods.

### Value

object with additional components `cutoff` and `print.loadings`.

### See Also

[princomp](#)

### Examples

```
summary(pc.cr <- princomp(USArrests, cor=TRUE))  
print(summary(princomp(USArrests, cor=TRUE),  
            loadings = TRUE, cutoff = 0.2), digits = 2)
```

---

supsmu

*Friedman's SuperSmoother*


---

### Description

Smooth the (x, y) values by Friedman's 'super smoother'.

### Usage

```
supsmu(x, y, wt, span = "cv", periodic = FALSE, bass = 0)
```

### Arguments

x	x values for smoothing
y	y values for smoothing
wt	case weights, by default all equal
span	the fraction of the observations in the span of the running lines smoother, or "cv" to choose this by leave-one-out cross-validation.
periodic	if TRUE, the x values are assumed to be in [0, 1] and of period 1.
bass	controls the smoothness of the fitted curve. Values of up to 10 indicate increasing smoothness.

### Details

supsmu is a running lines smoother which chooses between three spans for the lines. The running lines smoothers are symmetric, with  $k/2$  data points each side of the predicted point, and values of  $k$  as  $0.5 * n$ ,  $0.2 * n$  and  $0.05 * n$ , where  $n$  is the number of data points. If `span` is specified, a single smoother with span `span * n` is used.

The best of the three smoothers is chosen by cross-validation for each prediction. The best spans are then smoothed by a running lines smoother and the final prediction chosen by linear interpolation.

The FORTRAN code says: "For small samples ( $n < 40$ ) or if there are substantial serial correlations between observations close in x-value, then a pre-specified fixed span smoother (`span > 0`) should be used. Reasonable span values are 0.2 to 0.4."

Cases with non-finite values of `x`, `y` or `wt` are dropped, with a warning.

### Value

A list with components

x	the input values in increasing order with duplicates removed.
y	the corresponding y values on the fitted curve.

### References

Friedman, J. H. (1984) SMART User's Guide. Laboratory for Computational Statistics, Stanford University Technical Report No. 1.

Friedman, J. H. (1984) A variable span scatterplot smoother. Laboratory for Computational Statistics, Stanford University Technical Report No. 5.

**See Also**[ppr](#)**Examples**

```
require(graphics)

with(cars, {
  plot(speed, dist)
  lines(supsmu(speed, dist))
  lines(supsmu(speed, dist, bass = 7), lty = 2)
})
```

symnum

*Symbolic Number Coding***Description**

Symbolically encode a given numeric or logical vector or array. Particularly useful for visualization of structured matrices, e.g., correlation, sparse, or logical ones.

**Usage**

```
symnum(x, cutpoints = c(0.3, 0.6, 0.8, 0.9, 0.95),
       symbols = if(numeric.x) c(" ", ".", ",", "+", "*", "B")
         else c(".", "|"),
       legend = length(symbols) >= 3,
       na = "?", eps = 1e-5, numeric.x = is.numeric(x),
       corr = missing(cutpoints) && numeric.x,
       show.max = if(corr) "1", show.min = NULL,
       abbr.colnames = has.colnames,
       lower.triangular = corr && is.numeric(x) && is.matrix(x),
       diag.lower.tri = corr && !is.null(show.max))
```

**Arguments**

<code>x</code>	numeric or logical vector or array.
<code>cutpoints</code>	numeric vector whose values <code>cutpoints[j] = c<sub>j</sub></code> ( <i>after</i> augmentation, see <code>corr</code> below) are used for intervals.
<code>symbols</code>	character vector, one shorter than (the <i>augmented</i> , see <code>corr</code> below) <code>cutpoints</code> . <code>symbols[j] = s<sub>j</sub></code> are used as ‘code’ for the (half open) interval $(c_j, c_{j+1}]$ . When <code>numeric.x</code> is FALSE, i.e., by default when argument <code>x</code> is logical, the default is <code>c(" ", " ")</code> (graphical 0/1s).
<code>legend</code>	logical indicating if a "legend" attribute is desired.
<code>na</code>	character or logical. How NAs are coded. If <code>na == FALSE</code> , NAs are coded invisibly, <i>including</i> the "legend" attribute below, which otherwise mentions NA coding.
<code>eps</code>	absolute precision to be used at left and right boundary.

`numeric.x` logical indicating if `x` should be treated as numbers, otherwise as logical.  
`corr` logical. If TRUE, `x` contains correlations. The cutpoints are augmented by 0 and 1 and `abs(x)` is coded.  
`show.max` if TRUE, or of mode `character`, the maximal cutpoint is coded especially.  
`show.min` if TRUE, or of mode `character`, the minimal cutpoint is coded especially.  
`abbr.colnames` logical, integer or NULL indicating how column names should be abbreviated (if they are); if NULL (or FALSE and `x` has no column names), the column names will all be empty, i.e., ""; otherwise if `abbr.colnames` is false, they are left unchanged. If TRUE or integer, existing column names will be abbreviated to `abbreviate(*, minlength = abbr.colnames)`.  
`lower.triangular` logical. If TRUE and `x` is a matrix, only the *lower triangular* part of the matrix is coded as non-blank.  
`diag.lower.tri` logical. If `lower.triangular` and this are TRUE, the *diagonal* part of the matrix is shown.

### Value

An atomic character object of class `noquote` and the same dimensions as `x`.

If `legend` is TRUE (as by default when there are more than two classes), the result has an attribute "legend" containing a legend of the returned character codes, in the form

$$c_1s_1c_2s_2 \dots s_n c_{n+1}$$

where  $c_j = \text{cutpoints}[j]$  and  $s_j = \text{symbols}[j]$ .

### Note

The optional (mostly logical) arguments all try to use smart defaults. Specifying them explicitly may lead to considerably improved output in many cases.

### Author(s)

Martin Maechler <maechler@stat.math.ethz.ch>

### See Also

[as.character](#); [image](#)

### Examples

```

ii <- 0:8; names(ii) <- ii
symnum(ii, cut= 2*(0:4), sym = c(".", "-", "+", "$"))
symnum(ii, cut= 2*(0:4), sym = c(".", "-", "+", "$"), show.max=TRUE)

symnum(1:12 %% 3 == 0) # --> "|" = TRUE, "." = FALSE for logical

## Pascal's Triangle modulo 2 -- odd and even numbers:
N <- 38
pascal <- t(sapply(0:N, function(n) round(choose(n, 0:N - (N-n)%/2))))
rownames(pascal) <- rep("", 1+N) # <-- to improve "graphic"
  
```



```

symnum(pascal %% 2, symbols = c(" ", "A"), numeric = FALSE)

##-- Symbolic correlation matrices:
symnum(cor(attitude), diag = FALSE)
symnum(cor(attitude), abbr.= NULL)
symnum(cor(attitude), abbr.= FALSE)
symnum(cor(attitude), abbr.= 2)

symnum(cor(rbind(1, rnorm(25), rnorm(25)^2)))
symnum(cor(matrix(rexp(30, 1), 5, 18))) # <<-- PATTERN ! --
symnum(cm1 <- cor(matrix(rnorm(90) , 5, 18))) # < White Noise SMALL n
symnum(cm1, diag=FALSE)
symnum(cm2 <- cor(matrix(rnorm(900), 50, 18))) # < White Noise "BIG" n
symnum(cm2, lower=FALSE)

## NA's:
Cm <- cor(matrix(rnorm(60), 10, 6)); Cm[c(3,6), 2] <- NA
symnum(Cm, show.max=NULL)

## Graphical P-values (aka "significance stars"):
pval <- rev(sort(c(outer(1:6, 10^-(1:3))))))
symp <- symnum(pval, corr=FALSE,
               cutpoints = c(0, .001, .01, .05, .1, 1),
               symbols = c("***", "**", "*", ".", " "))
noquote(cbind(P.val = format(pval), Signif= symp))

```

---

t.test

*Student's t-Test*


---

## Description

Performs one and two sample t-tests on vectors of data.

## Usage

```

t.test(x, ...)

## Default S3 method:
t.test(x, y = NULL,
       alternative = c("two.sided", "less", "greater"),
       mu = 0, paired = FALSE, var.equal = FALSE,
       conf.level = 0.95, ...)

## S3 method for class 'formula':
t.test(formula, data, subset, na.action, ...)

```

## Arguments

**x** a (non-empty) numeric vector of data values.

**y** an optional (non-empty) numeric vector of data values.

**alternative** a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.

<code>mu</code>	a number indicating the true value of the mean (or difference in means if you are performing a two sample test).
<code>paired</code>	a logical indicating whether you want a paired t-test.
<code>var.equal</code>	a logical variable indicating whether to treat the two variances as being equal. If <code>TRUE</code> then the pooled variance is used to estimate the variance otherwise the Welch (or Satterthwaite) approximation to the degrees of freedom is used.
<code>conf.level</code>	confidence level of the interval.
<code>formula</code>	a formula of the form <code>lhs ~ rhs</code> where <code>lhs</code> is a numeric variable giving the data values and <code>rhs</code> a factor with two levels giving the corresponding groups.
<code>data</code>	an optional matrix or data frame (or similar: see <code>model.frame</code> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>subset</code>	an optional vector specifying a subset of observations to be used.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. Defaults to <code>getOption("na.action")</code> .
<code>...</code>	further arguments to be passed to or from methods.

### Details

The formula interface is only applicable for the 2-sample tests.

`alternative = "greater"` is the alternative that `x` has a larger mean than `y`.

If `paired` is `TRUE` then both `x` and `y` must be specified and they must be the same length. Missing values are removed (in pairs if `paired` is `TRUE`). If `var.equal` is `TRUE` then the pooled estimate of the variance is used. By default, if `var.equal` is `FALSE` then the variance is estimated separately for both groups and the Welch modification to the degrees of freedom is used.

If the input data are effectively constant (compared to the larger of the two means) an error is generated.

### Value

A list with class `"htest"` containing the following components:

<code>statistic</code>	the value of the t-statistic.
<code>parameter</code>	the degrees of freedom for the t-statistic.
<code>p.value</code>	the p-value for the test.
<code>conf.int</code>	a confidence interval for the mean appropriate to the specified alternative hypothesis.
<code>estimate</code>	the estimated mean or difference in means depending on whether it was a one-sample test or a two-sample test.
<code>null.value</code>	the specified hypothesized value of the mean or mean difference depending on whether it was a one-sample test or a two-sample test.
<code>alternative</code>	a character string describing the alternative hypothesis.
<code>method</code>	a character string indicating what type of t-test was performed.
<code>data.name</code>	a character string giving the name(s) of the data.

### See Also

[prop.test](#)

**Examples**

```
require(graphics)

t.test(1:10,y=c(7:20))      # P = .00001855
t.test(1:10,y=c(7:20, 200)) # P = .1245    -- NOT significant anymore

## Classical example: Student's sleep data
plot(extra ~ group, data = sleep)
## Traditional interface
with(sleep, t.test(extra[group == 1], extra[group == 2]))
## Formula interface
t.test(extra ~ group, data = sleep)
```

TDist

*The Student t Distribution***Description**

Density, distribution function, quantile function and random generation for the t distribution with `df` degrees of freedom (and optional non-centrality parameter `ncp`).

**Usage**

```
dt(x, df, ncp, log = FALSE)
pt(q, df, ncp, lower.tail = TRUE, log.p = FALSE)
qt(p, df, ncp, lower.tail = TRUE, log.p = FALSE)
rt(n, df, ncp)
```

**Arguments**

<code>x, q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
<code>df</code>	degrees of freedom ( $> 0$ , maybe non-integer). <code>df = Inf</code> is allowed.
<code>ncp</code>	non-centrality parameter $\delta$ ; currently except for <code>rt()</code> , only for <code>abs(ncp) &lt;= 37.62</code> . If omitted, use the central t distribution.
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .

**Details**

The *t* distribution with `df` =  $\nu$  degrees of freedom has density

$$f(x) = \frac{\Gamma((\nu + 1)/2)}{\sqrt{\pi\nu}\Gamma(\nu/2)}(1 + x^2/\nu)^{-(\nu+1)/2}$$

for all real  $x$ . It has mean 0 (for  $\nu > 1$ ) and variance  $\frac{\nu}{\nu-2}$  (for  $\nu > 2$ ).

The general *non-central t* with parameters  $(\nu, \delta) = (\text{df}, \text{ncp})$  is defined as the distribution of  $T_\nu(\delta) := (U + \delta)/\sqrt{V/\nu}$  where  $U$  and  $V$  are independent random variables,  $U \sim \mathcal{N}(0, 1)$  and  $V \sim \chi_\nu^2$  (see [Chisquare](#)).

The most used applications are power calculations for  $t$ -tests:

Let  $T = \frac{\bar{X} - \mu_0}{S/\sqrt{n}}$  where  $\bar{X}$  is the [mean](#) and  $S$  the sample standard deviation ([sd](#)) of  $X_1, X_2, \dots, X_n$  which are i.i.d.  $\mathcal{N}(\mu, \sigma^2)$  Then  $T$  is distributed as non-central  $t$  with  $\text{df} = n - 1$  degrees of freedom and non-centrality parameter  $\text{ncp} = (\mu - \mu_0)\sqrt{n}/\sigma$ .

### Value

`dt` gives the density, `pt` gives the distribution function, `qt` gives the quantile function, and `rt` generates random deviates.

Invalid arguments will result in return value `NaN`, with a warning.

### Note

Setting `ncp = 0` is *not* equivalent to omitting `ncp`. **R** uses the non-centrality functionality whenever `ncp` is specified which provides continuous behavior at `ncp = 0`.

The code for non-zero `ncp` is principally intended to be used for moderate values of `ncp`: it will not be highly accurate, especially in the tails, for large values.

### Source

The central `dt` is computed via an accurate formula provided by Catherine Loader (see the reference in [dbinom](#)).

For the non-central case of `dt`, C code contributed by Claus Ekstrøm based on the relationship (for  $x \neq 0$ ) to the cumulative distribution.

For the central case of `pt`, a normal approximation in the tails, otherwise via [pbeta](#).

For the non-central case of `pt` based on a C translation of

Lenth, R. V. (1989). *Algorithm AS 243* — Cumulative distribution function of the non-central  $t$  distribution, *Applied Statistics* **38**, 185–189.

This computes the lower tail only, so the upper tail suffers from cancellation and a warning will be given when this is likely to be significant.

For central `qt`, a C translation of

Hill, G. W. (1970) Algorithm 396: Student's  $t$ -quantiles. *Communications of the ACM*, **13(10)**, 619–620.

altered to take account of

Hill, G. W. (1981) Remark on Algorithm 396, *ACM Transactions on Mathematical Software*, **7**, 250–1.

The non-central case is done by inversion.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole. (Except non-central versions.)

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 2, chapters 28 and 31. Wiley, New York.

### See Also

[df](#) for the F distribution.

**Examples**

```
require(graphics)

1 - pt(1:5, df = 1)
qt(.975, df = c(1:10,20,50,100,1000))

tt <- seq(0,10, len=21)
ncp <- seq(0,6, len=31)
ptn <- outer(tt,ncp, function(t,d) pt(t, df = 3, ncp=d))
t.tit <- "Non-central t - Probabilities"
image(tt,ncp,ptn, zlim=c(0,1), main = t.tit)
persp(tt,ncp,ptn, zlim=0:1, r=2, phi=20, theta=200, main=t.tit,
      xlab = "t", ylab = "non-centrality parameter",
      zlab = "Pr(T <= t)")

plot(function(x) dt(x, df = 3, ncp = 2), -3, 11, ylim = c(0, 0.32),
      main="Non-central t - Density", yaxs="i")
```

termplot

*Plot Regression Terms***Description**

Plots regression terms against their predictors, optionally with standard errors and partial residuals added.

**Usage**

```
termplot(model, data = NULL, envir = environment(formula(model)),
  partial.resid = FALSE, rug = FALSE,
  terms = NULL, se = FALSE,
  xlabs = NULL, ylabs = NULL, main = NULL,
  col.term = 2, lwd.term = 1.5,
  col.se = "orange", lty.se = 2, lwd.se = 1,
  col.res = "gray", cex = 1, pch = par("pch"),
  col.smth = "darkred", lty.smth = 2, span.smth = 2/3,
  ask = dev.interactive() && nb.fig < n.tms,
  use.factor.levels = TRUE, smooth = NULL, ylim = "common",
  ...)
```

**Arguments**

model	fitted model object
data	data frame in which variables in model can be found
envir	environment in which variables in model can be found
partial.resid	logical; should partial residuals be plotted?
rug	add <a href="#">rugplots</a> (jittered 1-d histograms) to the axes?
terms	which terms to plot (default NULL means all terms)
se	plot pointwise standard errors?

xlabs	vector of labels for the x axes
ylabs	vector of labels for the y axes
main	logical, or vector of main titles; if TRUE, the model's call is taken as main title, NULL or FALSE mean no titles.
col.term, lwd.term	color and line width for the 'term curve', see <a href="#">lines</a> .
col.se, lty.se, lwd.se	color, line type and line width for the 'twice-standard-error curve' when se = TRUE.
col.res, cex, pch	color, plotting character expansion and type for partial residuals, when partial.resid = TRUE, see <a href="#">points</a> .
ask	logical; if TRUE, the user is asked before each plot, see <a href="#">par</a> (ask=.).
use.factor.levels	Should x-axis ticks use factor levels or numbers for factor terms?
smooth	NULL or a function with the same arguments as <a href="#">panel.smooth</a> to draw a smooth through the partial residuals for non-factor terms
lty.smth, col.smth, span.smth	Passed to smooth
ylim	an optional range for the y axis, or "common" when a range sufficient for all the plot will be computed, or "free" when limits are computed for each plot.
...	other graphical parameters.

## Details

The model object must have a predict method that accepts type=terms, eg [glm](#) in the **base** package, [coxph](#) and [survreg](#) in the **survival** package.

For the partial.resid=TRUE option it must have a [residuals](#) method that accepts type="partial", which [lm](#) and [glm](#) do.

The data argument should rarely be needed, but in some cases `termplot` may be unable to reconstruct the original data frame. Using `na.action=na.exclude` makes these problems less likely.

Nothing sensible happens for interaction terms.

## See Also

For (generalized) linear models, [plot.lm](#) and [predict.glm](#).

## Examples

```
require(graphics)

had.splines <- "package:splines" %in% search()
if(!had.splines) rs <- require(splines)
x <- 1:100
z <- factor(rep(LETTERS[1:4],25))
y <- rnorm(100, sin(x/10)+as.numeric(z))
model <- glm(y ~ ns(x,6) + z)

par(mfrow=c(2,2)) ## 2 x 2 plots for same model :
termplot(model, main = paste("termplot( ", deparse(model$call), " ...")))
```

```
termpart(model, rug=TRUE)
termpart(model, partial.resid=TRUE, se = TRUE, main = TRUE)
termpart(model, partial.resid=TRUE, smooth=panel.smooth, span.smth=1/4)
if(!had.splines && rs) detach("package:splines")
```

---

terms

*Model Terms*

---

## Description

The function `terms` is a generic function which can be used to extract *terms* objects from various kinds of R data objects.

## Usage

```
terms(x, ...)
```

## Arguments

`x` object used to select a method to dispatch.  
`...` further arguments passed to or from other methods.

## Details

There are methods for classes "aovlist", and "terms" "formula" (see [terms.formula](#)): the default method just extracts the `terms` component of the object (if any).

There are [print](#) and [labels](#) methods for class "terms": the latter prints the term labels (see [terms.object](#)).

## Value

An object of class `c("terms", "formula")` which contains the *terms* representation of a symbolic model. See [terms.object](#) for its structure.

## References

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models*. Chapter 2 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

## See Also

[terms.object](#), [terms.formula](#), [lm](#), [glm](#), [formula](#).

---

terms.formula	<i>Construct a terms Object from a Formula</i>
---------------	--

---

### Description

This function takes a formula and some optional arguments and constructs a terms object. The terms object can then be used to construct a `model.matrix`.

### Usage

```
## S3 method for class 'formula':
terms(x, specials = NULL, abb = NULL, data = NULL, neg.out = TRUE,
      keep.order = FALSE, simplify = FALSE, ...,
      allowDotAsName = FALSE)
```

### Arguments

x	a formula.
specials	which functions in the formula should be marked as special in the <code>terms</code> object.
abb	Not implemented in R.
data	a data frame from which the meaning of the special symbol <code>.</code> can be inferred. It is unused if there is no <code>.</code> in the formula.
neg.out	Not implemented in R.
keep.order	a logical value indicating whether the terms should keep their positions. If <code>FALSE</code> the terms are reordered so that main effects come first, followed by the interactions, all second-order, all third-order and so on. Effects of a given order are kept in the order specified.
simplify	should the formula be expanded and simplified, the pre-1.7.0 behaviour?
...	further arguments passed to or from other methods.
allowDotAsName	normally <code>.</code> in a formula refers to the remaining variables contained in <code>data</code> . Exceptionally, <code>.</code> can be treated as a name for non-standard uses of formulae.

### Details

Not all of the options work in the same way that they do in S and not all are implemented.

### Value

A `terms.object` object is returned. The object itself is the re-ordered (unless `keep.order = TRUE`) formula. In all cases variables within an interaction term in the formula are re-ordered by the ordering of the `"variables"` attribute, which is the order in which the variables occur in the formula.

### See Also

[terms](#), [terms.object](#)



---

<code>terms.object</code>	<i>Description of Terms Objects</i>
---------------------------	-------------------------------------

---

### Description

An object of class `terms` holds information about a model. Usually the model was specified in terms of a `formula` and that formula was used to determine the terms object.

### Value

The object itself is simply the formula supplied to the call of `terms.formula`. The object has a number of attributes and they are used to construct the model frame:

<code>factors</code>	A matrix of variables by terms showing which variables appear in which terms. The entries are 0 if the variable does not occur in the term, 1 if it does occur and should be coded by contrasts, and 2 if it occurs and should be coded via dummy variables for all levels (as when an intercept or lower-order term is missing). If there are no terms other than an intercept and offsets, this is <code>numeric(0)</code> .
<code>term.labels</code>	A character vector containing the labels for each of the terms in the model, except for offsets. Non-syntactic names will be quoted by backticks. Note that these are after possible re-ordering (unless argument <code>keep.order</code> was false).
<code>variables</code>	A call to <code>list</code> of the variables in the model.
<code>intercept</code>	Either 0, indicating no intercept is to be fit, or 1 indicating that an intercept is to be fit.
<code>order</code>	A vector of the same length as <code>term.labels</code> indicating the order of interaction for each term.
<code>response</code>	The index of the variable (in <code>variables</code> ) of the response (the left hand side of the formula). Zero, if there is no response.
<code>offset</code>	If the model contains <code>offset</code> terms there is an <code>offset</code> attribute indicating which variable(s) are offsets
<code>specials</code>	If a <code>specials</code> argument was given to <code>terms.formula</code> there is a <code>specials</code> attribute, a list of vectors (one for each specified special function) giving numeric indices of the arguments of the list returned as the <code>variables</code> attribute which contain these special functions.
<code>dataClasses</code>	optional. A named character vector giving the classes (as given by <code>.MFclass</code> ) of the variables used in a fit.

The object has class `c("terms", "formula")`.

### Note

These objects are different from those found in S. In particular there is no `formula` attribute, instead the object is itself a formula. Thus, the mode of a terms object is different as well.

Examples of the `specials` argument can be seen in the `avov` and `coxph` functions, the latter from package **survival**.

### See Also

`terms`, `formula`.

**Examples**

```
## use of specials (as used for gam() in packages mgcv and gam)
(tf <- terms(y ~ x + x:z + s(x), specials = "s"))
## Note that the "factors" attribute has variables as row names
## and term labels as column names, both as character vectors.
attr(tf, "specials")      # index 's' variable(s)
rownames(attr(tf, "factors"))[attr(tf, "specials")]$s

## we can keep the order by
terms(y ~ x + x:z + s(x), specials = "s", keep.order = TRUE)
```

time

*Sampling Times of Time Series***Description**

`time` creates the vector of times at which a time series was sampled.

`cycle` gives the positions in the cycle of each observation.

`frequency` returns the number of samples per unit time and `deltat` the time interval between observations (see [ts](#)).

**Usage**

```
time(x, ...)
## Default S3 method:
time(x, offset=0, ...)

cycle(x, ...)
frequency(x, ...)
deltat(x, ...)
```

**Arguments**

<code>x</code>	a univariate or multivariate time-series, or a vector or matrix.
<code>offset</code>	can be used to indicate when sampling took place in the time unit. 0 (the default) indicates the start of the unit, 0.5 the middle and 1 the end of the interval.
<code>...</code>	extra arguments for future methods.

**Details**

These are all generic functions, which will use the `ts` attribute of `x` if it exists. `time` and `cycle` have methods for class `ts` that coerce the result to that class.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[ts](#), [start](#), [tsp](#), [window](#).

[date](#) for clock time, [system.time](#) for CPU usage.

**Examples**

```
require(graphics)

cycle(presidents)
# a simple series plot
plot(as.vector(time(presidents)), as.vector(presidents), type="l")
```

---

toeplitz

*Form Symmetric Toeplitz Matrix*

---

**Description**

Forms a symmetric Toeplitz matrix given its first row.

**Usage**

```
toeplitz(x)
```

**Arguments**

`x` the first row to form the Toeplitz matrix.

**Value**

The Toeplitz matrix.

**Author(s)**

A. Trapletti

**Examples**

```
x <- 1:5
toeplitz(x)
```

---

 ts *Time-Series Objects*


---

**Description**

The function `ts` is used to create time-series objects.

`as.ts` and `is.ts` coerce an object to a time-series and test whether an object is a time series.

**Usage**

```
ts(data = NA, start = 1, end = numeric(0), frequency = 1,
   deltat = 1, ts.eps = getOption("ts.eps"), class = , names = )
as.ts(x, ...)
is.ts(x)
```

**Arguments**

<code>data</code>	a numeric vector or matrix of the observed time-series values. A data frame will be coerced to a numeric matrix via <code>data.matrix</code> .
<code>start</code>	the time of the first observation. Either a single number or a vector of two integers, which specify a natural time unit and a (1-based) number of samples into the time unit. See the examples for the use of the second form.
<code>end</code>	the time of the last observation, specified in the same way as <code>start</code> .
<code>frequency</code>	the number of observations per unit of time.
<code>deltat</code>	the fraction of the sampling period between successive observations; e.g., 1/12 for monthly data. Only one of <code>frequency</code> or <code>deltat</code> should be provided.
<code>ts.eps</code>	time series comparison tolerance. Frequencies are considered equal if their absolute difference is less than <code>ts.eps</code> .
<code>class</code>	class to be given to the result, or <code>NULL</code> or <code>"none"</code> . The default is <code>"ts"</code> for a single series, <code>c("mts", "ts")</code> for multiple series.
<code>names</code>	a character vector of names for the series in a multiple series: defaults to the <code>colnames</code> of <code>data</code> , or <code>Series 1, Series 2, ...</code> .
<code>x</code>	an arbitrary R object.
<code>...</code>	arguments passed to methods (unused for the default method).

**Details**

The function `ts` is used to create time-series objects. These are vector or matrices with class of `"ts"` (and additional attributes) which represent data which has been sampled at equispaced points in time. In the matrix case, each column of the matrix `data` is assumed to contain a single (univariate) time series. Time series must have at least one observation, and although they need not be numeric there is very limited support for non-numeric series.

Class `"ts"` has a number of methods. In particular arithmetic will attempt to align time axes, and subsetting to extract subsets of series can be used (e.g., `EuStockMarkets[, "DAX"]`). However, subsetting the first (or only) dimension will return a matrix or vector, as will matrix subsetting. Subassignment can be used to replace values but not to extend a series (see [window](#)). There is a method for `t` that transposes the series as a matrix (a one-column matrix if a vector) and hence returns a result that does not inherit from class `"ts"`.

The value of argument `frequency` is used when the series is sampled an integral number of times in each unit time interval. For example, one could use a value of 7 for `frequency` when the data are sampled daily, and the natural time period is a week, or 12 when the data are sampled monthly and the natural time period is a year. Values of 4 and 12 are assumed in (e.g.) `print` methods to imply a quarterly and monthly series respectively.

`as.ts` is generic. Its default method will use the `tsp` attribute of the object if it has one to set the start and end times and frequency.

`is.ts` tests if an object is a time series. It is generic: you can write methods to handle specific classes of objects, see [InternalMethods](#).

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

`tsp`, `frequency`, `start`, `end`, `time`, `window`; `print.ts`, the print method for time series objects; `plot.ts`, the plot method for time series objects.

## Examples

```
require(graphics)

ts(1:10, frequency = 4, start = c(1959, 2)) # 2nd Quarter of 1959
print( ts(1:10, frequency = 7, start = c(12, 2)), calendar = TRUE)
# print.ts(.)
## Using July 1954 as start date:
gnp <- ts(cumsum(1 + round(rnorm(100), 2)),
          start = c(1954, 7), frequency = 12)
plot(gnp) # using 'plot.ts' for time-series plot

## Multivariate
z <- ts(matrix(rnorm(300), 100, 3), start=c(1961, 1), frequency=12)
class(z)
plot(z)
plot(z, plot.type="single", lty=1:3)

## A phase plot:
plot(nhtemp, c(nhtemp[-1], NA), cex = .8, col="blue",
      main = "Lag plot of New Haven temperatures")
## a clearer way to do this would be
## Not run:
plot(nhtemp, lag(nhtemp, 1), cex = .8, col="blue",
      main = "Lag plot of New Haven temperatures")

## End(Not run)
```

**Description**

Methods for objects of class "ts", typically the result of `ts`.

**Usage**

```
## S3 method for class 'ts':
diff(x, lag = 1, differences = 1, ...)

## S3 method for class 'ts':
na.omit(object, ...)
```

**Arguments**

`x` an object of class "ts" containing the values to be differenced.  
`lag` an integer indicating which lag to use.  
`differences` an integer indicating the order of the difference.  
`object` a univariate or multivariate time series.  
`...` further arguments to be passed to or from methods.

**Details**

The `na.omit` method omits initial and final segments with missing values in one or more of the series. 'Internal' missing values will lead to failure.

**Value**

For the `na.omit` method, a time series without missing values. The class of `object` will be preserved.

**See Also**

`diff`; `na.omit`, `na.fail`, `na.contiguous`.

ts.plot

*Plot Multiple Time Series***Description**

Plot several time series on a common plot. Unlike `plot.ts` the series can have a different time bases, but they should have the same frequency.

**Usage**

```
ts.plot(..., gpars = list())
```

**Arguments**

`...` one or more univariate or multivariate time series.  
`gpars` list of named graphics parameters to be passed to the plotting functions. Those commonly used can be supplied directly in `...`

**Value**

None.

**Note**

Although this can be used for a single time series, `plot` is easier to use and is preferred.

**See Also**

[plot.ts](#)

**Examples**

```
require(graphics)

ts.plot(ldeaths, mdeaths, fdeaths,
        gpars=list(xlab="year", ylab="deaths", lty=c(1:3)))
```

---

ts.union

*Bind Two or More Time Series*

---

**Description**

Bind time series which have a common frequency. `ts.union` pads with NAs to the total time coverage, `ts.intersect` restricts to the time covered by all the series.

**Usage**

```
ts.intersect(..., dframe = FALSE)
ts.union(..., dframe = FALSE)
```

**Arguments**

`...` two or more univariate or multivariate time series, or objects which can coerced to time series.

`dframe` logical; if TRUE return the result as a data frame.

**Details**

As a special case, `...` can contain vectors or matrices of the same length as the combined time series of the time series present, as well as those of a single row.

**Value**

A time series object if `dframe` is FALSE, otherwise a data frame.

**See Also**

[cbind](#).

## Examples

```
ts.union(mdeaths, fdeaths)
cbind(mdeaths, fdeaths) # same as the previous line
ts.intersect(window(mdeaths, 1976), window(fdeaths, 1974, 1978))

sales1 <- ts.union(BJsales, lead = BJsales.lead)
ts.intersect(sales1, lead3 = lag(BJsales.lead, -3))
```

---

tsdiag

*Diagnostic Plots for Time-Series Fits*

---

## Description

A generic function to plot time-series diagnostics.

## Usage

```
tsdiag(object, gof.lag, ...)
```

## Arguments

object	a fitted time-series model
gof.lag	the maximum number of lags for a Portmanteau goodness-of-fit test
...	further arguments to be passed to particular methods

## Details

This is a generic function. It will generally plot the residuals, often standardized, the autocorrelation function of the residuals, and the p-values of a Portmanteau test for all lags up to `gof.lag`.

The methods for `arima` and `StructTS` objects plots residuals scaled by the estimate of their (individual) variance, and use the Ljung–Box version of the portmanteau test.

## Value

None. Diagnostics are plotted.

## See Also

`arima`, `StructTS`, `Box.test`

## Examples

```
## Not run: require(graphics)

fit <- arima(lh, c(1,0,0))
tsdiag(fit)

## see also examples(arima)

(fit <- StructTS(log10(JohnsonJohnson), type="BSM"))
tsdiag(fit)

## End(Not run)
```



---

tsp	<i>Tsp Attribute of Time-Series-like Objects</i>
-----	--

---

### Description

tsp returns the tsp attribute (or NULL). It is included for compatibility with S version 2. tsp<- sets the tsp attribute. hasTsp ensures x has a tsp attribute, by adding one if needed.

### Usage

```
tsp(x)
tsp(x) <- value
hasTsp(x)
```

### Arguments

x	a vector or matrix or univariate or multivariate time-series.
value	a numeric vector of length 3 or NULL.

### Details

The tsp attribute was previously described here as `c(start(x), end(x), frequency(x))`, but this is incorrect. It gives the start time *in time units*, the end time and the frequency.

Assignments are checked for consistency.

Assigning NULL which removes the tsp attribute *and* any "ts" (or "mts") class of x.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[ts](#), [time](#), [start](#).

---

tsSmooth	<i>Use Fixed-Interval Smoothing on Time Series</i>
----------	--

---

### Description

Performs fixed-interval smoothing on a univariate time series via a state-space model. Fixed-interval smoothing gives the best estimate of the state at each time point based on the whole observed series.

### Usage

```
tsSmooth(object, ...)
```

**Arguments**

object a time-series fit. Currently only class "[StructTS](#)" is supported  
 . . . possible arguments for future methods.

**Value**

A time series, with as many dimensions as the state space and results at each time point of the original series. (For seasonal models, only the current seasonal component is returned.)

**Author(s)**

B. D. Ripley

**References**

Durbin, J. and Koopman, S. J. (2001) *Time Series Analysis by State Space Methods*. Oxford University Press.

**See Also**

[KalmanSmooth](#), [StructTS](#).

For examples consult [AirPassengers](#), [JohnsonJohnson](#) and [Nile](#).

Tukey

*The Studentized Range Distribution*

**Description**

Functions of the distribution of the studentized range,  $R/s$ , where  $R$  is the range of a standard normal sample and  $df \times s^2$  is independently distributed as chi-squared with  $df$  degrees of freedom, see [pchisq](#).

**Usage**

```
ptukey(q, nmeans, df, nranges = 1, lower.tail = TRUE, log.p = FALSE)
qtukey(p, nmeans, df, nranges = 1, lower.tail = TRUE, log.p = FALSE)
```

**Arguments**

q vector of quantiles.  
 p vector of probabilities.  
 nmeans sample size for range (same for each group).  
 df degrees of freedom for  $s$  (see below).  
 nranges number of *groups* whose **maximum** range is considered.  
 log.p logical; if TRUE, probabilities  $p$  are given as  $\log(p)$ .  
 lower.tail logical; if TRUE (default), probabilities are  $P[X \leq x]$ , otherwise,  $P[X > x]$ .

**Details**

If  $n_g = \text{nranges}$  is greater than one,  $R$  is the *maximum* of  $n_g$  groups of  $n_{\text{means}}$  observations each.

**Value**

`ptukey` gives the distribution function and `qtukey` its inverse, the quantile function.

**Note**

A Legendre 16-point formula is used for the integral of `ptukey`. The computations are relatively expensive, especially for `qtukey` which uses a simple secant method for finding the inverse of `ptukey`. `qtukey` will be accurate to the 4th decimal place.

**References**

Copenhaver, Margaret Diponzio and Holland, Burt S. (1988) Multiple comparisons of simple effects in the two-way analysis of variance with fixed effects. *Journal of Statistical Computation and Simulation*, **30**, 1–15.

**See Also**

[pnorm](#) and [qnorm](#) for the corresponding functions for the normal distribution.

**Examples**

```
if(interactive())
  curve(ptukey(x, nm=6, df=5), from=-1, to=8, n=101)
(ptt <- ptukey(0:10, 2, df= 5))
(qtt <- qtukey(.95, 2, df= 2:11))
## The precision may be not much more than about 8 digits:
summary(abs(.95 - ptukey(qtt,2, df = 2:11)))
```

---

 TukeyHSD

---

*Compute Tukey Honest Significant Differences*


---

**Description**

Create a set of confidence intervals on the differences between the means of the levels of a factor with the specified family-wise probability of coverage. The intervals are based on the Studentized range statistic, Tukey's 'Honest Significant Difference' method. There is a `plot` method.

**Usage**

```
TukeyHSD(x, which, ordered = FALSE, conf.level = 0.95, ...)
```

**Arguments**

<code>x</code>	A fitted model object, usually an <code>av</code> fit.
<code>which</code>	A character vector listing terms in the fitted model for which the intervals should be calculated. Defaults to all the terms.
<code>ordered</code>	A logical value indicating if the levels of the factor should be ordered according to increasing average in the sample before taking differences. If <code>ordered</code> is true then the calculated differences in the means will all be positive. The significant differences will be those for which the <code>lwr</code> end point is positive.
<code>conf.level</code>	A numeric value between zero and one giving the family-wise confidence level to use.
<code>...</code>	Optional additional arguments. None are used at present.

**Details**

When comparing the means for the levels of a factor in an analysis of variance, a simple comparison using t-tests will inflate the probability of declaring a significant difference when it is not in fact present. This because the intervals are calculated with a given coverage probability for each interval but the interpretation of the coverage is usually with respect to the entire family of intervals.

John Tukey introduced intervals based on the range of the sample means rather than the individual differences. The intervals returned by this function are based on this Studentized range statistics.

Technically the intervals constructed in this way would only apply to balanced designs where there are the same number of observations made at each level of the factor. This function incorporates an adjustment for sample size that produces sensible intervals for mildly unbalanced designs.

If `which` specifies non-factor terms these will be dropped with a warning: if no terms are left this is an error.

**Value**

A list with one component for each term requested in `which`. Each component is a matrix with columns `diff` giving the difference in the observed means, `lwr` giving the lower end point of the interval, `upr` giving the upper end point and `p.adj` giving the p-value after adjustment for the multiple comparisons.

**Author(s)**

Douglas Bates

**References**

- Miller, R. G. (1981) *Simultaneous Statistical Inference*. Springer.
- Yandell, B. S. (1997) *Practical Data Analysis for Designed Experiments*. Chapman & Hall.

**See Also**

[av](#), [qtukey](#), [model.tables](#), [glht](#) in package **multcomp**.

**Examples**

```
require(graphics)

summary(fm1 <- aov(breaks ~ wool + tension, data = warpbreaks))
TukeyHSD(fm1, "tension", ordered = TRUE)
plot(TukeyHSD(fm1, "tension"))
```

Uniform

*The Uniform Distribution***Description**

These functions provide information about the uniform distribution on the interval from `min` to `max`. `dunif` gives the density, `punif` gives the distribution function `qunif` gives the quantile function and `runif` generates random deviates.

**Usage**

```
dunif(x, min=0, max=1, log = FALSE)
punif(q, min=0, max=1, lower.tail = TRUE, log.p = FALSE)
qunif(p, min=0, max=1, lower.tail = TRUE, log.p = FALSE)
runif(n, min=0, max=1)
```

**Arguments**

<code>x, q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>n</code>	number of observations. If <code>length(n) &gt; 1</code> , the length is taken to be the number required.
<code>min, max</code>	lower and upper limits of the distribution. Must be finite.
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as <code>log(p)</code> .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .

**Details**

If `min` or `max` are not specified they assume the default values of 0 and 1 respectively.

The uniform distribution has density

$$f(x) = \frac{1}{\max - \min}$$

for  $\min \leq x \leq \max$ .

For the case of  $u := \min == \max$ , the limit case of  $X \equiv u$  is assumed, although there is no density in that case and `dunif` will return `NaN` (the error condition).

`runif` will not generate either of the extreme values unless `max = min` or `max-min` is small compared to `min`, and in particular not for the default arguments.

**Note**

The characteristics of output from pseudo-random number generators (such as precision and periodicity) vary widely. See [.Random.seed](#) for more information on R's random number generation algorithms.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

[.Random.seed](#) about random number generation, [rnorm](#), etc for other distributions.

**Examples**

```
u <- runif(20)

## The following relations always hold :
punif(u) == u
dunif(u) == 1

var(runif(10000))#- ~ = 1/12 = .08333
```

---

uniroot

*One Dimensional Root (Zero) Finding*


---

**Description**

The function `uniroot` searches the interval from `lower` to `upper` for a root (i.e., zero) of the function `f` with respect to its first argument.

**Usage**

```
uniroot(f, interval, ...,
        lower = min(interval), upper = max(interval),
        f.lower = f(lower, ...), f.upper = f(upper, ...),
        tol = .Machine$double.eps^0.25, maxiter = 1000)
```

**Arguments**

<code>f</code>	the function for which the root is sought.
<code>interval</code>	a vector containing the end-points of the interval to be searched for the root.
<code>...</code>	additional named or unnamed arguments to be passed to <code>f</code>
<code>lower, upper</code>	the lower and upper end points of the interval to be searched.
<code>f.lower, f.upper</code>	the same as <code>f(upper)</code> and <code>f(lower)</code> , respectively. Passing these values from the caller where they are often known is more economical as soon as <code>f()</code> contains non-trivial computations.
<code>tol</code>	the desired accuracy (convergence tolerance).
<code>maxiter</code>	the maximum number of iterations.

## Details

Note that arguments after `...` must be matched exactly.

Either `interval` or both `lower` and `upper` must be specified: the upper endpoint must be strictly larger than the lower endpoint. The function values at the endpoints must be of opposite signs (or zero).

The function uses Fortran subroutine "zeroin" (from Netlib) based on algorithms given in the reference below. They assume a continuous function (which then is known to have at least one root in the interval).

Convergence is declared either if  $f(x) == 0$  or the change in  $x$  for one step of the algorithm is less than `tol` (plus an allowance for representation error in  $x$ ).

If the algorithm does not converge in `maxiter` steps, a warning is printed and the current approximation is returned.

`f` will be called as `f(x, ...)` for a numeric value of  $x$ .

## Value

A list with four components: `root` and `f.root` give the location of the root and the value of the function evaluated at that point. `iter` and `estim.prec` give the number of iterations used and an approximate estimated precision for `root`. (If the root occurs at one of the endpoints, the estimated precision is NA.)

## Source

Based on 'zeroin.c' in <http://www.netlib.org/c/brent.shar>.

## References

Brent, R. (1973) *Algorithms for Minimization without Derivatives*. Englewood Cliffs, NJ: Prentice-Hall.

## See Also

[polyroot](#) for all complex roots of a polynomial; [optimize](#), [nlm](#).

## Examples

```
require(utils) # for str

f <- function(x,a) x - a
str(xmin <- uniroot(f, c(0, 1), tol = 0.0001, a = 1/3))
str(uniroot(function(x) x*(x^2-1) + .5, lower = -2, upper = 2,
             tol = 0.0001), dig = 10)
str(uniroot(function(x) x*(x^2-1) + .5, lower = -2, upper = 2,
             tol = 1e-10 ), dig = 10)

## Find the smallest value x for which exp(x) > 0 (numerically):
r <- uniroot(function(x) 1e80*exp(x)-1e-300, c(-1000,0), tol = 1e-15)
str(r, digits= 15) ##> around -745, depending on the platform.

exp(r$root)      # = 0, but not for r$root * 0.999...
minexp <- r$root * (1 - 10*.Machine$double.eps)
exp(minexp)     # typically denormalized
```

---

update	<i>Update and Re-fit a Model Call</i>
--------	---------------------------------------

---

**Description**

`update` will update and (by default) re-fit a model. It does this by extracting the call stored in the object, updating the call and (by default) evaluating that call. Sometimes it is useful to call `update` with only one argument, for example if the data frame has been corrected.

**Usage**

```
update(object, ...)

## Default S3 method:
update(object, formula., ..., evaluate = TRUE)
```

**Arguments**

<code>object</code>	An existing fit from a model function such as <code>lm</code> , <code>glm</code> and many others.
<code>formula.</code>	Changes to the formula – see <code>update.formula</code> for details.
<code>...</code>	Additional arguments to the call, or arguments with changed values. Use <code>name=NULL</code> to remove the argument <code>name</code> .
<code>evaluate</code>	If true evaluate the new call else return the call.

**Value**

If `evaluate = TRUE` the fitted object, otherwise the updated call.

**References**

Chambers, J. M. (1992) *Linear models*. Chapter 4 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

[update.formula](#)

**Examples**

```
oldcon <- options(contrasts = c("contr.treatment", "contr.poly"))
## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.
ctl <- c(4.17, 5.58, 5.18, 6.11, 4.50, 4.61, 5.17, 4.53, 5.33, 5.14)
trt <- c(4.81, 4.17, 4.41, 3.59, 5.87, 3.83, 6.03, 4.89, 4.32, 4.69)
group <- gl(2, 10, 20, labels = c("Ctl", "Trt"))
weight <- c(ctl, trt)
lm.D9 <- lm(weight ~ group)
lm.D9
summary(lm.D9 <- update(lm.D9, . ~ . - 1))
options(contrasts = c("contr.helmert", "contr.poly"))
update(lm.D9)
options(oldcon)
```



---

update.formula      *Model Updating*

---

### Description

update.formula is used to update model formulae. This typically involves adding or dropping terms, but updates can be more general.

### Usage

```
## S3 method for class 'formula':  
update(old, new, ...)
```

### Arguments

old	a model formula to be updated.
new	a formula giving a template which specifies how to update.
...	further arguments passed to or from other methods.

### Details

Either or both of `old` and `new` can be objects such as length-one character vectors which can be coerced to a formula via [as.formula](#).

The function works by first identifying the *left-hand side* and *right-hand side* of the `old` formula. It then examines the `new` formula and substitutes the *lhs* of the `old` formula for any occurrence of `'.'` on the left of `new`, and substitutes the *rhs* of the `old` formula for any occurrence of `'.'` on the right of `new`. The result is then simplified via [terms.formula](#)(`simplify = TRUE`).

### Value

The updated formula is returned. The environment of the result is that of `old`.

### See Also

[terms](#), [model.matrix](#).

### Examples

```
update(y ~ x,      ~ . + x2) #> y ~ x + x2  
update(y ~ x, log(.) ~ . ) #> log(y) ~ x
```

var.test

*F Test to Compare Two Variances***Description**

Performs an F test to compare the variances of two samples from normal populations.

**Usage**

```
var.test(x, ...)

## Default S3 method:
var.test(x, y, ratio = 1,
         alternative = c("two.sided", "less", "greater"),
         conf.level = 0.95, ...)

## S3 method for class 'formula':
var.test(formula, data, subset, na.action, ...)
```

**Arguments**

<code>x, y</code>	numeric vectors of data values, or fitted linear model objects (inheriting from class "lm").
<code>ratio</code>	the hypothesized ratio of the population variances of <code>x</code> and <code>y</code> .
<code>alternative</code>	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
<code>conf.level</code>	confidence level for the returned confidence interval.
<code>formula</code>	a formula of the form <code>lhs ~ rhs</code> where <code>lhs</code> is a numeric variable giving the data values and <code>rhs</code> a factor with two levels giving the corresponding groups.
<code>data</code>	an optional matrix or data frame (or similar: see <a href="#">model.frame</a> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>subset</code>	an optional vector specifying a subset of observations to be used.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. Defaults to <code>getOption("na.action")</code> .
<code>...</code>	further arguments to be passed to or from methods.

**Details**

The null hypothesis is that the ratio of the variances of the populations from which `x` and `y` were drawn, or in the data to which the linear models `x` and `y` were fitted, is equal to `ratio`.

**Value**

A list with class "htest" containing the following components:

<code>statistic</code>	the value of the F test statistic.
<code>parameter</code>	the degrees of the freedom of the F distribution of the test statistic.

<code>p.value</code>	the p-value of the test.
<code>conf.int</code>	a confidence interval for the ratio of the population variances.
<code>estimate</code>	the ratio of the sample variances of $x$ and $y$ .
<code>null.value</code>	the ratio of population variances under the null.
<code>alternative</code>	a character string describing the alternative hypothesis.
<code>method</code>	the character string "F test to compare two variances".
<code>data.name</code>	a character string giving the names of the data.

### See Also

[bartlett.test](#) for testing homogeneity of variances in more than two samples from normal distributions; [ansari.test](#) and [mood.test](#) for two rank based (nonparametric) two-sample tests for difference in scale.

### Examples

```
x <- rnorm(50, mean = 0, sd = 2)
y <- rnorm(30, mean = 1, sd = 1)
var.test(x, y) # Do x and y have the same variance?
var.test(lm(x ~ 1), lm(y ~ 1)) # The same.
```

---

varimax

*Rotation Methods for Factor Analysis*

---

### Description

These functions ‘rotate’ loading matrices in factor analysis.

### Usage

```
varimax(x, normalize = TRUE, eps = 1e-5)
promax(x, m = 4)
```

### Arguments

<code>x</code>	A loadings matrix, with $p$ rows and $k < p$ columns
<code>m</code>	The power used the target for <code>promax</code> . Values of 2 to 4 are recommended.
<code>normalize</code>	logical. Should Kaiser normalization be performed? If so the rows of $x$ are re-scaled to unit length before rotation, and scaled back afterwards.
<code>eps</code>	The tolerance for stopping: the relative change in the sum of singular values.

### Details

These seek a ‘rotation’ of the factors  $x \%*\% T$  that aims to clarify the structure of the loadings matrix. The matrix  $T$  is a rotation (possibly with reflection) for `varimax`, but a general linear transformation for `promax`, with the variance of the factors being preserved.

**Value**

A list with components

loadings      The ‘rotated’ loadings matrix,  $x \%*\% \text{rotmat}$ , of class "loadings".  
 rotmat        The ‘rotation’ matrix.

**References**

Hendrickson, A. E. and White, P. O. (1964) Promax: a quick method for rotation to orthogonal oblique structure. *British Journal of Statistical Psychology*, **17**, 65–70.

Horst, P. (1965) *Factor Analysis of Data Matrices*. Holt, Rinehart and Winston. Chapter 10.

Kaiser, H. F. (1958) The varimax criterion for analytic rotation in factor analysis. *Psychometrika* **23**, 187–200.

Lawley, D. N. and Maxwell, A. E. (1971) *Factor Analysis as a Statistical Method*. Second edition. Butterworths.

**See Also**

[factanal](#), [Harman74.cor](#).

**Examples**

```
## varimax with normalize = TRUE is the default
fa <- factanal( ~., 2, data = swiss)
varimax(loadings(fa), normalize = FALSE)
promax(loadings(fa))
```

---

 vcov

*Calculate Variance-Covariance Matrix for a Fitted Model Object*

---

**Description**

Returns the variance-covariance matrix of the main parameters of a fitted model object.

**Usage**

```
vcov(object, ...)
```

**Arguments**

object        a fitted model object.  
 ...          additional arguments for method functions. For the [glm](#) method this can be used to pass a `dispersion` parameter.

**Details**

This is a generic function. Functions with names beginning in `vcov.` will be methods for this function. Classes with methods for this function include: `lm`, `mlm`, `glm`, `nls`, `negbin`, `polr`, `rmlm` (in package **MASS**), `multinom` (in package **nnet**) `gls`, `lme` (in package **nlme**, `coxph` and `survreg` (in package **survival**)).

**Value**

A matrix of the estimated covariances between the parameter estimates in the linear or non-linear predictor of the model.

---

 Weibull

*The Weibull Distribution*


---

**Description**

Density, distribution function, quantile function and random generation for the Weibull distribution with parameters `shape` and `scale`.

**Usage**

```
dweibull(x, shape, scale = 1, log = FALSE)
pweibull(q, shape, scale = 1, lower.tail = TRUE, log.p = FALSE)
qweibull(p, shape, scale = 1, lower.tail = TRUE, log.p = FALSE)
rweibull(n, shape, scale = 1)
```

**Arguments**

`x`, `q` vector of quantiles.  
`p` vector of probabilities.  
`n` number of observations. If `length(n) > 1`, the length is taken to be the number required.  
`shape`, `scale` shape and scale parameters, the latter defaulting to 1.  
`log`, `log.p` logical; if TRUE, probabilities `p` are given as `log(p)`.  
`lower.tail` logical; if TRUE (default), probabilities are  $P[X \leq x]$ , otherwise,  $P[X > x]$ .

**Details**

The Weibull distribution with shape parameter  $a$  and scale parameter  $\sigma$  has density given by

$$f(x) = (a/\sigma)(x/\sigma)^{a-1} \exp(-(x/\sigma)^a)$$

for  $x > 0$ . The cumulative distribution function is  $F(x) = 1 - \exp(-(x/\sigma)^a)$  on  $x > 0$ , the mean is  $E(X) = \sigma\Gamma(1 + 1/a)$ , and the  $Var(X) = \sigma^2(\Gamma(1 + 2/a) - (\Gamma(1 + 1/a))^2)$ .

**Value**

`dweibull` gives the density, `pweibull` gives the distribution function, `qweibull` gives the quantile function, and `rweibull` generates random deviates.

Invalid arguments will result in return value `NaN`, with a warning.

**Note**

The cumulative hazard  $H(t) = -\log(1 - F(t))$  is `-pweibull(t, a, b, lower = FALSE, log = TRUE)` which is just  $H(t) = (t/b)^a$ .

**Source**

[dpq]weibull are calculated directly from the definitions. rweibull uses inversion.

**References**

Johnson, N. L., Kotz, S. and Balakrishnan, N. (1995) *Continuous Univariate Distributions*, volume 1, chapter 21. Wiley, New York.

**See Also**

The [Exponential](#) is a special case of the Weibull distribution.

**Examples**

```
x <- c(0, rlnorm(50))
all.equal(dweibull(x, shape = 1), dexp(x))
all.equal(pweibull(x, shape = 1, scale = pi), pexp(x, rate = 1/pi))
## Cumulative hazard H():
all.equal(pweibull(x, 2.5, pi, lower.tail=FALSE, log.p=TRUE), -(x/pi)^2.5,
          tol = 1e-15)
all.equal(qweibull(x/11, shape = 1, scale = pi), qexp(x/11, rate = 1/pi))
```

---

weighted.mean	<i>Weighted Arithmetic Mean</i>
---------------	---------------------------------

---

**Description**

Compute a weighted mean.

**Usage**

```
weighted.mean(x, w, ...)

## Default S3 method:
weighted.mean(x, w, ..., na.rm = FALSE)
```

**Arguments**

x	an object containing the values whose weighted mean is to be computed.
w	a numerical vector of weights the same length as x giving the weights to use for elements of x.
...	arguments to be passed to or from methods.
na.rm	a logical value indicating whether NA values in x should be stripped before the computation proceeds.

**Details**

This is a generic function and methods can be defined for the first argument `x`: apart from the default methods there are methods for the date-time classes "POSIXct", "POSIXlt", "difftime" and "Date". The default method will work for any numeric-like object for which `[]`, multiplication and `sum` have suitable methods, including complex vectors.

If `w` is missing then all elements of `x` are given the same weight, otherwise the weights coerced to numeric by `as.numeric` and normalized to sum to one (if possible: if their sum is zero or infinite the value is likely to be NaN).

Missing values in `w` are not handled specially and so give a missing value as the result. However, as from R 2.11.0 zero weights *are* handled specially and the corresponding `x` values are omitted from the sum.

**Value**

For the default method, a length-one numeric vector.

**See Also**

`mean`

**Examples**

```
## GPA from Siegel 1994
wt <- c(5, 5, 4, 1)/15
x <- c(3.7, 3.3, 3.5, 2.8)
xm <- weighted.mean(x, wt)
```

---

`weighted.residuals` *Compute Weighted Residuals*

---

**Description**

Computed weighted residuals from a linear model fit.

**Usage**

```
weighted.residuals(obj, drop0 = TRUE)
```

**Arguments**

<code>obj</code>	R object, typically of class <code>lm</code> or <code>glm</code> .
<code>drop0</code>	logical. If TRUE, drop all cases with <code>weights == 0</code> .

**Details**

Weighted residuals are based on the deviance residuals, which for a `lm` fit are the raw residuals  $R_i$  multiplied by  $\sqrt{w_i}$ , where  $w_i$  are the `weights` as specified in `lm`'s call.

Dropping cases with weights zero is compatible with `influence` and related functions.

**Value**

Numeric vector of length  $n'$ , where  $n'$  is the number of non-0 weights (`drop0 = TRUE`) or the number of observations, otherwise.

**See Also**

[residuals](#), [lm.influence](#), etc.

**Examples**

```
utils::example("lm")
all.equal(weighted.residuals(lm.D9),
          residuals(lm.D9))
x <- 1:10
w <- 0:9
y <- rnorm(x)
weighted.residuals(lmxy <- lm(y ~ x, weights = w))
weighted.residuals(lmxy, drop0 = FALSE)
```

---

wilcox.test

*Wilcoxon Rank Sum and Signed Rank Tests*

---

**Description**

Performs one and two sample Wilcoxon tests on vectors of data; the latter is also known as ‘Mann-Whitney’ test.

**Usage**

```
wilcox.test(x, ...)

## Default S3 method:
wilcox.test(x, y = NULL,
            alternative = c("two.sided", "less", "greater"),
            mu = 0, paired = FALSE, exact = NULL, correct = TRUE,
            conf.int = FALSE, conf.level = 0.95, ...)

## S3 method for class 'formula':
wilcox.test(formula, data, subset, na.action, ...)
```

**Arguments**

<code>x</code>	numeric vector of data values. Non-finite (e.g. infinite or missing) values will be omitted.
<code>y</code>	an optional numeric vector of data values.
<code>alternative</code>	a character string specifying the alternative hypothesis, must be one of "two.sided" (default), "greater" or "less". You can specify just the initial letter.
<code>mu</code>	a number specifying an optional parameter used to form the null hypothesis. See ‘Details’.



<code>paired</code>	a logical indicating whether you want a paired test.
<code>exact</code>	a logical indicating whether an exact p-value should be computed.
<code>correct</code>	a logical indicating whether to apply continuity correction in the normal approximation for the p-value.
<code>conf.int</code>	a logical indicating whether a confidence interval should be computed.
<code>conf.level</code>	confidence level of the interval.
<code>formula</code>	a formula of the form <code>lhs ~ rhs</code> where <code>lhs</code> is a numeric variable giving the data values and <code>rhs</code> a factor with two levels giving the corresponding groups.
<code>data</code>	an optional matrix or data frame (or similar: see <code>model.frame</code> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>subset</code>	an optional vector specifying a subset of observations to be used.
<code>na.action</code>	a function which indicates what should happen when the data contain NAs. Defaults to <code>getOption("na.action")</code> .
<code>...</code>	further arguments to be passed to or from methods.

### Details

The formula interface is only applicable for the 2-sample tests.

If only `x` is given, or if both `x` and `y` are given and `paired` is `TRUE`, a Wilcoxon signed rank test of the null that the distribution of `x` (in the one sample case) or of `x - y` (in the paired two sample case) is symmetric about `mu` is performed.

Otherwise, if both `x` and `y` are given and `paired` is `FALSE`, a Wilcoxon rank sum test (equivalent to the Mann-Whitney test: see the Note) is carried out. In this case, the null hypothesis is that the distributions of `x` and `y` differ by a location shift of `mu` and the alternative is that they differ by some other location shift (and the one-sided alternative `"greater"` is that `x` is shifted to the right of `y`).

By default (if `exact` is not specified), an exact p-value is computed if the samples contain less than 50 finite values and there are no ties. Otherwise, a normal approximation is used.

Optionally (if argument `conf.int` is true), a nonparametric confidence interval and an estimator for the pseudomedian (one-sample case) or for the difference of the location parameters `x-y` is computed. (The pseudomedian of a distribution  $F$  is the median of the distribution of  $(u + v)/2$ , where  $u$  and  $v$  are independent, each with distribution  $F$ . If  $F$  is symmetric, then the pseudomedian and median coincide. See Hollander & Wolfe (1973), page 34.) If exact p-values are available, an exact confidence interval is obtained by the algorithm described in Bauer (1972), and the Hodges-Lehmann estimator is employed. Otherwise, the returned confidence interval and point estimate are based on normal approximations. These are continuity-corrected for the interval but *not* the estimate (as the correction depends on the `alternative`).

With small samples it may not be possible to achieve very high confidence interval coverages. If this happens a warning will be given and an interval with lower coverage will be substituted.

### Value

A list with class `"htest"` containing the following components:

<code>statistic</code>	the value of the test statistic with a name describing it.
<code>parameter</code>	the parameter(s) for the exact distribution of the test statistic.
<code>p.value</code>	the p-value for the test.
<code>null.value</code>	the location parameter <code>mu</code> .

alternative	a character string describing the alternative hypothesis.
method	the type of test applied.
data.name	a character string giving the names of the data.
conf.int	a confidence interval for the location parameter. (Only present if argument <code>conf.int = TRUE</code> .)
estimate	an estimate of the location parameter. (Only present if argument <code>conf.int = TRUE</code> .)

### Warning

This function can use large amounts of memory and stack (and even crash R if the stack limit is exceeded) if `exact = TRUE` and one sample is large (several thousands or more).

### Note

The literature is not unanimous about the definitions of the Wilcoxon rank sum and Mann-Whitney tests. The two most common definitions correspond to the sum of the ranks of the first sample with the minimum value subtracted or not: R subtracts and S-PLUS does not, giving a value which is larger by  $m(m+1)/2$  for a first sample of size  $m$ . (It seems Wilcoxon's original paper used the unadjusted sum of the ranks but subsequent tables subtracted the minimum.)

R's value can also be computed as the number of all pairs  $(x[i], y[j])$  for which  $y[j]$  is not greater than  $x[i]$ , the most common definition of the Mann-Whitney test.

### References

David F. Bauer (1972), Constructing confidence sets using rank statistics. *Journal of the American Statistical Association* **67**, 687–690.

Myles Hollander and Douglas A. Wolfe (1973), *Nonparametric Statistical Methods*. New York: John Wiley & Sons. Pages 27–33 (one-sample), 68–75 (two-sample).

Or second edition (1999).

### See Also

[psignrank](#), [pwilcox](#).

[wilcox\\_test](#) in package **coin** for exact, asymptotic and Monte Carlo *conditional* p-values, including in the presence of ties.

[kruskal.test](#) for testing homogeneity in location parameters in the case of two or more samples; [t.test](#) for an alternative under normality assumptions [or large samples]

### Examples

```
require(graphics)
## One-sample test.
## Hollander & Wolfe (1973), 29f.
## Hamilton depression scale factor measurements in 9 patients with
## mixed anxiety and depression, taken at the first (x) and second
## (y) visit after initiation of a therapy (administration of a
## tranquilizer).
x <- c(1.83, 0.50, 1.62, 2.48, 1.68, 1.88, 1.55, 3.06, 1.30)
y <- c(0.878, 0.647, 0.598, 2.05, 1.06, 1.29, 1.06, 3.14, 1.29)
wilcox.test(x, y, paired = TRUE, alternative = "greater")
wilcox.test(y - x, alternative = "less") # The same.
```

```
wilcox.test(y - x, alternative = "less",
            exact = FALSE, correct = FALSE) # H&W large sample
                                           # approximation

## Two-sample test.
## Hollander & Wolfe (1973), 69f.
## Permeability constants of the human chorioamnion (a placental
## membrane) at term (x) and between 12 to 26 weeks gestational
## age (y). The alternative of interest is greater permeability
## of the human chorioamnion for the term pregnancy.
x <- c(0.80, 0.83, 1.89, 1.04, 1.45, 1.38, 1.91, 1.64, 0.73, 1.46)
y <- c(1.15, 0.88, 0.90, 0.74, 1.21)
wilcox.test(x, y, alternative = "g")          # greater
wilcox.test(x, y, alternative = "greater",
            exact = FALSE, correct = FALSE) # H&W large sample
                                           # approximation

wilcox.test(rnorm(10), rnorm(10, 2), conf.int = TRUE)

## Formula interface.
boxplot(Ozone ~ Month, data = airquality)
wilcox.test(Ozone ~ Month, data = airquality,
            subset = Month %in% c(5, 8))
```

---

 Wilcoxon

*Distribution of the Wilcoxon Rank Sum Statistic*


---

## Description

Density, distribution function, quantile function and random generation for the distribution of the Wilcoxon rank sum statistic obtained from samples with size  $m$  and  $n$ , respectively.

## Usage

```
dwilcox(x, m, n, log = FALSE)
pwilcox(q, m, n, lower.tail = TRUE, log.p = FALSE)
qwilcox(p, m, n, lower.tail = TRUE, log.p = FALSE)
rwilcox(nn, m, n)
```

## Arguments

<code>x, q</code>	vector of quantiles.
<code>p</code>	vector of probabilities.
<code>nn</code>	number of observations. If <code>length(nn) &gt; 1</code> , the length is taken to be the number required.
<code>m, n</code>	numbers of observations in the first and second sample, respectively. Can be vectors of positive integers.
<code>log, log.p</code>	logical; if TRUE, probabilities <code>p</code> are given as $\log(p)$ .
<code>lower.tail</code>	logical; if TRUE (default), probabilities are $P[X \leq x]$ , otherwise, $P[X > x]$ .

**Details**

This distribution is obtained as follows. Let  $x$  and  $y$  be two random, independent samples of size  $m$  and  $n$ . Then the Wilcoxon rank sum statistic is the number of all pairs  $(x[i], y[j])$  for which  $y[j]$  is not greater than  $x[i]$ . This statistic takes values between 0 and  $m * n$ , and its mean and variance are  $m * n / 2$  and  $m * n * (m + n + 1) / 12$ , respectively.

If any of the first three arguments are vectors, the recycling rule is used to do the calculations for all combinations of the three up to the length of the longest vector.

**Value**

`dwilcox` gives the density, `pwilcox` gives the distribution function, `qwilcox` gives the quantile function, and `rwilcox` generates random deviates.

**Warning**

These functions can use large amounts of memory and stack (and even crash **R** if the stack limit is exceeded and stack-checking is not in place) if one sample is large (several thousands or more).

**Note**

S-PLUS uses a different (but equivalent) definition of the Wilcoxon statistic: see [wilcox.test](#) for details.

**Author(s)**

Kurt Hornik

**Source**

These are calculated via recursion, based on `cwilcox(k, m, n)`, the number of choices with statistic  $k$  from samples of size  $m$  and  $n$ , which is itself calculated recursively and the results cached. Then `dwilcox` and `pwilcox` sum appropriate values of `cwilcox`, and `qwilcox` is based on inversion.

`rwilcox` generates a random permutation of ranks and evaluates the statistic.

**See Also**

[wilcox.test](#) to calculate the statistic from data, find p values and so on.

[dsignrank](#) etc, for the distribution of the *one-sample* Wilcoxon signed rank statistic.

**Examples**

```
require(graphics)

x <- -1:(4*6 + 1)
fx <- dwilcox(x, 4, 6)
Fx <- pwilcox(x, 4, 6)

layout(rbind(1,2), widths=1, heights=c(3,2))
plot(x, fx,type='h', col="violet",
      main= "Probabilities (density) of Wilcoxon-Statist.(n=6,m=4) ")
plot(x, Fx,type="s", col="blue",
      main= "Distribution of Wilcoxon-Statist.(n=6,m=4) ")
```

```

abline(h=0:1, col="gray20",lty=2)
layout(1)# set back

N <- 200
hist(U <- rwilcox(N, m=4,n=6), breaks=0:25 - 1/2,
     border="red", col="pink", sub = paste("N =",N))
mtext("N * f(x), f() = true \"density\"", side=3, col="blue")
lines(x, N*f(x), type='h', col='blue', lwd=2)
points(x, N*f(x), cex=2)

## Better is a Quantile-Quantile Plot
qqplot(U, qw <- qwilcox((1:N - 1/2)/N, m=4,n=6),
       main = paste("Q-Q-Plot of empirical and theoretical quantiles",
                    "Wilcoxon Statistic, (m=4, n=6)",sep="\n"))
n <- as.numeric(names(print(tU <- table(U))))
text(n+.2, n+.5, labels=tU, col="red")

```

---

window

*Time Windows*

---

## Description

`window` is a generic function which extracts the subset of the object `x` observed between the times `start` and `end`. If a frequency is specified, the series is then re-sampled at the new frequency.

## Usage

```

window(x, ...)
## S3 method for class 'ts':
window(x, ...)
## Default S3 method:
window(x, start = NULL, end = NULL,
       frequency = NULL, deltat = NULL, extend = FALSE, ...)

window(x, ...) <- value
## S3 method for class 'ts':
window(x, start, end, frequency, deltat, ...) <- value

```

## Arguments

<code>x</code>	a time-series (or other object if not replacing values).
<code>start</code>	the start time of the period of interest.
<code>end</code>	the end time of the period of interest.
<code>frequency, deltat</code>	the new frequency can be specified by either (or both if they are consistent).
<code>extend</code>	logical. If true, the <code>start</code> and <code>end</code> values are allowed to extend the series. If false, attempts to extend the series give a warning and are ignored.
<code>...</code>	further arguments passed to or from other methods.
<code>value</code>	replacement values.

**Details**

The start and end times can be specified as for `ts`. If there is no observation at the new `start` or `end`, the immediately following (`start`) or preceding (`end`) observation time is used.

The replacement function has a method for `ts` objects, and is allowed to extend the series (with a warning). There is no default method.

**Value**

The value depends on the method. `window.default` will return a vector or matrix with an appropriate `tsp` attribute.

`window.ts` differs from `window.default` only in ensuring the result is a `ts` object.

If `extend = TRUE` the series will be padded with NAs if needed.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`time`, `ts`.

**Examples**

```
window(presidents, 1960, c(1969,4)) # values in the 1960's
window(presidents, deltat=1) # All Qtr1s
window(presidents, start=c(1945,3), deltat=1) # All Qtr3s
window(presidents, 1944, c(1979,2), extend=TRUE)

pres <- window(presidents, 1945, c(1949,4)) # values in the 1940's
window(pres, 1945.25, 1945.50) <- c(60, 70)
window(pres, 1944, 1944.75) <- 0 # will generate a warning
window(pres, c(1945,4), c(1949,4), frequency=1) <- 85:89
pres
```

---

xtabs

*Cross Tabulation*


---

**Description**

Create a contingency table (optionally a sparse matrix) from cross-classifying factors, usually contained in a data frame, using a formula interface.

**Usage**

```
xtabs(formula = ~., data = parent.frame(), subset, sparse = FALSE, na.action,
      exclude = c(NA, NaN), drop.unused.levels = FALSE)
```

## Arguments

<code>formula</code>	a <a href="#">formula</a> object with the cross-classifying variables (separated by <code>+</code> ) on the right hand side (or an object which can be coerced to a formula). Interactions are not allowed. On the left hand side, one may optionally give a vector or a matrix of counts; in the latter case, the columns are interpreted as corresponding to the levels of a variable. This is useful if the data have already been tabulated, see the examples below.
<code>data</code>	an optional matrix or data frame (or similar: see <a href="#">model.frame</a> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>subset</code>	an optional vector specifying a subset of observations to be used.
<code>sparse</code>	logical specifying if the result should be a <i>sparse</i> matrix, i.e., inheriting from <a href="#">sparseMatrix</a> Only works for two factors (since there are no higher-order sparse array classes yet).
<code>na.action</code>	a function which indicates what should happen when the data contain NAs.
<code>exclude</code>	a vector of values to be excluded when forming the set of levels of the classifying factors.
<code>drop.unused.levels</code>	a logical indicating whether to drop unused levels in the classifying factors. If this is <code>FALSE</code> and there are unused levels, the table will contain zero marginals, and a subsequent chi-squared test for independence of the factors will not work.

## Details

There is a `summary` method for contingency table objects created by `table` or `xtabs(*, sparse=FALSE)`, which gives basic information and performs a chi-squared test for independence of factors (note that the function `chisq.test` currently only handles 2-d tables).

If a left hand side is given in `formula`, its entries are simply summed over the cells corresponding to the right hand side; this also works if the lhs does not give counts.

## Value

By default, when `sparse=FALSE`, a contingency table in array representation of S3 class `c("xtabs", "table")`, with a `"call"` attribute storing the matched call.

When `sparse=TRUE`, a sparse numeric matrix, specifically an object of S4 class `dgTMatrix` from package **Matrix**.

## See Also

[table](#) for traditional cross-tabulation, and [as.data.frame.table](#) which is the inverse operation of `xtabs` (see the DF example below).

[sparseMatrix](#) on sparse matrices in package **Matrix**.

## Examples

```
## 'esoph' has the frequencies of cases and controls for all levels of
## the variables 'agegp', 'alcgp', and 'tobgp'.
xtabs(cbind(ncases, ncontrols) ~ ., data = esoph)
## Output is not really helpful ... flat tables are better:
ftable(xtabs(cbind(ncases, ncontrols) ~ ., data = esoph))
## In particular if we have fewer factors ...
```

```
fable(xtabs(cbind(ncases, ncontrols) ~ agegp, data = esoph))

## This is already a contingency table in array form.
DF <- as.data.frame(UCBAdmissions)
## Now 'DF' is a data frame with a grid of the factors and the counts
## in variable 'Freq'.
DF
## Nice for taking margins ...
xtabs(Freq ~ Gender + Admit, DF)
## And for testing independence ...
summary(xtabs(Freq ~ ., DF))

## Create a nice display for the warp break data.
warpbreaks$replicate <- rep(1:9, len = 54)
fable(xtabs(breaks ~ wool + tension + replicate, data = warpbreaks))

### ---- Sparse Examples ----

if(require("Matrix")) {
  ## similar to "nlme"s 'ergoStool' :
  d.ergo <- data.frame(Type = paste("T", rep(1:4, 9*4), sep=""),
                      Subj = gl(9,4, 36*4))
  print(xtabs(~ Type + Subj, data=d.ergo)) # 4 replicates each
  set.seed(15) # a subset of cases:
  print(xtabs(~ Type + Subj, data=d.ergo[sample(36, 10),], sparse=TRUE))

  ## Hypothetical two level setup:
  inner <- factor(sample(letters[1:25], 100, replace = TRUE))
  inout <- factor(sample(LETTERS[1:5], 25, replace = TRUE))
  fr <- data.frame(inner = inner, outer = inout[as.integer(inner)])
  print(xtabs(~ inner + outer, fr, sparse = TRUE))
}
```





## Chapter 8

# The `tools` package

---

`tools-package`      *Tools for Package Development*

---

### Description

Tools for package development, administration and documentation.

### Details

This package contains tools for manipulating R packages and their documentation.

For a complete list of functions, use `library(help="tools")`.

### Author(s)

Kurt Hornik and Friedrich Leisch

Maintainer: R Core Team <R-core@r-project.org>

---

`buildVignettes`      *List and Build Package Vignettes*

---

### Description

Run [Sweave](#) and [texi2dvi](#) on all vignettes of a package.

### Usage

```
buildVignettes(package, dir, lib.loc = NULL, quiet = TRUE, clean = TRUE)
pkgVignettes(package, dir, lib.loc = NULL)
```

**Arguments**

<code>package</code>	a character string naming an installed package. If given, Sweave files are searched in subdirectory <code>'doc'</code> .
<code>dir</code>	a character string specifying the path to a package's root source directory. This subdirectory <code>'inst/doc'</code> is searched for Sweave files.
<code>lib.loc</code>	a character vector of directory names of R libraries, or <code>NULL</code> . The default value of <code>NULL</code> corresponds to all libraries currently known. The specified library trees are used to search for <code>package</code> .
<code>quiet</code>	logical. Run <code>Sweave</code> and <code>texi2dvi</code> in quiet mode.
<code>clean</code>	Remove all files generated by the build, even if there were copies there before.

**Value**

`buildVignettes` is called for its side effect of creating the PDF versions of all vignettes.  
`pkgVignettes` returns an object of class `"pkgVignettes"`.

---

charsets

*Conversion Tables between Character Sets*


---

**Description**

`charset_to_Unicode` is a matrix of Unicode points with columns for the common 8-bit encodings.

`Adobe_glyphs` is a dataframe which gives Adobe glyph names for Unicode points. It has two character columns, `"adobe"` and `"unicode"` (a 4-digit hex representation).

**Usage**

```
charset_to_Unicode
```

```
Adobe_glyphs
```

**Details**

`charset_to_Unicode` is an integer matrix of class `c("noquote", "hexmode")` so prints in hexadecimal. The mappings are those used by `libiconv`: there are differences in the way quotes and minus/hyphen are mapped between sources (and the postscript encoding files use a different mapping).

`Adobe_glyphs` include all the Adobe glyph names which correspond to single Unicode characters. It is sorted by Unicode point and within a point alphabetically on the glyph (there can be more than one name for a Unicode point). The data are in the file `'R_HOME/share/encodings/Adobe_glyphlist'`.

**Source**

<http://partners.adobe.com/public/developer/en/opentype/glyphlist.txt>

**Examples**

```
## find Adobe names for ISOLatin2 chars.
latin2 <- charset_to_Unicode[, "ISOLatin2"]
aUnicode <- as.numeric(paste("0x", Adobe_glyphs$unicode, sep=""))
keep <- aUnicode %in% latin2
aUnicode <- aUnicode[keep]
aAdobe <- Adobe_glyphs[keep, 1]
## first match
aLatin2 <- aAdobe[match(latin2, aUnicode)]
## all matches
bLatin2 <- lapply(1:256, function(x) aAdobe[aUnicode == latin2[x]])
format(bLatin2, justify="none")
```

checkFF

*Check Foreign Function Calls***Description**

Performs checks on calls to compiled code from R code. Currently only checks whether the interface functions such as `.C` and `.Fortran` are called with a `"NativeSymbolInfo"` first argument or with argument `PACKAGE` specified, which is highly recommended to avoid name clashes in foreign function calls.

**Usage**

```
checkFF(package, dir, file, lib.loc = NULL,
        verbose = getOption("verbose"))
```

**Arguments**

<code>package</code>	a character string naming an installed package. If given, the installed R code of the package is checked.
<code>dir</code>	a character string specifying the path to a package's root source directory. This should contain the subdirectory 'R' (for R code). Only used if <code>package</code> is not given.
<code>file</code>	the name of a file containing R code to be checked. Used if neither <code>package</code> nor <code>dir</code> are given.
<code>lib.loc</code>	a character vector of directory names of R libraries, or <code>NULL</code> . The default value of <code>NULL</code> corresponds to all libraries currently known. The specified library trees are used to search for <code>package</code> .
<code>verbose</code>	a logical. If <code>TRUE</code> , additional diagnostics are printed (and the result is returned invisibly).

**Details**

Note that we can only check if the `name` argument is a symbol or a character string, not what class of object the symbol resolves to at run-time.

If the package has a name space and if that contains a `useDynLib` directive, calls in top-level functions in the package are not reported as their symbols will be preferentially looked up in the DLL named in the first `useDynLib` directive.

**Value**

An object of class "checkFF", which currently is a list of the (parsed) foreign function calls with a character first argument and no PACKAGE argument.

There is a `print` method to display the information contained in such objects.

**Warning**

This function is still experimental. Both name and interface might change in future versions.

**See Also**

`.C`, `.Fortran`; `Foreign`.

**Examples**

```
checkFF(package = "stats", verbose = TRUE)
```

---

checkMD5sums

*Check and Create MD5 Checksum Files*

---

**Description**

`checkMD5sums` checks the files against a file 'MD5'.

**Usage**

```
checkMD5sums(package, dir)
```

**Arguments**

<code>package</code>	the name of an installed package
<code>dir</code>	the path to the top-level directory of an installed package.

**Details**

The file 'MD5' which is created is in a format which can be checked by `md5sum -c MD5` if a suitable command-line version of `md5sum` is available. (For Windows, one is supplied in the bundle at <http://www.murdoch-sutherland.com/Rtools/tools.zip>.)

If `dir` is missing, an installed package of name `package` is searched for.

The private function `tools:::installMD5sums` is used to create MD5 files in the Windows build.

**Value**

`checkMD5sums` returns a logical, NA if there is no 'MD5' file to be checked.

**See Also**

`md5sum`

checkRd

*Check an Rd Object***Description**

Check an help file or the output of the `parse_Rd` function.

**Usage**

```
checkRd(Rd, defines = .Platform$OS.type, stages = "render",
        unknownOK = TRUE, listOK = TRUE, ..., def_enc = FALSE)
```

**Arguments**

<code>Rd</code>	a filename or Rd object to use as input.
<code>defines</code>	string(s) to use in <code>#ifdef</code> tests.
<code>stages</code>	at which stage ("build", "install", or "render") should <code>\Sexpr</code> macros be executed? See the notes below.
<code>unknownOK</code>	unrecognized macros are treated as errors if <code>FALSE</code> , otherwise warnings.
<code>listOK</code>	unnecessary non-empty braces (e.g., around text, not as an argument) are treated as errors if <code>FALSE</code> , otherwise warnings.
<code>...</code>	additional parameters to pass to <code>parse_Rd</code> when <code>Rd</code> is a filename. One that is often useful is <code>encoding</code> .
<code>def_enc</code>	logical: has the package declared an encoding, so tests for non-ASCII text are suppressed?

**Details**

`checkRd` performs consistency checks on an Rd file, confirming that required sections are present, etc.

It accepts a filename for an Rd file, and will use `parse_Rd` to parse it before applying the checks. If so, warnings from `parse_Rd` are collected, together with those from the internal function `prepare_Rd`, which does the `#ifdef` and `\Sexpr` processing, drops sections that would not be rendered or are duplicated (and should not be) and removes empty sections.

An Rd object is passed through `prepare_Rd`, but it may already have been (and installed Rd objects have).

Warnings are given a ‘level’: those from `prepare_Rd` have level 0. These include

```
All text must be in a section
Only one \examples section is allowed: the first will be used
Only one \encoding section is allowed: the first will be used
Section name is unrecognized and will be dropped
Dropping empty section name
```

`checkRd` itself can show

```
7 Tag tag name not recognized
```

- 7 \tabular format must be simple text
- 7 Unrecognized \tabular format: ...
- 7 Only *n* columns allowed in this table
- 7 Must have a *tag name*
- 7 Only one *tag name* is allowed
- 7 Tag *tag name* must not be empty
- 7 'docType' must be plain text
- 5 Tag \method is only valid in \usage
- 5 Tag \dontrun is only valid in \examples
- 5 Tag *tag name* is invalid in a *block name* block
- 5 Title of \section must be non-empty plain text
- 5 \title content must be plain text
- 3 Empty section *tag name*
- 1 Non-ASCII contents without declared encoding
- 1 Non-ASCII contents in second part of \enc
- 3 Tag ... is not valid in a code block
- 3 Apparent non-ASCII contents without declared encoding
- 3 Apparent non-ASCII contents in second part of \enc
- 3 Unnecessary braces at ...
- 3 \method not valid outside a code block

and variations with \method replaced by \S3method or \S4method.

Note that both `prepare_Rd` and `checkRd` have tests for an empty section: that in `checkRd` is stricter (essentially that nothing is output).

### Value

This may fail through an R error, but otherwise warnings are collected as returned as an object of class "checkRd", a character vector of messages. This class has a `print` method which only prints unique messages, and has argument `minlevel` that can be used to select only more serious messages. (This is set to `-1` in R CMD `check`.)

Possible fatal errors are those from running the parser (e.g. a non-existent file, unclosed quoted string, non-ASCII input without a specified encoding) or from `prepare_Rd` (multiple `\Rdversion` declarations, invalid `\encoding` or `\docType` or `\name` sections, and missing or duplicate `\name` or `\title` sections).

### Author(s)

Duncan Murdoch, Brian Ripley

### See Also

[parse\\_Rd](#), [Rd2HTML](#).

---

checkRdaFiles	<i>Report on Details of Saved Images or Re-saves them</i>
---------------	---

---

### Description

This reports for each of the files produced by `save` the size, if it was saved in ASCII or XDR binary format, and if it was compressed (and if so in what format).

Usually such files have extension `‘.rda’` or `‘.RData’`, hence the name of the function.

### Usage

```
checkRdaFiles(paths)
resaveRdaFiles(paths, compress = c("auto", "gzip", "bzip2", "xz"),
               compression_level)
```

### Arguments

<code>paths</code>	A character vector of paths to save files. If this specifies a single directory, it is taken to refer to all <code>‘.rda’</code> and <code>‘.RData’</code> files in that directory.
<code>compress, compression_level</code>	type and level of compression: see <a href="#">save</a> .

### Details

`compress = "auto"` asks **R** to choose the compression and ignores `compression_level`. It will try `"gzip"`, `"bzip2"` and if the `"gzip"` compressed size is over 10Kb, `"xz"` and choose the smallest compressed file (but with a 10% bias towards `"gzip"`). This can be slow.

### Value

For `checkRdaFiles`, a data frame with rows names `paths` and columns

<code>size</code>	numeric: file size in bytes, NA if the file does not exist.
<code>ASCII</code>	logical: true for <code>save(ASCII = TRUE)</code> , NA if the format is not that of an <b>R</b> save file.
<code>compress</code>	character: type of compression. One of <code>"gzip"</code> , <code>"bzip2"</code> , <code>"xz"</code> , <code>"none"</code> or <code>"unknown"</code> (which means that if this is an <b>R</b> save file it is from a later version of <b>R</b> ).
<code>version</code>	integer: the version of the save – usually 2 but 1 for very old files, and NA for other files.

### Examples

```
## Not run:
## from a package top-level source directory
paths <- sort(Sys.glob(c("data/*.rda", "data/*.RData")))
(res <- checkRdaFiles(paths))
## pick out some that may need attention
bad <- is.na(res$ASCII) | res$ASCII | (res$size > 1e4 & res$compress == "none")
res[bad, ]

## End(Not run)
```



---

`checkTnF`*Check R Packages or Code for T/F*

---

**Description**

Checks the specified R package or code file for occurrences of T or F, and gathers the expression containing these. This is useful as in R T and F are just variables which are set to the logicals TRUE and FALSE by default, but are not reserved words and hence can be overwritten by the user. Hence, one should always use TRUE and FALSE for the logicals.

**Usage**

```
checkTnF(package, dir, file, lib.loc = NULL)
```

**Arguments**

<code>package</code>	a character string naming an installed package. If given, the installed R code and the examples in the documentation files of the package are checked. R code installed as an image file cannot be checked.
<code>dir</code>	a character string specifying the path to a package's root source directory. This must contain the subdirectory 'R' (for R code), and should also contain 'man' (for documentation). Only used if <code>package</code> is not given. If used, the R code files and the examples in the documentation files are checked.
<code>file</code>	the name of a file containing R code to be checked. Used if neither <code>package</code> nor <code>dir</code> are given.
<code>lib.loc</code>	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. The specified library trees are used to search for <code>package</code> .

**Value**

An object of class "checkTnF" which is a list containing, for each file where occurrences of T or F were found, a list with the expressions containing these occurrences. The names of the list are the corresponding file names.

There is a `print` method for nicely displaying the information contained in such objects.

**Warning**

This function is still experimental. Both name and interface might change in future versions.

---

checkVignettes      *Check Package Vignettes*

---

### Description

Check all [Sweave](#) files of a package by running [Sweave](#) and/or [Stangle](#) on them. All R source code files found after the tangling step are [sourced](#) to check whether all code can be executed without errors.

### Usage

```
checkVignettes(package, dir, lib.loc = NULL,
               tangle = TRUE, weave = TRUE, latex = FALSE,
               workdir = c("tmp", "src", "cur"),
               keepfiles = FALSE)
```

### Arguments

package	a character string naming an installed package. If given, Sweave files are searched in subdirectory 'doc'.
dir	a character string specifying the path to a package's root source directory. This subdirectory 'inst/doc' is searched for Sweave files.
lib.loc	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. The specified library trees are used to search for package.
tangle	Perform a tangle and <a href="#">source</a> the extracted code?
weave	Perform a weave?
latex	logical: if tangle, weave and latex are TRUE and there is no 'Makefile' in the vignettes directory, run the tangled files through <code>pdflatex</code> .
workdir	Directory used as working directory while checking the vignettes. If "tmp" then a temporary directory is created, this is the default. If "src" then the directory containing the vignettes itself is used, if "cur" then the current working directory of R is used.
keepfiles	Delete file in temporary directory? This option is ignored when workdir != "tmp".

### Value

An object of class "checkVignettes" which is a list with the error messages found during the tangle and weave steps. There is a `print` method for nicely displaying the information contained in such objects.

---

codoc

*Check Code/Documentation Consistency*


---

## Description

Find inconsistencies between actual and documented ‘structure’ of R objects in a package. `codoc` compares names and optionally also corresponding positions and default values of the arguments of functions. `codocClasses` and `codocData` compare slot names of S4 classes and variable names of data sets, respectively.

## Usage

```
codoc(package, dir, lib.loc = NULL,
      use.values = NULL, verbose = getOption("verbose"))
codocClasses(package, lib.loc = NULL)
codocData(package, lib.loc = NULL)
```

## Arguments

<code>package</code>	a character string naming an installed package.
<code>dir</code>	a character string specifying the path to a package’s root source directory. This must contain the subdirectories ‘man’ with R documentation sources (in Rd format) and ‘R’ with R code. Only used if <code>package</code> is not given.
<code>lib.loc</code>	a character vector of directory names of R libraries, or <code>NULL</code> . The default value of <code>NULL</code> corresponds to all libraries currently known. The specified library trees are used to search for <code>package</code> .
<code>use.values</code>	if <code>FALSE</code> , do not use function default values when comparing code and docs. Otherwise, compare <i>all</i> default values if <code>TRUE</code> , and only the ones documented in the usage otherwise (default).
<code>verbose</code>	a logical. If <code>TRUE</code> , additional diagnostics are printed.

## Details

The purpose of `codoc` is to check whether the documented usage of function objects agrees with their formal arguments as defined in the R code. This is not always straightforward, in particular as the usage information for methods to generic functions often employs the name of the generic rather than the method.

The following algorithm is used. If an installed package is used, it is loaded (unless it is the **base** package), after possibly detaching an already loaded version of the package. Otherwise, if the sources are used, the R code files of the package are collected and sourced in a new environment. Then, the usage sections of the Rd files are extracted and parsed ‘as much as possible’ to give the formals documented. For interpreted functions in the code environment, the formals are compared between code and documentation according to the values of the argument `use.values`. Synopsis sections are used if present; their occurrence is reported if `verbose` is true.

If a package has a name space both exported and unexported objects are checked, as well as registered S3 methods. (In the unlikely event of differences the order is exported objects in the package, registered S3 methods and finally objects in the name space and only the first found is checked.)

Currently, the R documentation format has no high-level markup for the basic ‘structure’ of classes and data sets (similar to the usage sections for function synopses). Variable names for data frames in

documentation objects obtained by suitably editing ‘templates’ created by `prompt` are recognized by `codocData` and used provided that the documentation object is for a single data frame (i.e., only has one alias). `codocClasses` analogously handles slot names for classes in documentation objects obtained by editing shells created by `promptClass`.

Help files named ‘*pkgname-defunct.Rd*’ for the appropriate *pkgname* are checked more loosely, as they may have undocumented arguments.

### Value

`codoc` returns an object of class "codoc". Currently, this is a list which, for each Rd object in the package where an inconsistency was found, contains an element with a list of the mismatches (which in turn are lists with elements `code` and `docs`, giving the corresponding arguments obtained from the function’s code and documented usage).

`codocClasses` and `codocData` return objects of class "codocClasses" and "codocData", respectively, with a structure similar to class "codoc".

There are `print` methods for nicely displaying the information contained in such objects.

### Warning

Both `codocClasses` and `codocData` are still somewhat experimental. Names, interfaces and values might change in future versions.

### Note

The default for `use.values` has been changed from `FALSE` to `NULL`, for R versions 1.9.0 and later.

### See Also

[undoc](#), [QC](#)

---

delimMatch

*Delimited Pattern Matching*

---

### Description

Match delimited substrings in a character vector, with proper nesting.

### Usage

```
delimMatch(x, delim = c("{", "}"), syntax = "Rd")
```

### Arguments

<code>x</code>	a character vector.
<code>delim</code>	a character vector of length 2 giving the start and end delimiters. Future versions might allow for arbitrary regular expressions.
<code>syntax</code>	currently, always the string "Rd" indicating Rd syntax (i.e., ‘%’ starts a comment extending till the end of the line, and ‘\’ escapes). Future versions might know about other syntax, perhaps via ‘syntax tables’ allowing to flexibly specify comment, escape, and quote characters.

**Value**

An integer vector of the same length as `x` giving the starting position (in characters) of the first match, or `-1` if there is none, with attribute `"match.length"` giving the length (in characters) of the matched text (or `-1` for no match).

**See Also**

[regexpr](#) for ‘simple’ pattern matching.

**Examples**

```
x <- c("\\value{foo}", "function(bar)")
delimMatch(x)
delimMatch(x, c("(", ")"))
```

---

dependsOnPkgs

*Find Reverse Dependencies*

---

**Description**

Find ‘reverse’ dependencies of packages, that is those packages which depend on this one, and (optionally) so on recursively.

**Usage**

```
dependsOnPkgs(pkgs, dependencies = c("Depends", "Imports", "LinkingTo"),
             recursive = TRUE, lib.loc = NULL,
             installed = installed.packages(lib.loc, fields = "Enhances"))
```

**Arguments**

<code>pkgs</code>	a character vector of package names.
<code>dependencies</code>	a character vector listing the types of dependencies, a subset of <code>c("Depends", "Imports", "LinkingTo", "Suggests", "Enhances")</code> .
<code>recursive</code>	logical: should reverse dependencies of reverse dependencies (and so on) be included?
<code>lib.loc</code>	a character vector of R library trees, or <code>NULL</code> for all known trees (see <a href="#">.libPaths</a> ).
<code>installed</code>	a result of calling <code>installed.packages</code> .

**Value**

A character vector of package names, which does not include any from `pkgs`.

**Examples**

```
## there are few dependencies in a vanilla R installation
dependsOnPkgs("lattice")
```

---

 encoded\_text\_to\_latex

*Translate non-ASCII Text to LaTeX Escapes*


---

## Description

Translate non-ASCII characters in text to LaTeX escape sequences.

## Usage

```
encoded_text_to_latex(x,
                      encoding = c("latin1", "latin2", "latin9",
                                   "UTF-8", "utf8"))
```

## Arguments

<code>x</code>	a character vector.
<code>encoding</code>	the encoding to be assumed. "latin9" is officially ISO-8859-15 or Latin-9, but known as latin9 to LaTeX's inputenc package.

## Details

Non-ASCII characters in `x` are replaced by an appropriate LaTeX escape sequence, or '?' if there is no appropriate sequence.

Even if there is an appropriate sequence, it may not be supported by the font in use. Hyphen is mapped to '\-'.

## Value

A character vector of the same length as `x`.

## See Also

[iconv](#)

## Examples

```
x <- "fa\xE7ile"
encoded_text_to_latex(x, "latin1")
## Not run:
## create a tex file to show the upper half of 8-bit charsets
x <- rawToChar(as.raw(160:255), multiple=TRUE)
(x <- matrix(x, ncol=16, byrow=TRUE))
xx <- x
xx[] <- encoded_text_to_latex(x, "latin1") # or latin2 or latin9
xx <- apply(xx, 1, paste, collapse="&")
con <- file("test-encoding.tex", "w")
header <- c(
  "\\documentclass{article}",
  "\\usepackage[T1]{fontenc}",
  "\\usepackage{Rd}",
  "\\begin{document}",
```

```

"\\HeaderA{test}{}{test}",
"\\begin{Details}\\relax",
"\\Tabular{cccccccccccccc}{"}
trailer <- c(")", "\\end{Details}", "\\end{document}")
writeLines(header, con)
writeLines(paste(xx, "\\ ", sep=""), con)
writeLines(trailer, con)
close(con)
## and some UTF_8 chars
x <- intToUtf8(as.integer(
  c(160:383, 0x0192, 0x02C6, 0x02C7, 0x02CA, 0x02D8,
    0x02D9, 0x02DD, 0x200C, 0x2018, 0x2019, 0x201C,
    0x201D, 0x2020, 0x2022, 0x2026, 0x20AC)),
  multiple=TRUE)
x <- matrix(x, ncol=16, byrow=TRUE)
xx <- x
xx[] <- encoded_text_to_latex(x, "UTF-8")
xx <- apply(xx, 1, paste, collapse="&")
con <- file("test-utf8.tex", "w")
writeLines(header, con)
writeLines(paste(xx, "\\ ", sep=""), con)
writeLines(trailer, con)
close(con)

## End(Not run)

```

---

fileutils

*File Utilities*


---

## Description

Utilities for listing files, and manipulating file paths.

## Usage

```

file_ext(x)
file_path_as_absolute(x)
file_path_sans_ext(x, compression = FALSE)

list_files_with_exts(dir, exts, all.files = FALSE,
  full.names = TRUE)
list_files_with_type(dir, type, all.files = FALSE,
  full.names = TRUE, OS_subdirs = .OSType())

```

## Arguments

<code>x</code>	character vector giving file paths.
<code>compression</code>	logical: should compression extension <code>'gz'</code> , <code>'bz2'</code> or <code>'xz'</code> be removed first?
<code>dir</code>	a character string with the path name to a directory.
<code>exts</code>	a character vector of possible file extensions.
<code>all.files</code>	a logical. If <code>FALSE</code> (default), only visible files are considered; if <code>TRUE</code> , all files are used.

<code>full.names</code>	a logical indicating whether the full paths of the files found are returned (default), or just the file names.
<code>type</code>	a character string giving the ‘type’ of the files to be listed, as characterized by their extensions. Currently, possible values are "code" (R code), "data" (data sets), "demo" (demos), "docs" (R documentation), and "vignette" (vignettes).
<code>OS_subdirs</code>	a character vector with the names of OS-specific subdirectories to possibly include in the listing of R code and documentation files. By default, the value of the environment variable <code>R_OSTYPE</code> , or if this is empty, the value of <code>.Platform\$OS.type</code> , is used.

### Details

`file_ext` returns the file (name) extensions. (Only purely alphanumeric extensions are recognized.)

`file_path_as_absolute` turns a possibly relative file path absolute, performing tilde expansion if necessary. Currently, only a single existing path can be given.

`file_path_sans_ext` returns the file paths without extensions. (Only purely alphanumeric extensions are recognized.)

`list_files_with_exts` returns the paths or names of the files in directory `dir` with extension matching one of the elements of `exts`. Note that by default, full paths are returned, and that only visible files are used.

`list_files_with_type` returns the paths of the files in `dir` of the given ‘type’, as determined by the extensions recognized by R. When listing R code and documentation files, files in OS-specific subdirectories are included if present according to the value of `OS_subdirs`. Note that by default, full paths are returned, and that only visible files are used.

### See Also

[file.path](#), [file.info](#), [list.files](#)

### Examples

```
dir <- file.path(R.home(), "library", "stats")
list_files_with_exts(file.path(dir, "demo"), "R")
list_files_with_type(file.path(dir, "demo"), "demo") # the same
file_path_sans_ext(list.files(file.path(R.home(), "modules")))
```

### Description

Given a dependency matrix, will create a `DependsList` object for that package which will include the dependencies for that matrix, which ones are installed, which unresolved dependencies were found online, which unresolved dependencies were not found online, and any R dependencies.



**Usage**

```
getDepList(depMtrx, instPkgs, recursive = TRUE, local = TRUE,
           reduce = TRUE, lib.loc = NULL)

pkgDepends(pkg, recursive = TRUE, local = TRUE, reduce = TRUE,
           lib.loc = NULL)
```

**Arguments**

<code>depMtrx</code>	A dependency matrix as from <code>package.dependencies</code>
<code>pkg</code>	The name of the package
<code>instPkgs</code>	A matrix specifying all packages installed on the local system, as from <code>installed.packages</code>
<code>recursive</code>	Whether or not to include indirect dependencies
<code>local</code>	Whether or not to search only locally
<code>reduce</code>	Whether or not to collapse all sets of dependencies to a minimal value
<code>lib.loc</code>	What libraries to use when looking for installed packages. <code>NULL</code> indicates all library directories in the user's <code>.libPaths()</code> .

**Details**

The function `pkgDepends` is a convenience function which wraps `getDepList` and takes as input a package name. It will then query `installed.packages` and also generate a dependency matrix, calling `getDepList` with this information and returning the result.

These functions will retrieve information about the dependencies of the matrix, resulting in a `DependsList` object. This is a list with four elements:

**Depends** A vector of the dependencies for this package.

**Installed** A vector of the dependencies which have been satisfied by the currently installed packages.

**Found** A list representing the dependencies which are not in `Installed` but were found online. This list has element names which are the URLs for the repositories in which packages were found and the elements themselves are vectors of package names which were found in the respective repositories. If `local=TRUE`, the `Found` element will always be empty.

**R** Any R version dependencies.

If `recursive` is `TRUE`, any package that is specified as a dependency will in turn have its dependencies included (and so on), these are known as indirect dependencies. If `recursive` is `FALSE`, only the dependencies directly stated by the package will be used.

If `local` is `TRUE`, the system will only look at the user's local install and not online to find unresolved dependencies.

If `reduce` is `TRUE`, the system will collapse the fields in the `DependsList` object such that a minimal set of dependencies are specified (for instance if there was `'foo, foo (>= 1.0.0), foo (>= 1.3.0'`, it would only return `'foo (>= 1.3.0)'`).

**Value**

An object of class `"DependsList"`.

**Author(s)**

Jeff Gentry

**See Also**[installFoundDepends](#)**Examples**

```
pkgDepends("tools", local = FALSE)
```

---

`HTMLheader`*Generate a standard HTML header for R help.*

---

**Description**

This function generates the standard HTML header used on R help pages.

**Usage**

```
HTMLheader(title = "R", logo = TRUE, up = NULL, top = file.path(Rhome, "doc/html")  
           Rhome = "", headerTitle = paste("R:", title), outputEncoding = "UTF-8")
```

**Arguments**

<code>title</code>	The title to display and use in the HTML headers. Should have had any HTML escaping already done.
<code>logo</code>	Whether to display the R logo after the title.
<code>up</code>	Which page (if any) to link to on the “up” button.
<code>top</code>	Which page (if any) to link to on the “top” button.
<code>Rhome</code>	A relative path to the R home directory. See the Details.
<code>headerTitle</code>	The title used in the headers.
<code>outputEncoding</code>	The declared encoding for the whole page.

**Details**

The `up` and `top` links should be relative to the current page. The `Rhome` path default works with dynamic help; for static help, a relative path (e.g. `../..`) to it should be used.

**Value**

A character vector containing the lines of an HTML header which can be used to start a page in the R help system.

**Examples**

```
cat(HTMLheader("This is a sample header"), sep="\n")
```

HTMLlinks

*Collect HTML Links from Package Documentation***Description**

Compute relative file paths for URLs to other package's installed HTML documentation.

**Usage**

```
findHTMLlinks(pkgDir = "", lib.loc = NULL, level = 0:2)
```

**Arguments**

<code>pkgDir</code>	the top-level directory of an installed package. The default indicates no package.
<code>lib.loc</code>	character vector describing the location of R library trees to scan: the default indicates <code>.libPaths()</code> .
<code>level</code>	Which level(s) to include.

**Details**

`findHTMLlinks` tries to resolve links from one help page to another. It uses in decreasing priority

- The package in `pkgDir`: this is used when converting HTML help for that package (level 0).
- The base and recommended packages (level 1).
- Other packages found in the library trees specified by `lib.loc` in the order of the trees and alphabetically within a library tree (level 2).

**Value**

A named character vector of file paths, relative to the 'html' directory of an installed package. So these are of the form `"../somepkg/html/sometopic.html"`.

**Author(s)**

Duncan Murdoch, Brian Ripley

installFoundDepends

*A function to install unresolved dependencies***Description**

This function will take the `Found` element of a `pkgDependsList` object and attempt to install all of the listed packages from the specified repositories.

**Usage**

```
installFoundDepends(depPkgList, ...)
```

**Arguments**

depPkgList    A Found element from a pkgDependsList object  
 ...            Arguments to pass on to `install.packages`

**Details**

This function takes as input the Found list from a pkgDependsList object. This list will have element names being URLs corresponding to repositories and the elements will be vectors of package names. For each element, `install.packages` is called for that URL to install all packages listed in the vector.

**Author(s)**

Jeff Gentry

**See Also**

`pkgDepends`, `install.packages`

**Examples**

```
## Set up a temporary directory to install packages to
tmp <- tempfile()
dir.create(tmp)

pDL <- pkgDepends("tools", local=FALSE)
installFoundDepends(pDL$Found, destdir=tmp)
```

---

makeLazyLoading    *Lazy Loading of Packages*

---

**Description**

Tools for lazy loading of packages from a database.

**Usage**

```
makeLazyLoading(package, lib.loc = NULL, compress = TRUE,
                 keep.source = getOption("keep.source.pkgs"))
```

**Arguments**

package        package name string  
 lib.loc        library trees, as in `library`  
 keep.source    logical; should sources be kept when saving from source  
 compress       logical; whether to compress entries on the database.

**Details**

A tool to set up packages for lazy loading from a database. For packages other than **base** you can use `makeLazyLoading(package)` to convert them to use lazy loading.

**Author(s)**

Luke Tierney and Brian Ripley

**Examples**

```
## set up package "splines" for lazy loading -- already done
## Not run:
tools::makeLazyLoading("splines")

## End(Not run)
```

---

md5sum

*Compute MD5 Checksums*

---

**Description**

Compute the 32-byte MD5 checksums of one or more files.

**Usage**

```
md5sum(files)
```

**Arguments**

`files` character. The paths of file(s) to be check-summed.

**Value**

A character vector of the same length as `files`, with names equal to `files`. The elements will be NA for non-existent or unreadable files, otherwise a 32-character string of hexadecimal digits.

On Windows all files are read in binary mode (as the `md5sum` utilities there do): on other OSes the files are read in the default way.

**See Also**

[checkMD5sums](#)

**Examples**

```
md5sum(dir(R.home(), pattern="^COPY", full.names=TRUE))
```

---

`package.dependencies`*Check Package Dependencies*

---

**Description**

Parses and checks the dependencies of a package against the currently installed version of R (and other packages).

**Usage**

```
package.dependencies(x, check = FALSE,
                    depLevel = c("Depends", "Imports", "Suggests"))
```

**Arguments**

<code>x</code>	A matrix of package descriptions as returned by <a href="#">available.packages</a> .
<code>check</code>	If TRUE, return logical vector of check results. If FALSE, return parsed list of dependencies.
<code>depLevel</code>	Whether to look for Depends or Suggests level dependencies.

**Details**

Currently we only check if the package conforms with the currently running version of R. In the future we might add checks for inter-package dependencies.

**See Also**

[update.packages](#)

---

`parse_Rd`*Parse an Rd file*

---

**Description**

This function reads an R documentation (Rd) file and parses it, for processing by other functions.

**Usage**

```
parse_Rd(file, srcfile = NULL, encoding = "unknown", verbose = FALSE,
         fragment = FALSE, warningCalls = TRUE)
## S3 method for class 'Rd':
print(x, deparse = FALSE, ...)
## S3 method for class 'Rd':
as.character(x, deparse = FALSE, ...)
```

**Arguments**

<code>file</code>	A filename or text-mode connection. At present filenames work best.
<code>srcfile</code>	NULL, or a "srcfile" object. See the 'Details' section.
<code>encoding</code>	Encoding to be assumed for input strings.
<code>verbose</code>	Logical indicating whether detailed parsing information should be printed.
<code>fragment</code>	Logical indicating whether file represents a complete Rd file, or a fragment.
<code>warningCalls</code>	Logical: should parser warnings include the call?
<code>x</code>	An object of class Rd.
<code>deparse</code>	If TRUE, attempt to reinstate the escape characters so that the resulting characters will parse to the same object.
<code>...</code>	Further arguments to be passed to or from other methods.

**Details**

This function parses 'Rd' files according to the specification given in <http://developer.r-project.org/parseRd.pdf>. This is not identical to the rules used before version 2.10.x: it is somewhat stricter.

As from R 2.10.0, `parse_Rd` generates a warning for each parse error and attempts to continue parsing. In order to continue, it is generally necessary to drop some parts of the file, so such warnings should not be ignored.

**Value**

`parse_Rd` returns an object of class "Rd". The internal format of this object is subject to change. The `as.character()` and `print()` methods defined for the class return character vectors and print them, respectively.

Files without a marked encoding are by default assumed to be in the native encoding. An alternate default can be set using the `encoding` argument. All text in files is translated to the UTF-8 encoding in the parsed object.

**Author(s)**

Duncan Murdoch

**References**

<http://developer.r-project.org/parseRd.pdf>

**See Also**

[Rd2HTML](#) for the converters that use the output of `parse_Rd()`.

## Description

Functions for performing various quality checks.

## Usage

```
checkDocFiles(package, dir, lib.loc = NULL)
checkDocStyle(package, dir, lib.loc = NULL)
checkReplaceFuns(package, dir, lib.loc = NULL)
checkS3methods(package, dir, lib.loc = NULL)
```

## Arguments

<code>package</code>	a character string naming an installed package.
<code>dir</code>	a character string specifying the path to a package's root source directory. This should contain the subdirectories 'R' (for R code) and 'man' with R documentation sources (in Rd format). Only used if <code>package</code> is not given.
<code>lib.loc</code>	a character vector of directory names of R libraries, or <code>NULL</code> . The default value of <code>NULL</code> corresponds to all libraries currently known. The specified library trees are used to search for <code>package</code> .

## Details

`checkDocFiles` checks, for all Rd files in a package, whether all arguments shown in the usage sections of the Rd file are documented in its arguments section. It also reports duplicated entries in the arguments section, and 'over-documented' arguments which are given in the arguments section but not in the usage. Note that the match is for the usage section and not a possibly existing synopsis section, as the usage is what gets displayed.

`checkDocStyle` investigates how (S3) methods are shown in the usages of the Rd files in a package. It reports the methods shown by their full name rather than using the Rd `\method` markup for indicating S3 methods. Earlier versions of R also reported about methods shown along with their generic, which typically caused problems for the documentation of the primary argument in the generic and its methods. With `\method` now being expanded in a way that class information is preserved, joint documentation is no longer necessarily a problem. (The corresponding information is still contained in the object returned by `checkDocStyle`.)

`checkReplaceFuns` checks whether replacement functions or S3/S4 replacement methods in the package R code have their final argument named `value`.

`checkS3methods` checks whether all S3 methods defined in the package R code have all arguments of the corresponding generic, with positional arguments of the generics in the same positions for the method. As an exception, the first argument of a formula method *may* be called `formula` even if this is not the name used by the generic. The rules when `...` is involved are subtle: see the source code. Functions recognized as S3 generics are those with a call to `UseMethod` in their body, internal S3 generics (see [InternalMethods](#)), and S3 group generics (see [Math](#)). Possible dispatch under a different name is not taken into account. The generics are sought first in the given package, then in the **base** package and (currently) the packages **graphics**, **stats**, and **utils** added in R 1.9.0 by splitting the former **base**, and, if an installed package is tested, also in the loaded name spaces/packages listed in the package's 'DESCRIPTION' Depends field.



If using an installed package, the checks needing access to all R objects of the package will load the package (unless it is the **base** package), after possibly detaching an already loaded version of the package.

### Value

The functions return objects of class the same as the respective function names containing the information about problems detected. There are `print` methods for nicely displaying the information contained in such objects.

### Warning

These functions are still experimental. Names, interfaces and values might change in future versions.

---

Rd2HTML

*Rd Converters*

---

### Description

These functions take the output of the `parse_Rd` function and produce a help page from it. As they are mainly intended for internal use, their interfaces are subject to change.

### Usage

```
Rd2HTML(Rd, out = "", package = "", defines = .Platform$OS.type,
        Links = NULL, Links2 = NULL,
        stages = "render", outputEncoding = "UTF-8",
        dynamic = FALSE, no_links = FALSE, ...)
```

```
Rd2txt(Rd, out = "", package = "", defines = .Platform$OS.type,
        stages = "render", outputEncoding = "",
        width = getOption("help_text_width", 80L), ...)
```

```
Rd2latex(Rd, out = "", defines = .Platform$OS.type,
        stages = "render", outputEncoding = "ASCII", ...,
        writeEncoding = TRUE)
```

```
Rd2ex(Rd, out = "", defines = .Platform$OS.type,
        stages = "render", outputEncoding = "UTF-8", ...)
```

### Arguments

<code>Rd</code>	a filename or Rd object to use as input.
<code>out</code>	a filename or connection object to which to write the output.
<code>package</code>	the package to list in the output.
<code>defines</code>	string(s) to use in <code>#ifdef</code> tests.
<code>stages</code>	at which stage ("build", "install", or "render") should <code>\Sexpr</code> macros be executed? See the notes below.
<code>outputEncoding</code>	see the 'Encodings' section below.

<code>dynamic</code>	logical: set links for render-time resolution by dynamic help system.
<code>no_links</code>	logical: suppress hyperlinks to other help topics. Used by R CMD <code>Rdconv</code> .
<code>Links, Links2</code>	NULL or a named (by topics) character vector of links, as returned by <code>findHTMLlinks</code> .
<code>width</code>	The intended page width (in characters) for which the text rendering should be designed.
<code>...</code>	additional parameters to pass to <code>parse_Rd</code> when <code>Rd</code> is a filename.
<code>writeEncoding</code>	should <code>\inputencoding</code> lines be written in the file for non-ASCII encodings?

## Details

These functions convert help documents: `Rd2HTML` produces HTML, `Rd2txt` produces plain text, `Rd2latex` produces LaTeX. `Rd2ex` extracts the examples in the format used by `example` and R utilities.

Each of the functions accepts a filename for an Rd file, and will use `parse_Rd` to parse it before applying the conversions or checks.

The difference between arguments `Link` and `Link2` is that links are looked in them in turn, so lazy-evaluation can be used to only do a second-level search for links if required.

Note that the default for `Rd2latex` is to output ASCII, including using the second option of `\enc` markup. This was chosen because use of UTF-8 in LaTeX requires version ‘2005/12/01’ or later, and even with that version the coverage of UTF-8 glyphs is not extensive (and not even as complete as Latin-1).

`Rd2txt` will format text paragraphs to a width determined by `width`, with appropriate margins. The default is to be close to the rendering in versions of R < 2.10.0.

`Rd2txt` will use directional quotes (see `sQuote`) if option `"useFancyQuotes"` is true (the default) and the current encoding is UTF-8.

## Value

These functions are executed mainly for the side effect of writing the converted help page. Their value is the name of the output file (invisibly). For `Rd2latex`, the output name is given an attribute `"latexEncoding"` giving the encoding of the file in a form suitable for use with the LaTeX ‘`inputenc`’ package.

## Encodings

Rd files are normally intended to be rendered on a wide variety of systems, so care must be taken in the encoding of non-ASCII characters. In general, any such encoding should be declared using the ‘`encoding`’ section for there to be any hope of correct rendering.

For output, the `outputEncoding` argument will be used: `outputEncoding = ""` will choose the native encoding for the current system.

If the text cannot be converted to the `outputEncoding`, byte substitution will be used (see `iconv`): `Rd2latex` and `Rd2ex` give a warning.

**Note**

The `\Sexpr` macro is a new addition to Rd files. It includes R code that will be executed at one of three times: *build* time (when a package's source code is built into a tarball, not yet implemented), *install* time (when the package is installed or built into a binary package), and *render* time (when the man page is converted to a readable format).

Currently only text format man pages render when displayed; all other formats render when installed.

For example, this man page was:

1. built on

```
\Sexpr[stage=build]{format(Sys.time(), "%Y-%m-%d at %H:%M:%S")}
```

2. installed on 2010-05-31 at 13:13:25, and

3. rendered on 2010-05-31 at 15:14:09.

Because build-time execution is not yet supported, the first of these will display as a macro; the other two may or may not, depending on the build of R. (Note that escapes, e.g. for '%', may not be identical in this display, but the displayed Rd code should parse to the same object.)

**Author(s)**

Duncan Murdoch, Brian Ripley

**References**

<http://developer.r-project.org/parseRd.pdf>

**See Also**

[parse\\_Rd](#), [checkRd](#), [findHTMLlinks](#).

**Examples**

```
## Not run:
## Simulate install and rendering of this page in HTML and text format:

Rd <- file.path("src/library/tools/Rd2HTML.Rd")

outfile <- paste(tempfile(), ".html", sep="")
browseURL(Rd2HTML(Rd, outfile, package="tools", stages=c("install", "render")))

outfile <- paste(tempfile(), ".txt", sep="")
file.show(Rd2txt(Rd, outfile, package="tools", stages=c("install", "render")))

checkRd(con) # A stricter test than Rd2HTML uses

## End(Not run)
```

---

`Rdiff`*Difference R Output Files*

---

**Description**

Given two R output files, compute differences ignoring headers, footers and some encoding differences.

**Usage**

```
Rdiff(from, to, useDiff = FALSE, forEx = FALSE)
```

**Arguments**

<code>from, to</code>	filepaths to be compared
<code>useDiff</code>	should <code>diff</code> always be used to compare results?
<code>forEx</code>	logical: extra pruning for ‘-Ex.Rout’ files to exclude the header.

**Details**

The R startup banner and any timing information from R CMD BATCH are removed from both files, together with lines about loading packages. UTF-8 fancy quotes (see [sQuote](#)) and on Windows, Windows so-called ‘smart quotes’ are mapped to a simple quote. The files are then compared line-by-line. If there are the same number of lines and `useDiff` is false, a simple `diff`-like display of differences is printed, otherwise `diff -bw` is called on the edited files.

**Value**

0L if no differences were found, otherwise 1L

**See Also**

The shell script run as R CMD Rdiff.

---

`Rdindex`*Generate Index from Rd Files*

---

**Description**

Print a 2-column index table with names and titles from given R documentation files to a given output file or connection. The titles are nicely formatted between two column positions (typically 25 and 72, respectively).

**Usage**

```
Rdindex(RdFiles, outFile = "", type = NULL,  
        width = 0.9 * getOption("width"), indent = NULL)
```

**Arguments**

RdFiles	a character vector specifying the Rd files to be used for creating the index, either by giving the paths to the files, or the path to a single directory with the sources of a package.
outFile	a connection, or a character string naming the output file to print to. "" (the default) indicates output to the console.
type	a character string giving the documentation type of the Rd files to be included in the index, or NULL (the default). The type of an Rd file is typically specified via the <code>\docType</code> tag; if <code>type</code> is "data", Rd files whose <i>only</i> keyword is <code>datasets</code> are included as well.
width	a positive integer giving the target column for wrapping lines in the output.
indent	a positive integer specifying the indentation of the second column. Must not be greater than <code>width/2</code> , and defaults to <code>width/3</code> .

**Details**

If a name is not a valid alias, the first alias (or the empty string if there is none) is used instead.

---

RdTextFilter	<i>Select text in an Rd file.</i>
--------------	-----------------------------------

---

**Description**

This function blanks out all non-text in an Rd file, for spell checking or other uses.

**Usage**

```
RdTextFilter(ifile, encoding = "unknown", keepSpacing = TRUE,
             drop = character(), keep = character())
```

**Arguments**

ifile	An input file specified as a filename or connection, or an "Rd" object from <a href="#">parse_Rd</a> .
encoding	An encoding name to pass to <a href="#">parse_Rd</a> .
keepSpacing	Whether to try to leave the text in the same lines and columns as in the original file.
drop	Additional sections of the Rd to drop.
keep	Sections of the Rd file to keep.

**Details**

This function parses the Rd file, then walks through it, element by element. Items with tag "TEXT" are kept in the same position as they appeared in the original file, while other parts of the file are replaced with blanks, so a spell checker such as [aspell](#) can check only the text and report the position in the original file. (If `keepSpacing` is `FALSE`, blank filling will not occur, and text will not be output in its original location.)

By default, the tags `c("\docType", "\encoding", "\keyword", "\email", "\file", "\linkS4class", "\pkg", "\var", "\method", "\S3method", "\S4method", "\link")` are skipped. Additional tags can be skipped by listing them in the `drop` argument; listing tags in the `keep` argument will stop them from being skipped. It is also possible to keep any of the `c("RCODE", "COMMENT", "VERB")` tags, which correspond to R-like code, comments, and verbatim text respectively, or to drop "TEXT".

### Value

A character vector which if written to a file, one element per line, would duplicate the text elements of the original Rd file.

### Note

The filter attempts to merge text elements into single words when markup in the Rd file is used to highlight just the start of a word.

### Author(s)

Duncan Murdoch

### See Also

[aspell](#), for which this is an acceptable filter.

---

Rdutils

*Rd Utilities*

---

### Description

Utilities for computing on the information in Rd objects.

### Usage

```
Rd_db(package, dir, lib.loc = NULL)
```

### Arguments

<code>package</code>	a character string naming an installed package.
<code>dir</code>	a character string specifying the path to a package's root source directory. This should contain the subdirectory 'man' with R documentation sources (in Rd format). Only used if <code>package</code> is not given.
<code>lib.loc</code>	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. The specified library trees are used to search for <code>package</code> .

### Details

`Rd_db` builds a simple database of all Rd objects in a package, as a list of the results of running [parse\\_Rd](#) on the Rd source files in the package and processing platform conditionals.

**Warning**

Rd\_db is still experimental. Names, interface and value might change in future versions.

**See Also**

[parse\\_Rd](#)

**Examples**

```
## Build the Rd db for the (installed) base package.
db <- Rd_db("base")

## Keyword metadata per Rd object.
keywords <- lapply(db, tools:::Rd_get_metadata, "keyword")
## Tabulate the keyword entries.
kw_table <- sort(table(unlist(keywords)))
## The 5 most frequent ones:
rev(kw_table)[1 : 5]
## The "most informative" ones:
kw_table[kw_table == 1]

## Concept metadata per Rd file.
concepts <- lapply(db, tools:::Rd_get_metadata, "concept")
## How many files already have \concept metadata?
sum(sapply(concepts, length) > 0)
## How many concept entries altogether?
length(unlist(concepts))
```

---

read.00Index

*Read 00Index-style Files*

---

**Description**

Read item/description information from 00Index-style files. Such files are description lists rendered in tabular form, and currently used for the 'INDEX' and 'demo/00Index' files of add-on packages.

**Usage**

```
read.00Index(file)
```

**Arguments**

**file** the name of a file to read data values from. If the specified file is "", then input is taken from the keyboard (in this case input can be terminated by a blank line). Alternatively, **file** can be a [connection](#), which will be opened if necessary, and if so closed at the end of the function call.

**Value**

A character matrix with 2 columns named "Item" and "Description" which hold the items and descriptions.

**See Also**

[formatDL](#) for the inverse operation of creating a 00Index-style file from items and their descriptions.

---

readNEWS

*Read R's NEWS file or a similar one*


---

**Description**

Read R's 'NEWS' file or a similarly formatted one. This is an experimental feature, new in R 2.4.0 and may change in several ways.

**Usage**

```
readNEWS(file = file.path(R.home(), "NEWS"), trace = FALSE,
          chop = c("first", "1", "par1", "keepAll"))
checkNEWS(file = file.path(R.home(), "NEWS"))
```

**Arguments**

file	the name of the file which the data are to be read from. Alternatively, file can be a <a href="#">connection</a> , which will be opened if necessary, and can also be a complete URL. For more details, see the file argument of <a href="#">read.table</a> .
trace	logical indicating if the recursive reading should be traced, i.e., print what it is doing.
chop	a character string specifying how the news entries should be <i>chopped</i> ; chop = "keepAll" saves the full entries.

**Details**

`readNEWS()` reads a NEWS file; `checkNEWS()` checks for common errors in formatting. Currently it detects an incorrect number of spaces before the "o" item marker.

If non-ASCII characters are needed, the NEWS file may be encoded in UTF-8 with a byte-order mark (BOM) at the beginning, which `readNEWS()` will recognize. Other encodings will display incorrectly on some systems. However, BOMs are discouraged on many systems and not all editors recognize them, so NEWS files should normally be written in ASCII.

**Value**

`readNEWS()` returns an (S3) object of class "newsTree"; effectively a [list](#) of lists which is a tree of NEWS entries.

`checkNEWS()` returns TRUE if no suspected errors are found, or prints a message for each suspected error and returns FALSE.

Note that this is still experimental and may change in the future.



**Examples**

```

NEWStr <- readNEWS(trace = TRUE)# chop = "first" (= "first non-empty")
## keep the full NEWS entry text i.e. "no chopping":
NEWStrA <- readNEWS(chop = "keepAll")
object.size(NEWStr)
object.size(NEWStrA) ## (no chopping) ==> about double the size

str(NEWStr, max.level = 3)

str(NEWStr[[c("2.3", "2.3.1")]], max.level=2, vec.len=1)

NEWStr [[c("2.3", "2.3.1", "NEW FEATURES")]]
NEWStrA[[c("2.4", "2.4.0", "NEW FEATURES")]]

# Check the current NEWS file

stopifnot(checkNEWS())

```

---

showNonASCII

*Highlight non-ASCII characters*


---

**Description**

This function prints elements of a character vector which contain non-ASCII bytes, printing such bytes as an escape like '<fc>'.

**Usage**

```
showNonASCII(x)
```

**Arguments**

`x` a character vector.

**Details**

This was originally written to help detect non-portable text in files in packages.

It prints all lines of the files which contain non-ASCII characters, preceded by the line number and with non-ASCII bytes highlighted *via* `iconv(sub = "byte")`.

**Value**

The elements of `x` containing non-ASCII characters will be returned invisibly.

**Examples**

```

out <- c(
"fa\xe7ile test of showNonASCII():",
"\details{",
"  This is a good line",
"  This has an \xfcmlaut in it.",
"  OK again.",

```

```
"}")
f <- tempfile()
cat(out, file = f, sep = "\n")

showNonASCII(readLines(f))
unlink(f)
```

---

startDynamicHelp    *Start the Dynamic HTML Help System*

---

## Description

This function starts the internal help server, so that HTML help pages are rendered when requested.

## Usage

```
startDynamicHelp(start=TRUE)
```

## Arguments

`start`            logical: whether to start or shut down the dynamic help system.

## Details

This function starts the internal HTTP server, which runs on the loopback interface (127.0.0.1). If `options("help.ports")` is set to a vector of integer values, `startDynamicHelp` will try those ports in order; otherwise, it tries up to 10 random ports to find one not in use. It can be disabled by setting the environment variable `R_DISABLE_HTTPD` to a non-empty value.

`startDynamicHelp` is called by functions that need to use the server, so would rarely be called directly by a user.

Note that `options(help_type="html")` must be set to actually make use of HTML help, although it might be the default for an R installation.

If the server cannot be started or is disabled, `help.start` will be unavailable and requests for HTML help will give text help (with a warning).

The browser in use does need to be able to connect to the loopback interface: occasionally it is set to use a proxy for HTTP on all interfaces, which will not work – the solution is to add an exception for 127.0.0.1.

## Value

The chosen port number is returned invisibly (which will be 0 if the server has been stopped).

## See Also

`help.start` and `help(help_type = "html")` will attempt to start the HTTP server if required

`Rd2HTML` is used to render the package help pages.

---

SweaveTeXFilter      *Strip R code out of Sweave file*

---

### Description

This function blanks out code chunks and Noweb markup in an Sweave input file, for spell checking or other uses.

### Usage

```
SweaveTeXFilter(ifile, encoding = "unknown")
```

### Arguments

<code>ifile</code>	Input file or connection.
<code>encoding</code>	Text encoding to pass to <code>readLines</code> .

### Details

This function blanks out all Noweb markup and code chunks from an Sweave input file, leaving behind the LaTeX source, so that a LaTeX-aware spelling checker can check it and report errors in their original locations.

### Value

A character vector which if written to a file, one element per line, would duplicate the text elements of the original Rd file.

### Author(s)

Duncan Murdoch

### See Also

`aspell`, for which this is used with `filter="Sweave"`.

---

testInstalledPackage  
*Test Installed Packages*

---

### Description

These functions allow an installed package to be tested, or all base and recommended packages.

**Usage**

```
testInstalledPackage(pkg, lib.loc = NULL, outDir = ".",
                    types = c("examples", "tests", "vignettes"))

testInstalledPackages(outDir = ".", errorsAreFatal = TRUE,
                    scope = c("both", "base", "recommended"),
                    types = c("examples", "tests", "vignettes"))

testInstalledBasic(scope = c("basic", "devel", "both"))
```

**Arguments**

<code>pkg</code>	name of an installed package.
<code>lib.loc</code>	library path(s) in which to look for the package. See <a href="#">library</a> .
<code>outDir</code>	the directory into which to write the output files: this should already exist.
<code>types</code>	type(s) of tests to be done.
<code>errorsAreFatal</code>	logical: should testing terminate at the first error?
<code>scope</code>	Which set(s) should be tested?

**Details**

These tests depend on having the package example files installed (which is the default). If package-specific tests are found in a ‘tests’ directory they can be tested: these are not installed by default, but will be if `R CMD INSTALL --install-tests` was used. Finally, the R code in any vignettes can be extracted and tested.

Package tests are run in a ‘*pkg-tests*’ subdirectory of ‘`outDir`’, and leave their output there.

`testInstalledBasic` runs the basic tests, if installed. This should be run with `LC_COLLATE=C` set: the function tries to set this by it may not work on all OSes.

The package-specific tests for the base and recommended packages are not normally installed, but make `install-tests` is provided to do so (as well as the basic tests).

**Value**

Invisibly 0L for success, 1L for failure.

---

 texi2dvi

*Compile LaTeX Files*


---

**Description**

Run `latex` and `bibtex` until all cross-references are resolved and create either a dvi or PDF file.

**Usage**

```
texi2dvi(file, pdf = FALSE, clean = FALSE, quiet = TRUE,
        texi2dvi = getOption("texi2dvi"), texinputs = NULL)
```

**Arguments**

<code>file</code>	character. Name of LaTeX source file.
<code>pdf</code>	logical. If TRUE, a PDF file is produced instead of the default dvi file ( <code>texi2dvi</code> command line option <code>--pdf</code> ).
<code>clean</code>	logical. If TRUE, all auxiliary files are removed ( <code>texi2dvi</code> command line option <code>--clean</code> ). May not work on some platforms.
<code>quiet</code>	logical. No output unless an error occurs. Ignored if emulation (see the <code>texi2dvi</code> argument) is used.
<code>texi2dvi</code>	character (or NULL). Script or program used to compile a TeX file to dvi or PDF, respectively. The default (selected by "" or NULL) is to look for an executable on the search path and otherwise emulate the script with <code>system</code> calls.
<code>texinputs</code>	NULL or a character vector of paths to add to the LaTeX and bibtex input search paths.

**Details**

Despite the name, this is used in R to compile LaTeX files, specifically those generated from vignettes. It ensures that the `'R_HOME/share/texmf'` directory is in the `TEXINPUTS` path, so R style files such as `'Sweave'` and `'Rd'` will be found. The search path used is first the existing `TEXINPUTS` setting (or the current directory if unset), then elements of `texinputs`, then `'R_HOME/share/texmf'` and finally the default path. Analogous changes are made to `BIBINPUTS` and `BSTINPUTS` settings.

MiKTeX has a `texi2dvi` executable but no other Windows TeX installation that we know of does, so emulation is used on e.g. TeXLive installations.

**Author(s)**

Achim Zeileis and R-core

---

toHTML

*Display an object in HTML.*

---

**Description**

This generic function generates a complete HTML page from an object.

**Usage**

```
toHTML(x, ...)
## S3 method for class 'packageIQR':
toHTML(x, ...)
## S3 method for class 'news_db':
toHTML(x, ...)
```

**Arguments**

<code>x</code>	An object to display.
<code>...</code>	Optional parameters for methods; the <code>"packageIQR"</code> and <code>"news_db"</code> methods pass these to <code>HTMLheader</code> .

**Value**

A character vector to display the object `x`. The `"packageIQR"` method is designed to display lists in the R help system.

**See Also**

[HTMLheader](#)

**Examples**

```
cat(toHTML(demo(package="base")), sep="\n")
```

---

tools-deprecated      *Deprecated Objects in Package tools*

---

**Description**

The functions or variables listed here are provided for compatibility with older versions of R only, and may be defunct as soon as of the next release.

**See Also**

[Deprecated](#), [Defunct](#)

---

undoc      *Find Undocumented Objects*

---

**Description**

Finds the objects in a package which are undocumented, in the sense that they are visible to the user (or data objects or S4 classes provided by the package), but no documentation entry exists.

**Usage**

```
undoc(package, dir, lib.loc = NULL)
```

**Arguments**

<code>package</code>	a character string naming an installed package.
<code>dir</code>	a character string specifying the path to a package's root source directory. This must contain the subdirectory 'man' with R documentation sources (in Rd format), and at least one of the 'R' or 'data' subdirectories with R code or data objects, respectively.
<code>lib.loc</code>	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. The specified library trees are used to search for <code>package</code> .

**Details**

This function is useful for package maintainers mostly. In principle, *all* user-level R objects should be documented.

The **base** package is special as it contains the primitives and these do not have definitions available at code level. We provide equivalent closures in environments `.ArgsEnv` and `.GenericArgsEnv` in the **base** package that are used for various purposes: `undoc("base")` checks that all the primitives that are not language constructs are prototyped in those environments and no others are.

**Value**

An object of class "undoc" which is a list of character vectors containing the names of the undocumented objects split according to documentation type. This representation is still experimental, and might change in future versions.

There is a `print` method for nicely displaying the information contained in such objects.

**See Also**

[codoc](#), [QC](#)

**Examples**

```
undoc("tools")           # Undocumented objects in 'tools'
```

---

`vignetteDepends`      *Retrieve Dependency Information for a Vignette*

---

**Description**

Given a vignette name, will create a `DependsList` object that reports information about the packages the vignette depends on.

**Usage**

```
vignetteDepends(vignette, recursive = TRUE, reduce = TRUE,
                 local = TRUE, lib.loc = NULL)
```

**Arguments**

<code>vignette</code>	The path to the vignette source
<code>recursive</code>	Whether or not to include indirect dependencies
<code>reduce</code>	Whether or not to collapse all sets of dependencies to a minimal value
<code>local</code>	Whether or not to search only locally
<code>lib.loc</code>	What libraries to search in locally

## Details

If `recursive` is `TRUE`, any package that is specified as a dependency will in turn have its dependencies included (and so on), these are known as indirect dependencies. If `recursive` is `FALSE`, only the dependencies directly named by the vignette will be used.

If `local` is `TRUE`, the system will only look at the user's local machine and not online to find dependencies.

If `reduce` is `TRUE`, the system will collapse the fields in the `DependsList` object such that a minimal set of dependencies are specified (for instance if there was `'foo, foo (>= 1.0.0), foo (>= 1.3.0)'`, it would only return `'foo (>= 1.3.0)'`).

## Value

An object of class `"DependsList"`.

## Author(s)

Jeff Gentry

## See Also

[pkgDepends](#)

## Examples

```
## This may not be installed
gridEx <- system.file("doc", "grid.Snw", package = "grid")
vignetteDepends(gridEx)
```

---

write_PACKAGES	<i>Generate PACKAGES files</i>
----------------	--------------------------------

---

## Description

Generate `'PACKAGES'` and `'PACKAGES.gz'` files for a repository of source or Mac/Windows binary packages.

## Usage

```
write_PACKAGES(dir = ".", fields = NULL,
               type = c("source", "mac.binary", "win.binary"),
               verbose = FALSE, unpacked = FALSE, subdirs = FALSE,
               latestOnly = TRUE, addFiles = FALSE)
```

## Arguments

`dir` Character vector describing the location of the repository (directory including source or binary packages) to generate the `'PACKAGES'` and `'PACKAGES.gz'` files from and write them to.



fields	a character vector giving the fields to be used in the 'PACKAGES' and 'PACKAGES.gz' files in addition to the default ones, or NULL (default). The default corresponds to the fields needed by <code>available.packages</code> : "Package", "Version", "Priority", "Depends", "Imports", "LinkingTo", "Suggests", "Enhances", "OS_type", and "License" and those fields will always be included, plus the file name in field "File" if <code>addFile = TRUE</code> and the path to the subdirectory in field "Path" if subdirectories are used.
type	Type of packages: currently source '.tar.gz' archives, and Mac or Windows binary ('.tgz' or '.zip', respectively) packages are supported. Defaults to "win.binary" on Windows and to "source" otherwise.
verbose	logical. Should packages be listed as they are processed?
unpacked	a logical indicating whether the package contents are available in unpacked form or not (default).
subdirs	either logical (to indicate if subdirectories should be included, recursively) or a character vector of name of subdirectories to include.
latestOnly	logical: if multiple versions of a package are available should only the latest version be included?
addFiles	logical: should the filenames be included as field 'File' in the 'PACKAGES' file.

### Details

Including non-latest versions of packages is only useful if they have less constraining version requirements, so for example `latestOnly = FALSE` could be used for a source repository when 'foo\_1.0' depends on 'R >= 2.10.0' but 'foo\_0.9' is available which depends on 'R >= 2.7.0'.

Support for repositories with subdirectories and hence for `subdirs != FALSE` was added in R 2.7.0: this depends on recording a "Path" field in the 'PACKAGES' file.

Support for more general file names (e.g. other types of compression) *via* a "File" field in the 'PACKAGES' file was added in R 2.10.0 and can be used by `download.packages`. If the file names are not of the standard form, use `addFiles = TRUE`.

`type = "win.binary"` uses `unz` connections to read all 'DESCRIPTION' files contained in the (zipped) binary packages for Windows in the given directory `dir`, and builds files 'PACKAGES' and 'PACKAGES.gz' files from this information.

### Value

Invisibly returns the number of packages described in the resulting 'PACKAGES' and 'PACKAGES.gz' files. If 0, no packages were found and no files were written.

### Note

Processing '.tar.gz' archives to extract the 'DESCRIPTION' files is quite slow.

This function can be useful on other OSes to prepare a repository to be accessed by Windows machines, so `type = "win.binary"` should work on all OSes.

### Author(s)

Uwe Ligges and R-core.

**See Also**

See [read.dcf](#) and [write.dcf](#) for reading ‘DESCRIPTION’ files and writing the ‘PACKAGES’ and ‘PACKAGES.gz’ files.

**Examples**

```
## Not run:
write_PACKAGES("c:/myFolder/myRepository") # on Windows
write_PACKAGES("/pub/RWin/bin/windows/contrib/2.9",
               type="win.binary") # on Linux

## End(Not run)
```

xgettext

*Extract Translatable Messages from R Files in a Package***Description**

For each file in the ‘R’ directory (including system-specific subdirectories) of a package, extract the unique arguments passed to [stop](#), [warning](#), [message](#), [gettext](#) and [gettextf](#), or to [ngettext](#).

**Usage**

```
xgettext(dir, verbose = FALSE, asCall = TRUE)

xngettext(dir, verbose = FALSE)

xgettext2pot(dir, potFile)
```

**Arguments**

<code>dir</code>	the directory of a source package.
<code>verbose</code>	logical: should each file be listed as it is processed?
<code>asCall</code>	logical: if TRUE each argument is returned whole, otherwise the strings within each argument are extracted.
<code>potFile</code>	name of po template file to be produced. Defaults to ‘R- <i>pkgname</i> .pot’ where <i>pkgname</i> is the basename of ‘dir’.

**Details**

Leading and trailing white space (space, tab and linefeed) is removed for calls to [gettext](#), [gettextf](#), [stop](#), [warning](#), and [message](#), as it is by the internal code that passes strings for translation.

We look to see if these functions were called with `domain = NA` and if so omit the call if `asCall = TRUE`: note that the call might contain a call to [gettext](#) which would be visible if `asCall = FALSE`.

`xgettext2pot` calls `xgettext` and then `xngettext`, and writes a PO template file for use with the **GNU Gettext** tools. This ensures that the strings for simple translation are unique in the file (as **GNU Gettext** requires), but does not do so for `ngettext` calls (and the rules are not stated in the Gettext manual).

If applied to the **base** package, this also looks in the ‘.R’ files in ‘[R\\_HOME](#)/share/R’.

**Value**

For `xgettext`, a list of objects of class `"xgettext"` (which has a `print` method), one per source file that potentially contains translatable strings.

For `xngettext`, a list of objects of class `"xngettext"`, which are themselves lists of length-2 character strings.

**Examples**

```
## Not run: ## in a source-directory build of R:  
xgettext(file.path(R.home(), "src", "library", "splines"))  
  
## End(Not run)
```

## Chapter 9

# The `utils` package

---

`utils-package`      *The R Utils Package*

---

### Description

R utility functions

### Details

This package contains a collection of utility functions.  
For a complete list, use `library(help="utils")`.

### Author(s)

R Development Core Team and contributors worldwide  
Maintainer: R Core Team <R-core@r-project.org>

---

`alarm`      *Alert the User*

---

### Description

Gives an audible or visual signal to the user.

### Usage

```
alarm()
```

### Details

`alarm()` works by sending a `"\a"` character to the console. On most platforms this will ring a bell, beep, or give some other signal to the user (unless standard output has been redirected).

**Value**

No useful value is returned.

**Examples**

```
alarm()
```

---

```
apropos
```

*Find Objects by (Partial) Name*

---

**Description**

`apropos()` returns a character vector giving the names of all objects in the search list matching `what`.

`find()` is a different user interface to the same task.

**Usage**

```
apropos(what, where = FALSE, ignore.case = TRUE, mode = "any")
```

```
find(what, mode = "any", numeric = FALSE, simple.words = TRUE)
```

**Arguments**

<code>what</code>	character string with name of an object, or more generally a <a href="#">regular expression</a> to match against.
<code>where, numeric</code>	a logical indicating whether positions in the search list should also be returned
<code>ignore.case</code>	logical indicating if the search should be case-insensitive, TRUE by default. Note that in R versions prior to 2.5.0, the default was implicitly <code>ignore.case = FALSE</code> .
<code>mode</code>	character; if not "any", only objects whose <code>mode</code> equals <code>mode</code> are searched.
<code>simple.words</code>	logical; if TRUE, the <code>what</code> argument is only searched as whole word.

**Details**

If `mode != "any"` only those objects which are of `mode mode` are considered. If `where` is TRUE, the positions in the search list are returned as the `names` attribute.

`find` is a different user interface for the same task as `apropos`. However, by default (`simple.words == TRUE`), only full words are searched with [grep](#) (`fixed = TRUE`).

**Value**

For `apropos` character vector, sorted by name, possibly with names giving the (numerical) positions on the search path.

For `find`, either a character vector of environment names, or for `numeric = TRUE`, a numerical vector of positions on the search path, with names giving the names of the corresponding environments.

**Author(s)**

Kurt Hornik and Martin Maechler (May 1997).

**See Also**

[glob2rx](#) to convert wildcard patterns to regular expressions.

[objects](#) for listing objects from one place, [help.search](#) for searching the help system, [search](#) for the search path.

**Examples**

```
require(stats)

## Not run: apropos("lm")
apropos("GLM") # more than a dozen
## that may include internal objects starting '.__C__' if
## methods is attached
apropos("GLM", ignore.case = FALSE) # not one
apropos("lq")

cor <- 1:pi
find("cor") #> ".GlobalEnv" "package:stats"
find("cor", numeric=TRUE) # numbers with these names
find("cor", numeric=TRUE, mode="function") # only the second one
rm(cor)

## Not run: apropos(".", mode="list") # a long list

# need a DOUBLE backslash '\\\'' (in case you don't see it anymore)
apropos("\\[")

## Not run: # everything
length(apropos("."))

# those starting with 'pr'
apropos("^pr")

# the 1-letter things
apropos("^.?$")
# the 1-2-letter things
apropos("^..?$")
# the 2-to-4 letter things
apropos("^{2,4}$")

# the 8-and-more letter things
apropos("^{8,}$")
table(nchar(apropos("^{8,}$")))

## End(Not run)
```

aspell

*Aspell Interface***Description**

Spell check given files via Aspell.

**Usage**

```
aspell(files, filter, control = list(), encoding = "unknown")
```

**Arguments**

<code>files</code>	a character vector with the names of files to be checked.
<code>filter</code>	an optional filter for processing the files before spell checking, given as either a function (with formals <code>ifile</code> and <code>encoding</code> ), or a character string specifying a built-in filter, or a list with the name of a built-in filter and additional arguments to be passed to it. See <b>Details</b> for available filters. If missing or <code>NULL</code> , no filtering is performed.
<code>control</code>	a list or character vector of control options for Aspell.
<code>encoding</code>	the encoding of the files. Recycled as needed.

**Details**

It is assumed that the Aspell executable `aspell` is available in the system search path. See <http://aspell.net> for information on obtaining Aspell, and available dictionaries.

Currently the only available built-in filters are "Rd", corresponding to `RdTextFilter`, and "Sweave", corresponding to `SweaveTeXFilter`.

The print method has for the objects returned by `aspell` has an `indent` argument controlling the indentation of the positions of possibly mis-spelled words. The default is 2; Emacs users may find it useful to use an indentation of 0 and visit output in `grep-mode`.

**Value**

A data frame inheriting from `aspell` (which has a useful print method) with the information about possibly mis-spelled words.

**See Also**

Package **Aspell** on Omegahat (<http://www.omegahat.org/Aspell>) for a fine-grained R interface to the Aspell library.

**Examples**

```
## Not run:
# To check all Rd files in a directory, skipping the \references sections
files <- Sys.glob("*.Rd")
aspell(files, filter=list("Rd", drop="\references"))

# To check all Sweave files
files <- Sys.glob(c("*.Rnw", "*.Snw", "*.rnw", "*.snw"))
```

```

aspell(files, filter="Sweave", control="--mode=tex")

# To check all Texinfo files
files <- Sys.glob("*.texi")
aspell(files, control="--mode=texinfo")

## End(Not run)

```

---

available.packages *List Available Packages at CRAN-like Repositories*

---

## Description

`available.packages` returns a matrix of details corresponding to packages currently available at one or more repositories. The current list of packages is downloaded over the internet (or copied from a local mirror).

## Usage

```

available.packages(contriburl = contrib.url(getOption("repos"), type),
                  method, fields = NULL,
                  type = getOption("pkgType"),
                  filters = NULL)

```

## Arguments

<code>contriburl</code>	URL(s) of the ‘contrib’ sections of the repositories. Specify this argument only if your repository mirror is incomplete, e.g., because you burned only the ‘contrib’ section on a CD.
<code>method</code>	download method, see <a href="#">download.file</a> .
<code>type</code>	character string, indicate which type of packages: see <a href="#">install.packages</a> .
<code>fields</code>	a character vector giving the fields to extract from the ‘PACKAGES’ file(s) in addition to the default ones, or <code>NULL</code> (default). Unavailable fields result in <code>NA</code> values.
<code>filters</code>	a character vector or list or <code>NULL</code> (default). See ‘Details’.

## Details

By default, this includes only packages whose version and OS type requirements are met by the running version of R, and only information on the latest versions of packages with duplicates removed.

As from R 2.10.0 argument `filters` used to select which of the packages on the repositories are reported. It is called with its default value (`NULL`) by functions such as `install.packages`: this value corresponds to `getOption("available_packages_filters")` and to `c("R_version", "OS_type", "duplicates")` if that is unset or set to `NULL`.

The built-in filters are

"R\_version" exclude packages whose R version requirements are not met



"OS\_type" exclude packages whose OS requirement is incompatible with this version of R: that is exclude Windows-only packages on a Unix-alike platform and *vice versa*.

"duplicates" only report the latest version where more than one version is available, and only report the first-named repository (in `contriburl`) with the latest version if that is in more than one repository.

"license/FOSS" include only packages for which installation can proceed solely based on packages which can be verified as Free or Open Source Software (FOSS, e.g., <http://en.wikipedia.org/wiki/FOSS>) employing the available license specifications. Thus both the package and any packages that it depends on to load need to be *known to be* FOSS.

If all the filters are from this set they can be specified as a character vector; otherwise `filters` should be a list with elements which are character strings, user-defined function or `add = TRUE`.

User-defined filters are functions which take a single argument, a matrix of the form returned by `available.packages`, and return a matrix with a subset of the rows of the argument.

The special 'filter' `add=TRUE` appends the other elements of the filter list to the default filters.

### Value

A matrix with one row per package, row names the package names and column names "Package", "Version", "Priority", "Depends", "Imports", "LinkingTo", "Suggests", "Enhances", "OS\_type", "License", "File" and "Repository". Additional columns can be specified using the `fields` argument.

### See Also

[install.packages](#), [download.packages](#), [contrib.url](#).

The 'R Installation and Administration' manual for how to set up a repository.

BATCH

*Batch Execution of R*

### Description

Run R non-interactively with input from `infile` and send output (stdout/stderr) to another file.

### Usage

```
R CMD BATCH [options] infile [outfile]
```

### Arguments

<code>infile</code>	the name of a file with R code to be executed.
<code>options</code>	a list of R command line options, e.g., for setting the amount of memory available and controlling the load/save process. If <code>infile</code> starts with a '-', use '--' as the final option. The default options are '--restore --save --no-readline'.
<code>outfile</code>	the name of a file to which to write output. If not given, the name used is that of <code>infile</code> , with a possible '.R' extension stripped, and '.Rout' appended.

## Details

Use `R CMD BATCH --help` to be reminded of the usage.

By default, the input commands are printed along with the output. To suppress this behavior, add `options(echo = FALSE)` at the beginning of `infile`, or use option `'--slave'`.

The `infile` can have end of line marked by LF or CRLF (but not just CR), and files with an incomplete last line (missing end of line (EOL) mark) are processed correctly.

A final expression `'proc.time()'` will be executed after the input script unless the latter calls `q(runLast=FALSE)` or is aborted. This can be suppressed by the option `'--no-timing'`.

Additional options can be set by the environment variable `R_BATCH_OPTIONS`: these come after `'--restore --save --no-readline'` and before any options given on the command line.

## Note

Unlike `Splus BATCH`, this does not run the R process in the background. In most shells, `R CMD BATCH [options] infile [outfile] &` will do so.

Report bugs to [r-bugs@r-project.org](mailto:r-bugs@r-project.org).

---

 browseEnv

*Browse Objects in Environment*


---

## Description

The `browseEnv` function opens a browser with list of objects currently in `sys.frame()` environment.

## Usage

```
browseEnv(envir = .GlobalEnv, pattern,
          excludepatt = "^last\\.warning",
          html = .Platform$OS.type != "mac",
          expanded = TRUE, properties = NULL,
          main = NULL, debugMe = FALSE)
```

## Arguments

<code>envir</code>	an <a href="#">environment</a> the objects of which are to be browsed.
<code>pattern</code>	a <a href="#">regular expression</a> for object subselection is passed to the internal <code>ls()</code> call.
<code>excludepatt</code>	a regular expression for <i>dropping</i> objects with matching names.
<code>html</code>	is used on non Macintosh machines to display the workspace on a HTML page in your favorite browser.
<code>expanded</code>	whether to show one level of recursion. It can be useful to switch it to <code>FALSE</code> if your workspace is large. This option is ignored if <code>html</code> is set to <code>FALSE</code> .
<code>properties</code>	a named list of global properties (of the objects chosen) to be showed in the browser; when <code>NULL</code> (as per default), user, date, and machine information is used.
<code>main</code>	a title string to be used in the browser; when <code>NULL</code> (as per default) a title is constructed.
<code>debugMe</code>	logical switch; if true, some diagnostic output is produced.

**Details**

Very experimental code. Only allows one level of recursion into object structures. The HTML version is not dynamic.

It can be generalized. See sources ('.../library/base/R/databrowser.R') for details.

`wsbrowser()` is currently just an internally used function; its argument list will certainly change.

Most probably, this should rather work through using the 'tkWidget' package (from [www.Bioconductor.org](http://www.Bioconductor.org)).

**See Also**

`str`, `ls`.

**Examples**

```
if(interactive()) {
  ## create some interesting objects :
  ofa <- ordered(4:1)
  ex1 <- expression(1+ 0:9)
  ex3 <- expression(u,v, 1+ 0:9)
  example(factor, echo = FALSE)
  example(table, echo = FALSE)
  example(ftable, echo = FALSE)
  example(lm, echo = FALSE, ask = FALSE)
  example(str, echo = FALSE)

  ## and browse them:
  browseEnv()

  ## a (simple) function's environment:
  af12 <- approxfun(1:2, 1:2, method = "const")
  browseEnv(envir = environment(af12))
}
```

---

browseURL

*Load URL into a WWW Browser*

---

**Description**

Load a given URL into a WWW browser.

**Usage**

```
browseURL(url, browser = getOption("browser"), encodeIfNeeded = FALSE)
```

**Arguments**

<code>url</code>	a non-empty character string giving the URL to be loaded.
<code>browser</code>	a non-empty character string giving the name of the program to be used as hypertext browser. It should be in the PATH, or a full path specified. Alternatively, an R function to be called to invoke the browser. Under Windows NULL is also allowed (and is the default), and implies that the file association mechanism will be used.

encodeIfNeeded

Should the URL be encoded by `URLencode` before passing to the browser? This is not needed (and might be harmful) if the `browser` program/function itself does encoding, and can be harmful for `'file://'` URLs on some systems and for `'http://'` URLs passed to some CGI applications. Fortunately, most URLs do not need encoding.

## Details

The default browser is set by option `"browser"`, in turn set by the environment variable `R_BROWSER` which is by default set in file `'R_HOME/etc/Renviron'` to a choice made manually or automatically when R was configured. (See [Startup](#) for where to override that default value.)

If `browser` supports remote control and R knows how to perform it, the URL is opened in any already running browser or a new one if necessary. This mechanism currently is available for browsers which support the `"-remote openURL(...)"` interface (which includes Mozilla  $\geq$  0.9.5 and Mozilla Firefox), Galeon, KDE konqueror (*via* `kfmclient`) and the GNOME interface to Mozilla. Note that the type of browser is determined from its name, so this mechanism will only be used if the browser is installed under its canonical name.

Because `"-remote"` will use any browser displaying on the X server (whatever machine it is running on), the remote control mechanism is only used if `DISPLAY` points to the local host. This may not allow displaying more than one URL at a time from a remote host.

It is the caller's responsibility to encode `url` if necessary (see [URLencode](#)). This can be tricky for file URLs, where the format accepted can depend on the browser and OS.

## Examples

```
## Not run: ## for KDE users who want to open files in a new tab
options(browser="kfmclient newTab")
browseURL("http://www.r-project.org")

## End(Not run)
```

---

browseVignettes      *List Vignettes in an HTML Browser*

---

## Description

List available vignettes in an HTML browser with links to PDF, LaTeX/noweb source, and (tangled) R code (if available).

## Usage

```
browseVignettes(package = NULL, lib.loc = NULL, all = TRUE)

## S3 method for class 'browseVignettes':
print(x, ...)
```

## Arguments

package	a character vector with the names of packages to search through, or <code>NULL</code> in which "all" packages (as defined by argument <code>all</code> ) are searched.
lib.loc	a character vector of directory names of R libraries, or <code>NULL</code> . The default value of <code>NULL</code> corresponds to all libraries currently known.
all	logical; if <code>TRUE</code> search all available packages in the library trees specified by <code>lib.loc</code> , and if <code>FALSE</code> , search only attached packages.
x	Object of class <code>browseVignettes</code> .
...	Further arguments, ignored by the <code>print</code> method.

## Details

Function `browseVignettes` returns an object of the same class; the `print` method displays it as an HTML page in a browser (using `browseURL`).

## See Also

[browseURL](#), [vignette](#)

## Examples

```
## Not run:
## List vignettes from all *attached* packages
browseVignettes(all = FALSE)

## List vignettes from a specific package
browseVignettes("grid")

## End(Not run)
```

---

bug.report

*Send a Bug Report*

---

## Description

Invokes an editor to write a bug report or opens a web page for bug submission. Some standard information on the current version and configuration of R are included automatically.

## Usage

```
bug.report(subject = "",
           ccaddress = Sys.getenv("USER"),
           method = getOption("mailer"),
           address = "r-bugs@r-project.org",
           file = "R.bug.report",
           package = NULL,
           lib.loc = NULL)
```

**Arguments**

<code>subject</code>	Subject of the email. Please do not use single quotes (‘ ’) in the subject! File separate bug reports for multiple bugs
<code>ccaddress</code>	Optional email address for copies (default is current user). Use <code>ccaddress = FALSE</code> for no copies.
<code>method</code>	Submission method, one of "mailx", "gnudoit", "none", or "ess".
<code>address</code>	Recipient's email address.
<code>file</code>	File to use for setting up the email (or storing it when method is "none" or sending mail fails).
<code>package</code>	Optional character vector naming a single package which is the subject of the bug report.
<code>lib.loc</code>	A character vector describing the location of R library trees in which to search for the package, or NULL. The default value of NULL corresponds to all libraries currently known.

**Details**

If `package` is NULL, invokes an editor to write a bug report and optionally mail it to the automated r-bugs repository at <r-bugs@r-project.org>.

If `package` is specified, it is assumed that the bug report is about that package, and parts of its ‘DESCRIPTION’ file are added to the standard information. If the package has a `BugReports` field in the ‘DESCRIPTION’ file, that URL will be opened using `browseURL`, otherwise an email directed to the package maintainer will be generated.

Currently direct submission of bug reports works only on Unix systems. If the submission method is "mailx", then the default editor is used to write the bug report. Which editor is used can be controlled using `options`, type `getOption("editor")` to see what editor is currently defined. Please use the help pages of the respective editor for details of usage. After saving the bug report (in the temporary file opened) and exiting the editor the report is mailed using a Unix command line mail utility such as `mailx`. A copy of the mail is sent to the current user.

If method is "gnudoit", then an emacs mail buffer is opened and used for sending the email.

If method is "none" or NULL (and in every case on Windows systems), then only an editor is opened to help writing the bug report. The report can then be copied to your favorite email program and be sent to the r-bugs list.

If method is "ess" the body of the mail is simply sent to stdout.

**Value**

Nothing useful.

**When is there a bug?**

If R executes an illegal instruction, or dies with an operating system error message that indicates a problem in the program (as opposed to something like “disk full”), then it is certainly a bug.

Taking forever to complete a command can be a bug, but you must make certain that it was really R’s fault. Some commands simply take a long time. If the input was such that you KNOW it should have been processed quickly, report a bug. If you don’t know whether the command should take a long time, find out by looking in the manual or by asking for assistance.

If a command you are familiar with causes an R error message in a case where its usual definition ought to be reasonable, it is probably a bug. If a command does the wrong thing, that is a bug. But

be sure you know for certain what it ought to have done. If you aren't familiar with the command, or don't know for certain how the command is supposed to work, then it might actually be working right. Rather than jumping to conclusions, show the problem to someone who knows for certain.

Finally, a command's intended definition may not be best for statistical analysis. This is a very important sort of problem, but it is also a matter of judgement. Also, it is easy to come to such a conclusion out of ignorance of some of the existing features. It is probably best not to complain about such a problem until you have checked the documentation in the usual ways, feel confident that you understand it, and know for certain that what you want is not available. The mailing list `r-devel@r-project.org` is a better place for discussions of this sort than the bug list.

If you are not sure what the command is supposed to do after a careful reading of the manual this indicates a bug in the manual. The manual's job is to make everything clear. It is just as important to report documentation bugs as program bugs.

If the online argument list of a function disagrees with the manual, one of them must be wrong, so report the bug.

### How to report a bug

When you decide that there is a bug, it is important to report it and to report it in a way which is useful. What is most useful is an exact description of what commands you type, from when you start R until the problem happens. Always include the version of R, machine, and operating system that you are using; type `version` in R to print this. To help us keep track of which bugs have been fixed and which are still open please send a separate report for each bug.

The most important principle in reporting a bug is to report FACTS, not hypotheses or categorizations. It is always easier to report the facts, but people seem to prefer to strain to posit explanations and report them instead. If the explanations are based on guesses about how R is implemented, they will be useless; we will have to try to figure out what the facts must have been to lead to such speculations. Sometimes this is impossible. But in any case, it is unnecessary work for us.

For example, suppose that on a data set which you know to be quite large the command `data.frame(x, y, z, monday, tuesday)` never returns. Do not report that `data.frame()` fails for large data sets. Perhaps it fails when a variable name is a day of the week. If this is so then when we got your report we would try out the `data.frame()` command on a large data set, probably with no day of the week variable name, and not see any problem. There is no way in the world that we could guess that we should try a day of the week variable name.

Or perhaps the command fails because the last command you used was a `[]` method that had a bug causing R's internal data structures to be corrupted and making the `data.frame()` command fail from then on. This is why we need to know what other commands you have typed (or read from your startup file).

It is very useful to try and find simple examples that produce apparently the same bug, and somewhat useful to find simple examples that might be expected to produce the bug but actually do not. If you want to debug the problem and find exactly what caused it, that is wonderful. You should still report the facts as well as any explanations or solutions.

Invoking R with the `'--vanilla'` option may help in isolating a bug. This ensures that the site profile and saved data files are not read.

A bug report can be generated using the `bug.report()` function. This automatically includes the version information and sends the bug to the correct address. Alternatively the bug report can be emailed to `<r-bugs@r-project.org>` or submitted to the Web page at <http://bugs.r-project.org>.

Bug reports on **contributed packages** should be sent to the package maintainer rather than to `r-bugs`, by specifying the `package` argument to `bug.report()`.

**Author(s)**

This help page is adapted from the Emacs manual and the R FAQ

**See Also**

[help.request](#) which you possibly should try *before* `bug.report`. The R FAQ, also `sessionInfo()` from which you may add to the bug report.

---

capture.output      *Send Output to a Character String or File*

---

**Description**

Evaluates its arguments with the output being returned as a character string or sent to a file. Related to `sink` in the same way that `with` is related to `attach`.

**Usage**

```
capture.output(..., file = NULL, append = FALSE)
```

**Arguments**

<code>...</code>	Expressions to be evaluated.
<code>file</code>	A file name or a connection, or <code>NULL</code> to return the output as a character vector. If the connection is not open, it will be opened initially and closed on exit.
<code>append</code>	logical. If <code>file</code> a file name or unopened connection, append or overwrite?

**Details**

An attempt is made to write output as far as possible to `file` if there is an error in evaluating the expressions, but for `file = NULL` all output will be lost.

**Value**

A character string (if `file=NULL`), or invisible `NULL`.

**See Also**

[sink](#), [textConnection](#)

**Examples**

```
require(stats)
glmout <- capture.output(example(glm))
glmout[1:5]
capture.output(1+1, 2+2)
capture.output({1+1; 2+2})
## Not run:
## on Unix with enscript available
ps <- pipe("enscript -o tempout.ps", "w")
capture.output(example(glm), file=ps)
close(ps)

## End(Not run)
```



---

chooseBioCmirror *Select a Bioconductor Mirror*

---

### Description

Interact with the user to choose a Bioconductor mirror.

### Usage

```
chooseBioCmirror(graphics = getOption("menu.graphics"))
```

### Arguments

`graphics` Logical. If true, use a graphical list: on Windows or Mac OS X GUI use a list box, and on a Unix-alike if package `tk` and an X server are available, use a Tk widget. Otherwise use a text [menu](#).

### Details

This sets the option `"BioC_mirror"`: it needs to be used before a call to [setRepositories](#). Currently the Bioconductor master site (in Seattle, USA), NIH (Bethesda, USA) and the European mirror in Dortmund, Germany are available to select from.

### Value

None: this function is invoked for its side effect of updating options (`"BioC_mirror"`).

### See Also

[setRepositories](#), [chooseCRANmirror](#).

---

chooseCRANmirror *Select a CRAN Mirror*

---

### Description

Interact with the user to choose a CRAN mirror.

### Usage

```
chooseCRANmirror(graphics = getOption("menu.graphics"))
```

```
getCRANmirrors(all = FALSE, local.only = FALSE)
```

### Arguments

`graphics` Logical. If true, use a graphical list: on Windows or Mac OS X GUI use a list box, and on a Unix-alike if package `tk` and an X server are available, use a Tk widget. Otherwise use a text [menu](#).

`all` Logical, get all known mirrors or only the ones flagged as OK.

`local.only` Logical, try to get most recent list from CRAN or use file on local disk only.

**Details**

A list of mirrors is stored in file '`R_HOME/doc/CRAN_mirrors.csv`', but first an on-line list of current mirrors is consulted, and the file copy used only if the on-line list is inaccessible.

This function was originally written to support a Windows GUI menu item, but is also called by `contrib.url` if it finds the initial dummy value of `options("repos")`.

**Value**

None for `chooseCRANmirror()`, this function is invoked for its side effect of updating `options("repos")`.

`getCRANmirrors()` returns a data frame with mirror information.

**See Also**

`setRepositories`, `chooseBioCmirror`, `contrib.url`.

---

 citation

*Citing R and R Packages in Publications*


---

**Description**

How to cite R and R packages in publications.

**Usage**

```
citation(package = "base", lib.loc = NULL)
## S3 method for class 'citation':
toBibtex(object, ...)
## S3 method for class 'citationList':
toBibtex(object, ...)
```

**Arguments**

<code>package</code>	a character string with the name of a single package. An error occurs if more than one package name is given.
<code>lib.loc</code>	a character vector with path names of R libraries, or <code>NULL</code> . The default value of <code>NULL</code> corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries.
<code>object</code>	return object of <code>citation</code> .
<code>...</code>	currently not used.

**Details**

The R core development team and the very active community of package authors have invested a lot of time and effort in creating R as it is today. Please give credit where credit is due and cite R and R packages when you use them for data analysis.

Execute function `citation()` for information on how to cite the base R system in publications. If the name of a non-base package is given, the function either returns the information contained in the `CITATION` file of the package or auto-generates citation information. In the latter case the

package ‘DESCRIPTION’ file is parsed, the resulting citation object may be arbitrarily bad, but is quite useful (at least as a starting point) in most cases.

If only one reference is given, the print method shows both a text version and a BibTeX entry for it, if a package has more than one reference then only the text versions are shown. The BibTeX versions can be obtained using function `toBibtex` (see the examples below).

### Value

An object of class "citationList": see [readCitationFile](#).

### See Also

[citEntry](#)

### Examples

```
## the basic R reference
citation()

## references for a package -- might not have these installed
if(nchar(system.file(package="lattice"))) citation("lattice")
if(nchar(system.file(package="foreign"))) citation("foreign")

## extract the bibtex entry from the return value
x <- citation()
toBibtex(x)
```

---

citEntry

*Writing Package CITATION Files*

---

### Description

The ‘CITATION’ file of R packages contains an annotated list of references that should be used for citing the packages.

### Usage

```
citEntry(entry, textVersion, header = NULL, footer = NULL, ...)
citHeader(...)
citFooter(...)
readCitationFile(file, meta = NULL)
```

### Arguments

<code>entry</code>	a character string with a BibTeX entry type.
<code>textVersion</code>	a character string with a text representation of the reference.
<code>header</code>	a character string with optional header text.
<code>footer</code>	a character string with optional footer text.
<code>file</code>	a file name.
<code>...</code>	see ‘Details’.
<code>meta</code>	a list of package metadata as obtained by <a href="#">packageDescription</a> , or NULL (the default).

## Details

The 'CITATION' file of an R package should be placed in the 'inst' subdirectory of the package source. The file is an R source file and may contain arbitrary R commands including conditionals and computations. The file is `source()`ed by the R parser in a temporary environment and all resulting objects of class "citation" (the return value of `citEntry`) are collected.

Typically the file will contain zero or more calls to `citHeader`, then one or more calls to `citEntry`, and finally zero or more calls to `citFooter`. `citHeader` and `citFooter` are simply wrappers to `paste`, and their `...` argument is passed on to `paste` as is.

`readCitationFile` makes use of the `Encoding` element (if any) of `meta` to determine the encoding of the file.

## Value

`citEntry` returns an object of class "citation", for which there are `print` and `toBibtex` methods. This is a named list of entries with attributes "entry", "textversion" and optionally "header" and "footer".

`readCitationFile` returns an object of class "citationList", also with `print` and `toBibtex` methods. This is a list of one or more elements of class "citation" with optional attributes "header" and "footer".

## Entry Types

`citEntry` creates "citation" objects, which are modeled after BibTeX entries. The entry should be a valid BibTeX entry type, e.g.,

**article:** An article from a journal or magazine.

**book:** A book with an explicit publisher.

**inbook:** A part of a book, which may be a chapter (or section or whatever) and/or a range of pages.

**incollection:** A part of a book having its own title.

**inproceedings:** An article in a conference proceedings.

**manual:** Technical documentation like a software manual.

**mastersthesis:** A Master's thesis.

**misc:** Use this type when nothing else fits.

**phdthesis:** A PhD thesis.

**proceedings:** The proceedings of a conference.

**techreport:** A report published by a school or other institution, usually numbered within a series.

**unpublished:** A document having an author and title, but not formally published.

## Entry Fields

The `...` argument of `citEntry` can be any number of BibTeX fields, including

**address:** The address of the publisher or other type of institution.

**author:** The name(s) of the author(s), either as a character string in the format described in the LaTeX book, or a `personList` object.

**booktitle:** Title of a book, part of which is being cited.

**chapter:** A chapter (or section or whatever) number.

**editor:** Name(s) of editor(s), same format as `author`.

**institution:** The publishing institution of a technical report.

**journal:** A journal name.

**note:** Any additional information that can help the reader. The first word should be capitalized.

**number:** The number of a journal, magazine, technical report, or of a work in a series.

**pages:** One or more page numbers or range of numbers.

**publisher:** The publisher's name.

**school:** The name of the school where a thesis was written.

**series:** The name of a series or set of books.

**title:** The work's title.

**volume:** The volume of a journal or multi-volume book.

**year:** The year of publication.

### Examples

```
basecit <- system.file("CITATION", package="base")
source(basecit, echo=TRUE)
readCitationFile(basecit)
```

---

close.socket

*Close a Socket*

---

### Description

Closes the socket and frees the space in the file descriptor table. The port may not be freed immediately.

### Usage

```
close.socket(socket, ...)
```

### Arguments

socket	A socket object
...	further arguments passed to or from other methods.

### Value

logical indicating success or failure

### Author(s)

Thomas Lumley

### See Also

[make.socket](#), [read.socket](#)

combn

*Generate All Combinations of n Elements, Taken m at a Time***Description**

Generate all combinations of the elements of `x` taken `m` at a time. If `x` is a positive integer, returns all combinations of the elements of `seq(x)` taken `m` at a time. If argument `FUN` is not `NULL`, applies a function given by the argument to each point. If `simplify` is `FALSE`, returns a list; otherwise returns an [array](#), typically a [matrix](#). `...` are passed unchanged to the `FUN` function, if specified.

**Usage**

```
combn(x, m, FUN = NULL, simplify = TRUE, ...)
```

**Arguments**

<code>x</code>	vector source for combinations, or integer <code>n</code> for <code>x &lt;- seq(n)</code> .
<code>m</code>	number of elements to choose.
<code>FUN</code>	function to be applied to each combination; default <code>NULL</code> means the identity, i.e., to return the combination (vector of length <code>m</code> ).
<code>simplify</code>	logical indicating if the result should be simplified to an <a href="#">array</a> (typically a <a href="#">matrix</a> ); if <code>FALSE</code> , the function returns a <a href="#">list</a> . Note that when <code>simplify = TRUE</code> as by default, the dimension of the result is simply determined from <code>FUN(1st combination)</code> (for efficiency reasons). This will badly fail if <code>FUN(u)</code> is not of constant length.
<code>...</code>	optionally, further arguments to <code>FUN</code> .

**Value**

a [list](#) or [array](#) (in nondegenerate cases), see the `simplify` argument above.

**Author(s)**

Scott Chasalow wrote the original in 1994 for S; R package **combinat** and documentation by Vince Carey <stvjc@channing.harvard.edu>; small changes by the R core team, notably to return an array in all cases of `simplify = TRUE`, e.g., for `combn(5, 5)`.

**References**

Nijenhuis, A. and Wilf, H.S. (1978) *Combinatorial Algorithms for Computers and Calculators*; Academic Press, NY.

**See Also**

[choose](#) for fast computation of the *number* of combinations. [expand.grid](#) for creating a data frame from all combinations of factors or vectors.

**Examples**

```

combn(letters[1:4], 2)
(m <- combn(10, 5, min)) # minimum value in each combination
mm <- combn(15, 6, function(x) matrix(x, 2,3))
stopifnot(round(choose(10,5)) == length(m),
           c(2,3, round(choose(15,6))) == dim(mm))

## Different way of encoding points:
combn(c(1,1,1,1,2,2,2,3,3,4), 3, tabulate, nbins = 4)

## Compute support points and (scaled) probabilities for a
## Multivariate-Hypergeometric(n = 3, N = c(4,3,2,1)) p.f.:
# table.mat(t(combn(c(1,1,1,1,2,2,2,3,3,4), 3, tabulate,nbins=4)))

```

---

compareVersion      *Compare Two Package Version Numbers*

---

**Description**

Compare two package version numbers to see which is later.

**Usage**

```
compareVersion(a, b)
```

**Arguments**

`a`, `b`            Character strings representing package version numbers.

**Details**

R package version numbers are of the form  $x.y-z$  for integers  $x$ ,  $y$  and  $z$ , with components after  $x$  optionally missing (in which case the version number is older than those with the components present).

**Value**

0 if the numbers are equal, -1 if `b` is later and 1 if `a` is later (analogous to the C function `strcmp`).

**See Also**

[package\\_version](#), [library](#), [packageStatus](#).

**Examples**

```

compareVersion("1.0", "1.0-1")
compareVersion("7.2-0", "7.1-12")

```

---

 COMPILE

*Compile Files for Use with R*


---

**Description**

Compile given source files so that they can subsequently be collected into a shared library using R CMD SHLIB and be loaded into R using `dyn.load()`.

**Usage**

```
R CMD COMPILE [options] srcfiles
```

**Arguments**

<code>srcfiles</code>	A list of the names of source files to be compiled. Currently, C, C++, Objective C, Objective C++ and FORTRAN are supported; the corresponding files should have the extensions <code>‘.c’</code> , <code>‘.cc’</code> (or <code>‘.cpp’</code> or <code>‘.C’</code> ), <code>‘.m’</code> , <code>‘.mm’</code> (or <code>‘.M’</code> ) and <code>‘.f’</code> , respectively.
<code>options</code>	A list of compile-relevant settings, such as special values for CFLAGS or FFLAGS, or for obtaining information about usage and version of the utility.

**Details**

Note that Ratfor is not supported. If you have Ratfor source code, you need to convert it to FORTRAN. On many Solaris systems mixing Ratfor and FORTRAN code will work.

Objective C and Objective C++ support is optional and will work only if the corresponding compilers were available at R configure time.

**Note**

Some binary distributions of R have COMPILE in a separate bundle, e.g. an R-devel RPM.

**See Also**

[SHLIB](#), [dyn.load](#); the section on “Customizing compilation under Unix” in “R Administration and Installation” (see the `‘doc/manual’` subdirectory of the R source tree).

---

 contrib.url

*Find Appropriate Paths in CRAN-like Repositories*


---

**Description**

`contrib.url` adds the appropriate type-specific path within a repository to each URL in `repos`.

**Usage**

```
contrib.url(repos, type = getOption("pkgType"))
```



**Arguments**

`repos` character vector, the base URL(s) of the repositories to use.  
`type` character string, indicate which type of packages: see [install.packages](#).

**Value**

A character vector of the same length as `repos`.

**See Also**

[available.packages](#), [download.packages](#), [install.packages](#).

The ‘R Installation and Administration’ manual for how to set up a repository.

---

<code>count.fields</code>	<i>Count the Number of Fields per Line</i>
---------------------------	--

---

**Description**

`count.fields` counts the number of fields, as separated by `sep`, in each of the lines of `file` read.

**Usage**

```
count.fields(file, sep = "", quote = "\"'", skip = 0,
             blank.lines.skip = TRUE, comment.char = "#")
```

**Arguments**

`file` a character string naming an ASCII data file, or a [connection](#), which will be opened if necessary, and if so closed at the end of the function call.  
`sep` the field separator character. Values on each line of the file are separated by this character. By default, arbitrary amounts of whitespace can separate fields.  
`quote` the set of quoting characters  
`skip` the number of lines of the data file to skip before beginning to read data.  
`blank.lines.skip` logical: if TRUE blank lines in the input are ignored.  
`comment.char` character: a character vector of length one containing a single character or an empty string.

**Details**

This used to be used by [read.table](#) and can still be useful in discovering problems in reading a file by that function.

For the handling of comments, see [scan](#).

**Value**

A vector with the numbers of fields found.

**See Also**[read.table](#)**Examples**

```
cat("NAME", "1:John", "2:Paul", file = "foo", sep = "\n")
count.fields("foo", sep = ":")
unlink("foo")
```

data

*Data Sets***Description**

Loads specified data sets, or list the available data sets.

**Usage**

```
data(..., list = character(0), package = NULL, lib.loc = NULL,
      verbose = getOption("verbose"), envir = .GlobalEnv)
```

**Arguments**

<code>...</code>	a sequence of names or literal character strings.
<code>list</code>	a character vector.
<code>package</code>	a character vector giving the package(s) to look in for data sets, or <code>NULL</code> . By default, all packages in the search path are used, then the ‘data’ subdirectory (if present) of the current working directory.
<code>lib.loc</code>	a character vector of directory names of R libraries, or <code>NULL</code> . The default value of <code>NULL</code> corresponds to all libraries currently known.
<code>verbose</code>	a logical. If <code>TRUE</code> , additional diagnostics are printed.
<code>envir</code>	the <a href="#">environment</a> where the data should be loaded.

**Details**

Currently, four formats of data files are supported:

1. files ending ‘.R’ or ‘.r’ are `source()` d in, with the R working directory changed temporarily to the directory containing the respective file. (`data` ensures that the `utils` package is attached, in case it had been run *via* `utils::data`.)
2. files ending ‘.RData’ or ‘.rda’ are `load()` ed.
3. files ending ‘.tab’, ‘.txt’ or ‘.TXT’ are read using `read.table(..., header = TRUE)`, and hence result in a data frame.
4. files ending ‘.csv’ or ‘.CSV’ are read using `read.table(..., header = TRUE, sep = ";")`, and also result in a data frame.

If more than one matching file name is found, the first on this list is used. (Files with extensions `.txt`, `.tab` or `.csv` can be compressed, with or without further extension `.gz`, `.bz2` or `.xz`.)

The data sets to be loaded can be specified as a sequence of names or character strings, or as the character vector `list`, or as both.

For each given data set, the first two types (`.R` or `.r`, and `.RData` or `.rda` files) can create several variables in the load environment, which might all be named differently from the data set. The third and fourth types will always result in the creation of a single variable with the same name (without extension) as the data set.

If no data sets are specified, `data` lists the available data sets. It looks for a new-style data index in the `'Meta'` or, if this is not found, an old-style `'00Index'` file in the `'data'` directory of each specified package, and uses these files to prepare a listing. If there is a `'data'` area but no index, available data files for loading are computed and included in the listing, and a warning is given: such packages are incomplete. The information about available data sets is returned in an object of class `"packageIQR"`. The structure of this class is experimental. Where the datasets have a different name from the argument that should be used to retrieve them the index will have an entry like `beaver1 (beavers)` which tells us that dataset `beaver1` can be retrieved by the call `data(beaver)`.

If `lib.loc` and `package` are both `NULL` (the default), the data sets are searched for in all the currently loaded packages then in the `'data'` directory (if any) of the current working directory.

If `lib.loc = NULL` but `package` is specified as a character vector, the specified package(s) are searched for first amongst loaded packages and then in the default library/ies (see `.libPaths`).

If `lib.loc` is specified (and not `NULL`), packages are searched for in the specified library/ies, even if they are already loaded from another library.

To just look in the `'data'` directory of the current working directory, set `package = character(0)` (and `lib.loc = NULL`, the default).

### Value

A character vector of all data sets specified, or information about all available data sets in an object of class `"packageIQR"` if none were specified.

### Note

The data files can be many small files. On some file systems it is desirable to save space, and the files in the `'data'` directory of an installed package can be zipped up as a zip archive `'Rdata.zip'`. You will need to provide a single-column file `'filelist'` of file names in that directory.

One can take advantage of the search order and the fact that a `.R` file will change directory. If raw data are stored in `'mydata.txt'` then one can set up `'mydata.R'` to read `'mydata.txt'` and pre-process it, e.g., using `transform`. For instance one can convert numeric vectors to factors with the appropriate labels. Thus, the `.R` file can effectively contain a metadata specification for the plaintext formats.

### See Also

[help](#) for obtaining documentation on data sets, [save](#) for *creating* the second (`.rda`) kind of data, typically the most efficient one.

The `'Writing R Extensions'` for considerations in preparing the `'data'` directory of a package.

**Examples**

```
require(utils)
data() # list all available data sets
try(data(package = "rpart") )# list the data sets in the rpart package
data(USArrests, "VADeaths") # load the data sets 'USArrests' and 'VADeaths'
help(USArrests) # give information on data set 'USArrests'
```

dataentry

*Spreadsheet Interface for Entering Data***Description**

A spreadsheet-like editor for entering or editing data.

**Usage**

```
data.entry(..., Modes = NULL, Names = NULL)
dataentry(data, modes)
de(..., Modes = list(), Names = NULL)
```

**Arguments**

...	A list of variables: currently these should be numeric or character vectors or list containing such vectors.
Modes	The modes to be used for the variables.
Names	The names to be used for the variables.
data	A list of numeric and/or character vectors.
modes	A list of length up to that of <code>data</code> giving the modes of (some of) the variables. <code>list()</code> is allowed.

**Details**

The data entry editor is only available on some platforms and GUIs. Where available it provides a means to visually edit a matrix or a collection of variables (including a data frame) as described in the Notes section.

`data.entry` has side effects, any changes made in the spreadsheet are reflected in the variables. The functions `de`, `de.ncols`, `de.setup` and `de.restore` are designed to help achieve these side effects. If the user passes in a matrix, `X` say, then the matrix is broken into columns before `dataentry` is called. Then on return the columns are collected and glued back together and the result assigned to the variable `X`. If you don't want this behaviour use `dataentry` directly.

The primitive function is `dataentry`. It takes a list of vectors of possibly different lengths and modes (the second argument) and opens a spreadsheet with these variables being the columns. The columns of the `dataentry` window are returned as vectors in a list when the spreadsheet is closed.

`de.ncols` counts the number of columns which are supplied as arguments to `data.entry`. It attempts to count columns in lists, matrices and vectors. `de.setup` sets things up so that on return the columns can be regrouped and reassigned to the correct name. This is handled by `de.restore`.

**Value**

`de` and `dataentry` return the edited value of their arguments. `data.entry` invisibly returns a vector of variable names but its main value is its side effect of assigning new version of those variables in the user's workspace.

**Resources**

The data entry window responds to X resources of class `R_dataentry`. Resources `foreground`, `background` and `geometry` are utilized.

**Note**

The details of interface to the data grid may differ by platform and GUI. The following description applies to the X11-based implementation under Unix.

You can navigate around the grid using the cursor keys or by clicking with the (left) mouse button on any cell. The active cell is highlighted by thickening the surrounding rectangle. Moving to the right or down will scroll the grid as needed: there is no constraint to the rows or columns currently in use.

There are alternative ways to navigate using the keys. Return and (keypad) Enter and LineFeed all move down. Tab moves right and Shift-Tab move left. Home moves to the top left.

PageDown or Control-F moves down a page, and PageUp or Control-B up by a page. End will show the last used column and the last few rows used (in any column).

Using any other key starts an editing process on the currently selected cell: moving away from that cell enters the edited value whereas Esc cancels the edit and restores the previous value. When the editing process starts the cell is cleared. In numerical columns (the default) only letters making up a valid number (including `- . eE`) are accepted, and entering an invalid edited value (such as blank) enters NA in that cell. The last entered value can be deleted using the BackSpace or Del(ete) key. Only a limited number of characters (currently 29) can be entered in a cell, and if necessary only the start or end of the string will be displayed, with the omissions indicated by `>` or `<`. (The start is shown except when editing.)

Entering a value in a cell further down a column than the last used cell extends the variable and fills the gap (if any) by NAs (not shown on screen).

The column names can only be selected by clicking in them. This gives a popup menu to select the column type (currently Real (numeric) or Character) or to change the name. Changing the type converts the current contents of the column (and converting from Character to Real may generate NAs.) If changing the name is selected the header cell becomes editable (and is cleared). As with all cells, the value is entered by moving away from the cell by clicking elsewhere or by any of the keys for moving down (only).

New columns are created by entering values in them (and not by just assigning a new name). The mode of the column is auto-detected from the first value entered: if this is a valid number it gives a numeric column. Unused columns are ignored, so adding data in `var5` to a three-column grid adds one extra variable, not two.

The Copy button copies the currently selected cell: paste copies the last copied value to the current cell, and right-clicking selects a cell *and* copies in the value. Initially the value is blank, and attempts to paste a blank value will have no effect.

Control-L will refresh the display, recalculating field widths to fit the current entries.

In the default mode the column widths are chosen to fit the contents of each column, with a default of 10 characters for empty columns. you can specify fixed column widths by setting option `de.cellwidth` to the required fixed width (in characters). (set it to zero to return to variable widths). The displayed width of any field is limited to 600 pixels (and by the window width).

**See Also**

`vi`, `edit`: `edit` uses `dataentry` to edit data frames.

**Examples**

```
# call data entry with variables x and y
## Not run: data.entry(x,y)
```

---

debugger

*Post-Mortem Debugging*

---

**Description**

Functions to dump the evaluation environments (frames) and to examine dumped frames.

**Usage**

```
dump.frames(dumpto = "last.dump", to.file = FALSE)
debugger(dump = last.dump)
```

**Arguments**

<code>dumpto</code>	a character string. The name of the object or file to dump to.
<code>to.file</code>	logical. Should the dump be to an R object or to a file?
<code>dump</code>	An R dump object created by <code>dump.frames</code> .

**Details**

To use post-mortem debugging, set the option `error` to be a call to `dump.frames`. By default this dumps to an R object `"last.dump"` in the workspace, but it can be set to dump to a file (a dump of the object produced by a call to `save`). The dumped object contain the call stack, the active environments and the last error message as returned by `geterrmessage`.

When dumping to file, `dumpto` gives the name of the dumped object and the file name has `'rda'` appended.

A dump object of class `"dump.frames"` can be examined by calling `debugger`. This will give the error message and a list of environments from which to select repeatedly. When an environment is selected, it is copied and the `browser` called from within the copy.

If `dump.frames` is installed as the error handler, execution will continue even in non-interactive sessions. See the examples for how to dump and then quit.

**Value**

Invisible `NULL`.

**Note**

Functions such as `sys.parent` and `environment` applied to closures will not work correctly inside `debugger`.

If the error occurred when computing the default value of a formal argument the debugger will report "recursive default argument reference" when trying to examine that environment.

Of course post-mortem debugging will not work if R is too damaged to produce and save the dump, for example if it has run out of workspace.

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`options` for setting error options; `recover` is an interactive debugger working similarly to `debugger` but directly after the error occurs.

**Examples**

```
## Not run:
options(error=quote(dump.frames("testdump", TRUE)))

f <- function() {
  g <- function() stop("test dump.frames")
  g()
}
f() # will generate a dump on file "testdump.rda"
options(error=NULL)

## possibly in another R session
load("testdump.rda")
debugger(testdump)
Available environments had calls:
1: f()
2: g()
3: stop("test dump.frames")

Enter an environment number, or 0 to exit
Selection: 1
Browsing in the environment with call:
f()
Called from: debugger.look(ind)
Browse[1]> ls()
[1] "g"
Browse[1]> g
function() stop("test dump.frames")
<environment: 759818>
Browse[1]>
Available environments had calls:
1: f()
2: g()
3: stop("test dump.frames")

Enter an environment number, or 0 to exit
```

```

Selection: 0

## A possible setting for non-interactive sessions
options(error=quote({dump.frames(to.file=TRUE); q()}))

## End(Not run)

```

demo

*Demonstrations of R Functionality***Description**

`demo` is a user-friendly interface to running some demonstration R scripts. `demo()` gives the list of available topics.

**Usage**

```

demo(topic, package = NULL, lib.loc = NULL,
      character.only = FALSE, verbose = getOption("verbose"),
      echo = TRUE, ask = getOption("demo.ask"))

```

**Arguments**

<code>topic</code>	the topic which should be demonstrated, given as a <a href="#">name</a> or literal character string, or a character string, depending on whether <code>character.only</code> is <code>FALSE</code> (default) or <code>TRUE</code> . If omitted, the list of available topics is displayed.
<code>package</code>	a character vector giving the packages to look into for demos, or <code>NULL</code> . By default, all packages in the search path are used.
<code>lib.loc</code>	a character vector of directory names of R libraries, or <code>NULL</code> . The default value of <code>NULL</code> corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries.
<code>character.only</code>	logical; if <code>TRUE</code> , use <code>topic</code> as character string.
<code>verbose</code>	a logical. If <code>TRUE</code> , additional diagnostics are printed.
<code>echo</code>	a logical. If <code>TRUE</code> , show the R input when sourcing.
<code>ask</code>	a logical (or "default") indicating if <code>devAskNewPage</code> ( <code>ask=TRUE</code> ) should be called before graphical output happens from the demo code. The value "default" (the factory-fresh default) means to ask if <code>echo == TRUE</code> and the graphics device appears to be interactive. This parameter applies both to any currently opened device and to any devices opened by the demo code. If this is evaluated to <code>TRUE</code> and the session is <a href="#">interactive</a> , the user is asked to press RETURN to start.

**Details**

If no topics are given, `demo` lists the available demos. The corresponding information is returned in an object of class "packageIQR".

**See Also**

[source](#) and [devAskNewPage](#) which are called by `demo`.



**Examples**

```

demo() # for attached packages

## All available demos:
demo(package = .packages(all.available = TRUE))

## Display a demo, pausing between pages
demo(lm.glm, package="stats", ask=TRUE)

## Display it without pausing
demo(lm.glm, package="stats", ask=FALSE)

## Not run:
ch <- "scoping"
demo(ch, character = TRUE)

## End(Not run)

## Find the location of a demo
system.file("demo", "lm.glm.R", package="stats")

```

---

download.file

*Download File from the Internet*


---

**Description**

This function can be used to download a file from the Internet.

**Usage**

```

download.file(url, destfile, method, quiet = FALSE, mode = "w",
             cacheOK = TRUE)

```

**Arguments**

url	A character string naming the URL of a resource to be downloaded.
destfile	A character string with the name where the downloaded file is saved. Tilde-expansion is performed.
method	Method to be used for downloading files. Currently download methods "internal", "wget", "curl" and "lynx" are available, and there is a value "auto": see 'Details'. The method can also be set through the option "download.file.method": see <a href="#">options()</a> .
quiet	If TRUE, suppress status messages (if any), and the progress bar.
mode	character. The mode with which to write the file. Useful values are "w", "wb" (binary), "a" (append) and "ab". Only used for the "internal" method.
cacheOK	logical. Is a server-side cached value acceptable? Implemented for the "internal" and "wget" methods.

## Details

The function `download.file` can be used to download a single file as described by `url` from the internet and store it in `destfile`. The `url` must start with a scheme such as `'http://'`, `'ftp://'` or `'file://'`.

If `method = "auto"` is chosen (the default), the internal method is chosen for `'file://'` URLs, and for the others provided `capabilities("http/ftp")` is true (which it almost always is). Otherwise methods `"wget"`, `"curl"` and `"lynx"` are tried in turn.

`cacheOK = FALSE` is useful for `'http://'` URLs, and will attempt to get a copy directly from the site rather than from an intermediate cache. (Not all platforms support it.) It is used by `available.packages`.

The remaining details apply to method `"internal"` only.

Note that `'https://'` connections are not supported.

See `url` for how `'file://'` URLs are interpreted, especially on Windows. This function does decode encoded URLs.

The timeout for many parts of the transfer can be set by the option `timeout` which defaults to 60 seconds.

The level of detail provided during transfer can be set by the `quiet` argument and the `internet.info` option. The details depend on the platform and scheme, but setting `internet.info` to 0 gives all available details, including all server responses. Using 2 (the default) gives only serious messages, and 3 or more suppresses all messages.

A progress bar tracks the transfer. If the file length is known, an equals sign represents 2% of the transfer completed: otherwise a dot represents 10Kb.

Method `"wget"` can be used with proxy firewalls which require user/password authentication if proper values are stored in the configuration file for `wget`.

## Value

An (invisible) integer code, 0 for success and non-zero for failure. For the `"wget"` and `"lynx"` methods this is the status code returned by the external program. The `"internal"` method can return 1, but will in most cases throw an error.

## Setting Proxies

This applies to the internal code only.

Proxies can be specified via environment variables. Setting `"no_proxy"` to `"*"` stops any proxy being tried. Otherwise the setting of `"http_proxy"` or `"ftp_proxy"` (or failing that, the all upper-case version) is consulted and if non-empty used as a proxy site. For FTP transfers, the username and password on the proxy can be specified by `"ftp_proxy_user"` and `"ftp_proxy_password"`. The form of `"http_proxy"` should be `"http://proxy.dom.com/"` or `"http://proxy.dom.com:8080/"` where the port defaults to 80 and the trailing slash may be omitted. For `"ftp_proxy"` use the form `"ftp://proxy.dom.com:3128/"` where the default port is 21. These environment variables must be set before the download code is first used: they cannot be altered later by calling `Sys.setenv`.

Usernames and passwords can be set for HTTP proxy transfers via environment variable `http_proxy_user` in the form `user:passwd`. Alternatively, `http_proxy` can be of the form `"http://user:pass@proxy.dom.com:8080/"` for compatibility with `wget`. Only the HTTP/1.0 basic authentication scheme is supported.

**Note**

Methods "wget" and "lynx" are mainly for historical compatibility, but they and "curl" can be used for URLs (e.g. 'https://') URLs or those than use cookies) which the internal method does not support. They will block all other activity on the R process.

For methods "wget", "curl" and "lynx" a system call is made to the tool given by method, and the respective program must be installed on your system and be in the search path for executables.

**See Also**

[options](#) to set the HTTPUserAgent, timeout and internet.info options.

[url](#) for a finer-grained way to read data from URLs.

[url.show](#), [available.packages](#), [download.packages](#) for applications.

---

download.packages *Download Packages from CRAN-like Repositories*

---

**Description**

These functions can be used to automatically compare the version numbers of installed packages with the newest available version on the repositories and update outdated packages on the fly.

**Usage**

```
download.packages(pkgs, destdir, available = NULL,
                  repos = getOption("repos"),
                  contriburl = contrib.url(repos, type),
                  method, type = getOption("pkgType"), ...)
```

**Arguments**

pkgs	character vector of the names of packages whose latest available versions should be downloaded from the repositories.
destdir	directory where downloaded packages are to be stored.
available	an object as returned by <a href="#">available.packages</a> listing packages available at the repositories, or NULL which makes an internal call to <a href="#">available.packages</a> .
repos	character vector, the base URL(s) of the repositories to use, i.e., the URL of the CRAN master such as "http://cran.r-project.org" or its Statlib mirror, "http://lib.stat.cmu.edu/R/CRAN".
contriburl	URL(s) of the contrib sections of the repositories. Use this argument only if your repository mirror is incomplete, e.g., because you burned only the 'contrib' section on a CD. Overrides argument <code>repos</code> .
method	Download method, see <a href="#">download.file</a> .
type	character string, indicate which type of packages: see <a href="#">install.packages</a> .
...	additional arguments to be passed to <a href="#">download.file</a> .

**Details**

`download.packages` takes a list of package names and a destination directory, downloads the newest versions and saves them in `destdir`. If the list of available packages is not given as argument, it is obtained from repositories. If a repository is local, i.e. the URL starts with "file:", then the packages are not downloaded but used directly. Both "file:" and "file:///" are allowed as prefixes to a file path. Use the latter only for URLs: see [url](#) for their interpretation. (Other forms of 'file://' URLs are not supported.)

**Value**

A two-column matrix of names and destination file names of those packages successfully downloaded. If packages are not available or there is a problem with the download, suitable warnings are given.

**See Also**

[available.packages](#), [contrib.url](#).

The main use is by [install.packages](#).

See [download.file](#) for how to handle proxies and other options to monitor file transfers.

The 'R Installation and Administration' manual for how to set up a repository.

edit

*Invoke a Text Editor***Description**

Invoke a text editor on an R object.

**Usage**

```
## Default S3 method:
edit(name = NULL, file = "", title = NULL,
      editor = getOption("editor"), ...)

vi(name = NULL, file = "")
emacs(name = NULL, file = "")
pico(name = NULL, file = "")
xemacs(name = NULL, file = "")
xedit(name = NULL, file = "")
```

**Arguments**

<code>name</code>	a named object that you want to edit. If <code>name</code> is missing then the file specified by <code>file</code> is opened for editing.
<code>file</code>	a string naming the file to write the edited version to.
<code>title</code>	a display name for the object being edited.
<code>editor</code>	a string naming the text editor you want to use. On Unix the default is set from the environment variables <code>EDITOR</code> or <code>VISUAL</code> if either is set, otherwise <code>vi</code> is used. On Windows it defaults to <code>notepad</code> .
<code>...</code>	further arguments to be passed to or from methods.

## Details

`edit` invokes the text editor specified by `editor` with the object `name` to be edited. It is a generic function, currently with a default method and one for data frames and matrices.

`data.entry` can be used to edit data, and is used by `edit` to edit matrices and data frames on systems for which `data.entry` is available.

It is important to realize that `edit` does not change the object called `name`. Instead, a copy of `name` is made and it is that copy which is changed. Should you want the changes to apply to the object `name` you must assign the result of `edit` to `name`. (Try `fix` if you want to make permanent changes to an object.)

In the form `edit(name)`, `edit` deparses `name` into a temporary file and invokes the editor `editor` on this file. Quitting from the editor causes `file` to be parsed and that value returned. Should an error occur in parsing, possibly due to incorrect syntax, no value is returned. Calling `edit()`, with no arguments, will result in the temporary file being reopened for further editing.

Note that deparsing is not perfect, and the object recreated after editing can differ in subtle ways from that deparsed: see `dput` and `.deparseOpts`. (The deparse options used are the same as the defaults for `dump`.) Editing a function will preserve its environment. See `edit.data.frame` for further changes that can occur when editing a data frame or matrix.

Currently only the internal editor in Windows makes use of the `title` option; it displays the given name in the window header.

## Note

The functions `vi`, `emacs`, `pico`, `xemacs`, `xedit` rely on the corresponding editor being available and being on the path. This is system-dependent.

## See Also

`edit.data.frame`, `data.entry`, `fix`.

## Examples

```
## Not run:
# use xedit on the function mean and assign the changes
mean <- edit(mean, editor = "xedit")

# use vi on mean and write the result to file mean.out
vi(mean, file = "mean.out")

## End(Not run)
```

---

`edit.data.frame`      *Edit Data Frames and Matrices*

---

## Description

Use data editor on data frame or matrix contents.

**Usage**

```
## S3 method for class 'data.frame':
edit(name, factor.mode = c("character", "numeric"),
      edit.row.names = any(row.names(name) != 1:nrow(name)), ...)

## S3 method for class 'matrix':
edit(name, edit.row.names = !is.null(dn[[1]]), ...)
```

**Arguments**

<code>name</code>	A data frame or (numeric, logical or character) matrix.
<code>factor.mode</code>	How to handle factors (as integers or using character levels) in a data frame.
<code>edit.row.names</code>	logical. Show the row names (if they exist) be displayed as a separate editable column? It is an error to ask for this on a matrix with NULL row names.
<code>...</code>	further arguments passed to or from other methods.

**Details**

At present, this only works on simple data frames containing numeric, logical or character vectors and factors, and numeric, logical or character matrices. Any other mode of matrix will give an error, and a warning is given when the matrix has a class (which will be discarded).

Data frame columns are coerced on input to *character* unless numeric (in the sense of `is.numeric`), logical or factor. A warning is given when classes are discarded. Special characters (tabs, non-printing ASCII, etc.) will be displayed as escape sequences.

Factors columns are represented in the spreadsheet as either numeric vectors (which are more suitable for data entry) or character vectors (better for browsing). After editing, vectors are padded with NA to have the same length and factor attributes are restored. The set of factor levels can not be changed by editing in numeric mode; invalid levels are changed to NA and a warning is issued. If new factor levels are introduced in character mode, they are added at the end of the list of levels in the order in which they encountered.

It is possible to use the data-editor's facilities to select the mode of columns to swap between numerical and factor columns in a data frame. Changing any column in a numerical matrix to character will cause the result to be coerced to a character matrix. Changing the mode of logical columns is not supported.

For a data frame, the row names will be taken from the original object if `edit.row.names = FALSE` and the number of rows is unchanged, and from the edited output if `edit.row.names = TRUE` and there are no duplicates. (If the `row.names` column is incomplete, it is extended by entries like `row223`.) In all other cases the row names are replaced by `seq(length=nrows)`.

For a matrix, `colnames` will be added (of the form `col7`) if needed. The rownames will be taken from the original object if `edit.row.names = FALSE` and the number of rows is unchanged (otherwise NULL), and from the edited output if `edit.row.names = TRUE`. (If the `row.names` column is incomplete, it is extended by entries like `row223`.)

Editing a matrix or data frame will lose all attributes apart from the row and column names.

**Value**

The edited data frame or matrix.

**Note**

`fix(dataframe)` works for in-place editing by calling this function.

If the data editor is not available, a dump of the object is presented for editing using the default method of `edit`.

At present the data editor is limited to 65535 rows.

**Author(s)**

Peter Dalgaard

**See Also**

[data.entry](#), [edit](#)

**Examples**

```
## Not run:
edit(InsectSprays)
edit(InsectSprays, factor.mode="numeric")

## End(Not run)
```

---

example

*Run an Examples Section from the Online Help*

---

**Description**

Run all the R code from the **Examples** part of R's online help topic `topic` with two possible exceptions, `dontrun` and `dontshow`, see 'Details' below.

**Usage**

```
example(topic, package = NULL, lib.loc = NULL,
        local = FALSE, echo = TRUE,
        verbose = getOption("verbose"),
        setRNG = FALSE, ask = getOption("example.ask"),
        prompt.prefix = abbreviate(topic, 6))
```

**Arguments**

<code>topic</code>	name or literal character string: the online <a href="#">help</a> topic the examples of which should be run.
<code>package</code>	a character vector giving the package names to look into for the topic, or <code>NULL</code> (the default), when all packages on the <a href="#">search</a> path are used.
<code>lib.loc</code>	a character vector of directory names of R libraries, or <code>NULL</code> . The default value of <code>NULL</code> corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries.
<code>local</code>	logical: if <code>TRUE</code> evaluate locally, if <code>FALSE</code> evaluate in the workspace.
<code>echo</code>	logical; if <code>TRUE</code> , show the R input when sourcing.

<code>verbose</code>	logical; if <code>TRUE</code> , show even more when running example code.
<code>setRNG</code>	logical or expression; if not <code>FALSE</code> , the random number generator state is saved, then initialized to a specified state, the example is run and the (saved) state is restored. <code>setRNG = TRUE</code> sets the same state as R CMD <code>check</code> does for running a package's examples. This is currently equivalent to <code>setRNG = {RNGkind("default", "default"); set.seed(1)}</code> .
<code>ask</code>	logical (or "default") indicating if <code>devAskNewPage(ask=TRUE)</code> should be called before graphical output happens from the example code. The value "default" (the factory-fresh default) means to ask if <code>echo == TRUE</code> and the graphics device appears to be interactive. This parameter applies both to any currently opened device and to any devices opened by the example code.
<code>prompt.prefix</code>	character; prefixes the prompt to be used if <code>echo = TRUE</code> .

## Details

If `lib.loc` is not specified, the packages are searched for amongst those already loaded, then in the libraries given by `.libPaths()`. If `lib.loc` is specified, packages are searched for only in the specified libraries, even if they are already loaded from another library. The search stops at the first package found that has help on the topic.

An attempt is made to load the package before running the examples, but this will not replace a package loaded from another location.

If `local = TRUE` objects are not created in the workspace and so not available for examination after `example` completes: on the other hand they cannot overwrite objects of the same name in the workspace.

As detailed in the manual *Writing R Extensions*, the author of the help page can markup parts of the examples for two exception rules

`dontrun` encloses code that should not be run.

`dontshow` encloses code that is invisible on help pages, but will be run both by the package checking tools, and the `example()` function. This was previously `testonly`, and that form is still accepted.

## Value

The value of the last evaluated expression.

## Author(s)

Martin Maechler and others

## See Also

[demo](#)

## Examples

```
example(InsectSprays)
## force use of the standard package 'stats':
example("smooth", package="stats", lib.loc=.Library)

## set RNG *before* example as when R CMD check is run:
```



```
r1 <- example(quantile, setRNG = TRUE)
x1 <- rnorm(1)
u <- runif(1)
## identical random numbers
r2 <- example(quantile, setRNG = TRUE)
x2 <- rnorm(1)
stopifnot(identical(r1, r2))
## but x1 and x2 differ since the RNG state from before example()
## differs and is restored!
x1; x2
```

---

file.edit

*Edit One or More Files*

---

## Description

Edit one or more files in a text editor.

## Usage

```
file.edit(..., title = file, editor = getOption("editor"))
```

## Arguments

...	one or more character vectors containing the names of the files to be edited.
title	the title to use in the editor; defaults to the filename.
editor	the text editor to be used.

## Details

Path expansion (see [path.expand](#)) will be done on names.

The behaviour of this function is very system dependent. Currently files can be opened only one at a time on Unix; on Windows, the internal editor allows multiple files to be opened, but has a limit of 50 simultaneous edit windows.

The `title` argument is used for the window caption in Windows, and is ignored on other platforms.

## See Also

[files](#), [file.show](#), [edit](#), [fix](#),

## Examples

```
## Not run:
# open two R scripts for editing
file.edit("script1.R", "script2.R")

## End(Not run)
```

**Description**

Utility for shell-style file tests.

**Usage**

```
file_test(op, x, y)
```

**Arguments**

op	a character string specifying the test to be performed. Unary tests (only <code>x</code> is used) are <code>"-f"</code> (existence and not being a directory), <code>"-d"</code> (existence and directory) and <code>"-x"</code> (executable as a file or searchable as a directory). Binary tests are <code>"-nt"</code> (strictly newer than, using the modification dates) and <code>"-ot"</code> (strictly older than): in both cases the test is false unless both files exist.
x, y	character vectors giving file paths.

**Details**

'Existence' here means being on the file system and accessible by the `stat` system call (or a 64-bit extension) – on a Unix-alike this requires execute permission on all of the directories in the path that leads to the file, but no permissions on the file itself.

For the meaning of `"-x"` on Windows see [file.access](#).

**See Also**

[file.exists](#) which only tests for existence (`test -e` on some systems) but not for not being a directory.

[file.path](#), [file.info](#)

**Examples**

```
dir <- file.path(R.home(), "library", "stats")
file_test("-d", dir)
file_test("-nt", file.path(dir, "R"), file.path(dir, "demo"))
```

**Description**

These functions locate objects containing particular lines of source code, using the information saved when the code was parsed with `options(keep.source = TRUE)`.

**Usage**

```
findLineNum(srcfile, line, nameonly = TRUE, envir = parent.frame(),
            lastenv)
```

```
setBreakpoint(srcfile, line, nameonly = TRUE, envir = parent.frame(),
              lastenv, verbose = TRUE, tracer, print = FALSE, ...)
```

**Arguments**

<code>srcfile</code>	The name of the file containing the source code.
<code>line</code>	The line number within the file. See Details for an alternate way to specify this.
<code>nameonly</code>	If <code>TRUE</code> (the default), we require only a match to <code>basename(srcfile)</code> , not to the full path.
<code>envir</code>	Where do we start looking for function objects?
<code>lastenv</code>	Where do we stop? See the Details.
<code>verbose</code>	Should we print information on where breakpoints were set?
<code>tracer</code>	An optional <code>tracer</code> function to pass to <code>trace</code> . By default, a call to <code>browser</code> is inserted.
<code>print</code>	The <code>print</code> argument to pass to <code>trace</code> .
<code>...</code>	Additional arguments to pass to <code>trace</code> .

**Details**

The `findLineNum` function searches through all objects in environment `envir`, it's parent, grandparent, etc., all the way back to `lastenv`.

`lastenv` defaults to the global environment if `envir` is not specified, and to the root environment `emptyenv()` if `envir` is specified. (The first default tends to be quite fast, and will usually find all user code other than S4 methods; the second one is quite slow, as it will typically search all attached system libraries.)

`setBreakpoint` is a simple wrapper function for `trace`. It will set breakpoints at the locations found by `findLineNum`.

The `srcfile` is normally a filename entered as a character string, but it may be a "`srcfile`" object, or it may include a suffix like "`filename.R#nn`", in which case the number `nn` will be used as a default value for `line`.

As described in the description of the `where` argument on the man page for `trace`, the R package system uses a complicated scheme that may include more than one copy of a function in a package. The user will typically see the public one on the search path, while code in the package will see a private one in the package `NAMESPACE`. If you set `envir` to the environment of a function in the package, by default `findLineNum` will find both versions, and `setBreakpoint` will set the breakpoint in both. (This can be controlled using `lastenv`; e.g. `envir=environment(foo), lastenv=globalenv()` will find only the private copy, as the search is stopped before seeing the public copy.

S version 4 methods are also somewhat tricky to find. They are stored with the generic function, which may be in the `base` or other package, so it is usually necessary to have `lastenv=emptyenv()` in order to find them. In some cases transformations are done by R when storing them and `findLineNum` may not be able to find the original code. Many special cases, e.g. methods on primitive generics, are not yet supported.

**Value**

`findLineNum` returns a list of objects containing location information. A `print` method is defined for them.

`setBreakpoint` has no useful return value; it is called for the side effect of calling `trace`.

**Author(s)**

Duncan Murdoch

**See Also**

[trace](#)

**Examples**

```
## Not run:
# Find what function was defined in the file mysource.R at line 100:
findLineNum("mysource.R#100")

# Set a breakpoint in both copies of that function, assuming one is in the
# same namespace as myfunction and the other is on the search path
setBreakpoint("mysource.R#100", envir=environment(myfunction))

## End(Not run)
```

---

fix

*Fix an Object*

---

**Description**

`fix` invokes `edit` on `x` and then assigns the new (edited) version of `x` in the user's workspace.

**Usage**

```
fix(x, ...)
```

**Arguments**

`x` the name of an R object, as a name or a character string.  
`...` arguments to pass to editor: see [edit](#).

**Details**

The name supplied as `x` need not exist as an R object, in which case a function with no arguments and an empty body is supplied for editing.

Editing an R object may change it in ways other than are obvious: see the comment under [edit](#). See [edit.data.frame](#) for changes that can occur when editing a data frame or matrix.

**See Also**

[edit](#), [edit.data.frame](#)

**Examples**

```
## Not run:
## Assume 'my.fun' is a user defined function :
fix(my.fun)
## now my.fun is changed
## Also,
fix(my.data.frame) # calls up data editor
fix(my.data.frame, factor.mode="char") # use of ...

## End(Not run)
```

---

```
flush.console          Flush Output to A Console
```

---

**Description**

This does nothing except on console-based versions of R. On the Mac OS X and Windows GUIs, it ensures that the display of output in the console is current, even if output buffering is on.

**Usage**

```
flush.console()
```

---

```
format                 Format Unordered and Ordered Lists
```

---

**Description**

Format unordered (itemize) and ordered (enumerate) lists.

**Usage**

```
formatUL(x, label = "*", offset = 0,
         width = 0.9 * getOption("width"))
formatOL(x, type = "arabic", offset = 0, start = 1,
         width = 0.9 * getOption("width"))
```

**Arguments**

x	a character vector of list items.
label	a character string used for labelling the items.
offset	a non-negative integer giving the offset (indentation) of the list.
width	a positive integer giving the target column for wrapping lines in the output.
type	a character string specifying the ‘type’ of the labels in the ordered list. If "arabic" (default), arabic numerals are used. For "Alph" or "alph", single upper or lower case letters are employed (in this case, the number of the last item must not exceed 26. Finally, for "Roman" or "roman", the labels are given as upper or lower case roman numerals (with the number of the last item maximally 3899). type can be given as a unique abbreviation of the above, or as one of the HTML style tokens "1" (arabic), "A"/"a" (alphabetic), or "I"/"i" (roman), respectively.

start            a positive integer specifying the starting number of the first item in an ordered list.

**Value**

A character vector with the formatted entries.

**See Also**

[formatDL](#) for formatting description lists.

**Examples**

```
## A simpler recipe.
x <- c("Mix dry ingredients thoroughly.",
      "Pour in wet ingredients.",
      "Mix for 10 minutes.",
      "Bake for one hour at 300 degrees.")
## Format and output as an unordered list.
writeLines(formatUL(x))
## Format and output as an ordered list.
writeLines(formatOL(x))
## Ordered list using lower case roman numerals.
writeLines(formatOL(x, type = "i"))
## Ordered list using upper case letters and some offset.
writeLines(formatOL(x, type = "A", offset = 5))
```

---

getAnywhere

*Retrieve an R Object, Including from a Name Space*

---

**Description**

These functions locate all objects with name matching their argument, whether visible on the search path, registered as an S3 method or in a name space but not exported. `getAnywhere()` returns the objects and `argsAnywhere()` returns the arguments of any objects that are functions.

**Usage**

```
getAnywhere(x)
argsAnywhere(x)
```

**Arguments**

x            a character string or name.

**Details**

The functions look at all loaded name spaces, whether or not they are associated with a package on the search list.

The functions do not search literally “anywhere”: for example, local evaluation frames and name-spaces that are not loaded will not be searched.

Where functions are found as an S3 method, an attempt is made to find which name space registered them. This may not be correct, especially if a name space is unloaded.

**Value**

For `getAnywhere()` an object of class "getAnywhere". This is a list with components

<code>name</code>	the name searched for.
<code>objs</code>	a list of objects found
<code>where</code>	a character vector explaining where the object(s) were found
<code>visible</code>	logical: is the object visible
<code>dups</code>	logical: is the object identical to one earlier in the list.

Normally the structure will be hidden by the `print` method. There is a `[` method to extract one or more of the objects found.

For `argsAnywhere()` one or more argument lists as returned by `args`.

**See Also**

[get](#), [getFromNamespace](#), [args](#)

**Examples**

```
getAnywhere("format.dist")
getAnywhere("simpleLoess") # not exported from stats
argsAnywhere(format.dist)
```

---

`getFromNamespace`     *Utility functions for Developing Namespaces*

---

**Description**

Utility functions to access and replace the non-exported functions in a name space, for use in developing packages with name spaces.

**Usage**

```
getFromNamespace(x, ns, pos = -1, envir = as.environment(pos))

assignInNamespace(x, value, ns, pos = -1,
                  envir = as.environment(pos))

fixInNamespace(x, ns, pos = -1, envir = as.environment(pos), ...)
```

**Arguments**

<code>x</code>	an object name (given as a character string).
<code>value</code>	an R object.
<code>ns</code>	a name space, or character string giving the name space.
<code>pos</code>	where to look for the object: see <a href="#">get</a> .
<code>envir</code>	an alternative way to specify an environment to look in.
<code>...</code>	arguments to pass to the editor: see <a href="#">edit</a> .

**Details**

The name space can be specified in several ways. Using, for example, `ns = "stats"` is the most direct, but a loaded package with a name space can be specified via any of the methods used for [get](#): `ns` can also be the environment printed as `<namespace:foo>`.

`getFromNamespace` is similar to (but predates) the `:::` operator, but is more flexible in how the name space is specified.

`fixInNamespace` invokes [edit](#) on the object named `x` and assigns the revised object in place of the original object. For compatibility with `fix`, `x` can be unquoted.

**Value**

`getFromNamespace` returns the object found (or gives an error).

`assignInNamespace` and `fixInNamespace` are invoked for their side effect of changing the object in the name space.

**Note**

`assignInNamespace` and `fixInNamespace` change the copy in the name space, but not any copies already exported from the name space, in particular an object of that name in the package (if already attached) and any copies already imported into other name spaces. They are really intended to be used *only* for objects which are not exported from the name space. They do attempt to alter a copy registered as an S3 method if one is found.

They can only be used to change the values of objects in the name space, not to create new objects.

**See Also**

[get](#), [fix](#), [getS3method](#)

**Examples**

```
getFromNamespace("findGeneric", "utils")
## Not run:
fixInNamespace("predict.ppr", "stats")
stats:::predict.ppr
getS3method("predict", "ppr")
## alternatively
fixInNamespace("predict.ppr", pos = 3)
fixInNamespace("predict.ppr", pos = "package:stats")

## End(Not run)
```

---

getS3method

*Get An S3 Method*


---

**Description**

Get a method for an S3 generic, possibly from a name space.

**Usage**

```
getS3method(f, class, optional = FALSE)
```



**Arguments**

<code>f</code>	character: name of the generic.
<code>class</code>	character: name of the class.
<code>optional</code>	logical: should failure to find the generic or a method be allowed?

**Details**

S3 methods may be hidden in packages with name spaces, and will not then be found by `get`: this function can retrieve such functions, primarily for debugging purposes.

**Value**

The function found, or `NULL` if no function is found and `optional = TRUE`.

**See Also**

[methods](#), [get](#)

**Examples**

```
require(stats)
exists("predict.ppr") # false
getS3method("predict", "ppr")
```

---

glob2rx

*Change Wildcard or Globbing Pattern into Regular Expression*

---

**Description**

Change *wildcard* aka *globbing* patterns into the corresponding regular expressions ([regexp](#)).

**Usage**

```
glob2rx(pattern, trim.head = FALSE, trim.tail = TRUE)
```

**Arguments**

<code>pattern</code>	character vector
<code>trim.head</code>	logical specifying if leading " <code>^.*</code> " should be trimmed from the result.
<code>trim.tail</code>	logical specifying if trailing " <code>.*\$</code> " should be trimmed from the result.

**Details**

This takes a wildcard as used by most shells and returns an equivalent regular expression. `?` is mapped to `.` (match a single character), `*` to `.*` (match any string, including an empty one), and the pattern is anchored (it must start at the beginning and end at the end). Optionally, the resulting `regexp` is simplified.

Note that now even `(`, `[` and `{` can be used in `pattern`, but `glob2rx()` may not work correctly with arbitrary characters in `pattern`.

**Value**

A character vector of the same length as the input `pattern` where each wildcard is translated to the corresponding regular expression.

**Author(s)**

Martin Maechler, Unix/sed based version, 1991; current: 2004

**See Also**

[regex](#) about regular expression, [sub](#), etc about substitutions using regexps.

**Examples**

```
stopifnot(glob2rx("abc.*") == "^abc\\.\"",
          glob2rx("a?b.*") == "^a.b\\.\"",
          glob2rx("a?b.*", trim.tail=FALSE) == "^a.b\\.\\.\\.*$\"",
          glob2rx("*.doc") == "^.*\\.\\.doc$\"",
          glob2rx("*.doc", trim.head=TRUE) == "\\\\.doc$\"",
          glob2rx("*.t*") == "^.*\\.\\.t\"",
          glob2rx("*.t??") == "^.*\\.\\.t..*$\"",
          glob2rx("[*]") == "^.*\\\[\"
)
```

---

head

*Return the First or Last Part of an Object*

---

**Description**

Returns the first or last parts of a vector, matrix, table, data frame or function. Since `head()` and `tail()` are generic functions, they may also have been extended to other classes.

**Usage**

```
head(x, ...)
## Default S3 method:
head(x, n = 6L, ...)
## S3 method for class 'data.frame':
head(x, n = 6L, ...)
## S3 method for class 'matrix':
head(x, n = 6L, ...)
## S3 method for class 'ftable':
head(x, n = 6L, ...)
## S3 method for class 'table':
head(x, n = 6L, ...)
## S3 method for class 'function':
head(x, n = 6L, ...)

tail(x, ...)
## Default S3 method:
tail(x, n = 6L, ...)
## S3 method for class 'data.frame':
```

```
tail(x, n = 6L, ...)
## S3 method for class 'matrix':
tail(x, n = 6L, addrownums = TRUE, ...)
## S3 method for class 'ftable':
tail(x, n = 6L, addrownums = FALSE, ...)
## S3 method for class 'table':
tail(x, n = 6L, addrownums = TRUE, ...)
## S3 method for class 'function':
tail(x, n = 6L, ...)
```

### Arguments

<code>x</code>	an object
<code>n</code>	a single integer. If positive, size for the resulting object: number of elements for a vector (including lists), rows for a matrix or data frame or lines for a function. If negative, all but the <code>n</code> last/first number of elements of <code>x</code> .
<code>addrownums</code>	if there are no row names, create them from the row numbers.
<code>...</code>	arguments to be passed to or from other methods.

### Details

For matrices, 2-dim tables and data frames, `head()` (`tail()`) returns the first (last) `n` rows when `n > 0` or all but the last (first) `n` rows when `n < 0`. `head.matrix()` and `tail.matrix()` are exported. For functions, the lines of the deparsed function are returned as character strings.

If a matrix has no row names, then `tail()` will add row names of the form "`[n, ]`" to the result, so that it looks similar to the last lines of `x` when printed. Setting `addrownums = FALSE` suppresses this behaviour.

### Value

An object (usually) like `x` but generally smaller. For `ftable` objects `x`, a transformed `format(x)`.

### Author(s)

Patrick Burns, improved and corrected by R-Core. Negative argument added by Vincent Goulet.

### Examples

```
head(letters)
head(letters, n = -6L)

head(freeny.x, n = 10L)
head(freeny.y)

tail(letters)
tail(letters, n = -6L)

tail(freeny.x)
tail(freeny.y)

tail(library)

head(stats::ftable(Titanic))
```

## Description

help is the primary interface to the help systems.

## Usage

```
help(topic, package = NULL, lib.loc = NULL,
      verbose = getOption("verbose"),
      try.all.packages = getOption("help.try.all.packages"),
      help_type = getOption("help_type"))
```

## Arguments

topic	usually, a <a href="#">name</a> or character string specifying the topic for which help is sought. A character string (enclosed in explicit single or double quotes) is always taken as naming a topic. If the value of <code>topic</code> is a length-one character vector the topic is taken to be the value of the only element. Otherwise <code>topic</code> must be a name or a <a href="#">reserved</a> word (if syntactically valid) or character string. See ‘Details’ for what happens if this is omitted.
package	a name or character vector giving the packages to look into for documentation, or <code>NULL</code> . By default, all packages in the search path are used. To avoid a name being deparsed use e.g. <code>(pkg_ref)</code> .
lib.loc	a character vector of directory names of R libraries, or <code>NULL</code> . The default value of <code>NULL</code> corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries.
verbose	logical; if <code>TRUE</code> , the file name is reported.
try.all.packages	logical; see Note.
help_type	character string: the type of help required. Possible values are "text", "html", "postscript", "ps" and "pdf". Case is ignored, and partial matching is allowed.

## Details

The following types of help are available:

- Plain text help
- HTML help pages with hyperlinks to other topics, shown in a browser by [browseURL](#). (Where possible an existing browser window is re-used: the Mac OS X GUI uses its own browser window.) If for some reason HTML help is unavailable (see [startDynamicHelp](#)), plain text help will be used instead.
- For help only, typeset as a PostScript or PDF file – see the section on ‘Offline help’.

The ‘factory-fresh’ default is text help except from the Mac OS GUI, which uses HTML help displayed in its own browser window.

The rendering of text help will use directional quotes in suitable locales (UTF-8 and single-byte Windows locales): sometimes the fonts used do not support these quotes so this can be turned off by setting `options(useFancyQuotes = FALSE)`.

`topic` is not optional: if it is omitted `R` will give (text) information on the package (including hints to suitable help topics) if a package is specified, a (text) list of available packages if `lib.loc` only is specified, and help on `help` itself if none of the first three arguments is specified.

Some topics need to be quoted (by `backticks`) or given as a character string. There include those which cannot syntactically appear on their own such as unary and binary operators, `function` and control-flow `reserved` words (including `if`, `else`, `for`, `in`, `repeat`, `while`, `break` and `next`). The other `reserved` words can be used as if they were names, for example `TRUE`, `NA` and `Inf`.

If multiple help files matching `topic` are found, in interactive use a menu is presented for the user to choose one: in batch use the first on the search path is used. (For HTML help the menu will be an HTML page, otherwise a graphical menu if possible if `getOption("menu.graphics")` is true, the default.)

## Offline help

Typeset documentation is produced by running the LaTeX version of the help page through `latex` and `dvips` or, if `help_type = "PDF"`, `pdflatex`. This will produce either a PostScript or PDF file and possibly (depending on the configuration of `dvips`) send a PostScript file to a printer. You can set `options("dvipscmd")` to customize how `dvips` is called.

The appearance of the output can be customized through a file ‘`Rhelp.cfg`’ somewhere in your LaTeX search path: this will be input as a LaTeX style file after `Rd.sty`. Some `environment variables` are consulted, notably `R_PAPERSIZE` (via `getOption("papersize")`) and `R_RD4DVI` / `R_RD4PDF` (see ‘Making manuals’ in the ‘R Installation and Administration Manual’).

If there is a function `offline_help_helper` in the workspace or further down the search path it is used to do the typesetting, otherwise the function of that name in the `utils` name space (to which the first paragraph applies). It should have two arguments, the name of the LaTeX file to be typeset and the type.

## Note

Unless `lib.loc` is specified explicitly, the loaded packages are searched before those in the specified libraries. This ensures that if a library is loaded from a library not in the known library trees, then the help from the loaded library is used. If `lib.loc` is specified explicitly, the loaded packages are *not* searched.

If this search fails and argument `try.all.packages` is `TRUE` and neither `packages` nor `lib.loc` is specified, then all the packages in the known library trees are searched for help on `topic` and a list of (any) packages where help may be found is displayed (with hyperlinks for `help_type = "html"`). **NB:** searching all packages can be slow, especially the first time (caching of files by the OS can expedite subsequent searches dramatically).

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

? for shortcuts to help topics.

help.search() or ?? for finding help pages on a vague topic; help.start() which opens the HTML version of the R help pages; library() for listing available packages and the help objects they contain; data() for listing available data sets; methods().

Use prompt() to get a prototype for writing help pages of your own package.

**Examples**

```
help()
help(help)           # the same

help(lapply)

help("for")          # or ?"for", but quotes/backticks are needed

help(package="splines") # get help even when package is not loaded

topi <- "women"
help(topi)

try(help("bs", try.all.packages=FALSE)) # reports not found (an error)
help("bs", try.all.packages=TRUE)       # reports can be found
                                         # in package 'splines'
```

---

help.request                      *Send a Post to R-help*

---

**Description**

Prompts the user to check they have done all that is expected of them before sending a post to the R-help mailing list, provides a template for the post with session information included and optionally sends the email (on Unix systems).

**Usage**

```
help.request(subject = "",
              ccaddress = Sys.getenv("USER"),
              method = getOption("mailer"),
              address = "r-help@R-project.org",
              file = "R.help.request")
```

**Arguments**

subject	subject of the email. Please do not use single quotes (') in the subject! Post separate help requests for multiple queries.
ccaddress	optional email address for copies (default is current user). Use ccaddress = FALSE for no copies.
method	submission method: for Unix one of "mailx", "gnudoit", "none" or "ess"; for Windows either "none" (default) or "mailto".
address	recipient's email address.

`file` file to use for setting up the email (or storing it when method is "none" or sending mail fails).

## Details

This function is not intended to replace the posting guide. Please read the guide before posting to R-help or using this function (see <http://www.r-project.org/posting-guide.html>).

The `help.request` function:

- asks whether the user has consulted relevant resources, stopping and opening the relevant url if a negative response is given.
- checks whether the current version of R is being used and whether the add-on packages are up-to-date, giving the option of updating where necessary.
- asks whether the user has prepared appropriate (minimal, reproducible, self-contained, commented) example code ready to paste into the post.

Once this checklist has been completed a template post is prepared including current session information.

If method is "none" or NULL, then the default text editor is opened for the user to complete the post. Which editor is used can be controlled using `options`, type `getOption("editor")` to see what editor is currently defined. Please use the help pages of the respective editor for details of usage. The report can then be copied to your favorite email program and sent to the r-help list.

On Windows systems there is an experimental "mailto" option, which sends the template post to the system's default email program for the user to edit and send.

On Unix systems there are three options for direct submission of the post. If the submission method is "mailx", then the default editor is used to write the help request. After saving the help request (in the temporary file opened) and exiting the editor the report is mailed using a Unix command line mail utility such as `mailx`. A copy of the mail is sent to the current user. If method is "gnudoit", then an emacs mail buffer is opened and used for sending the email. If method is "ess" the body of the mail is simply sent to stdout.

## Value

Nothing useful.

## Author(s)

Heather Turner, based on code and help page of `bug.report()`.

## See Also

The posting guide (<http://www.r-project.org/posting-guide.html>), also `sessionInfo()` from which you may add to the help request.

---

help.search                      *Search the Help System*

---

### Description

Allows for searching the help system for documentation matching a given character string in the (file) name, alias, title, concept or keyword entries (or any combination thereof), using either [fuzzy matching](#) or [regular expression](#) matching. Names and titles of the matched help entries are displayed nicely formatted.

### Usage

```
help.search(pattern, fields = c("alias", "concept", "title"),
            apropos, keyword, whatis, ignore.case = TRUE,
            package = NULL, lib.loc = NULL,
            help.db = getOption("help.db"),
            verbose = getOption("verbose"),
            rebuild = FALSE, agrep = NULL, use_UTF8 = FALSE)
??pattern
field??pattern
```

### Arguments

pattern	a character string to be matched in the specified fields. If this is given, the arguments <code>apropos</code> , <code>keyword</code> , and <code>whatis</code> are ignored.
fields	a character vector specifying the fields of the help database to be searched. The entries must be abbreviations of "name", "title", "alias", "concept", and "keyword", corresponding to the help page's (file) name, its title, the topics and concepts it provides documentation for, and the keywords it can be classified to.
apropos	a character string to be matched in the help page topics and title.
keyword	a character string to be matched in the help page 'keywords'. 'Keywords' are really categories: the standard categories are listed in file <code>'R.home("doc")/KEYWORDS'</code> (see also the example) and some package writers have defined their own. If <code>keyword</code> is specified, <code>agrep</code> defaults to <code>FALSE</code> .
whatis	a character string to be matched in the help page topics.
ignore.case	a logical. If <code>TRUE</code> , case is ignored during matching; if <code>FALSE</code> , pattern matching is case sensitive.
package	a character vector with the names of packages to search through, or <code>NULL</code> in which case <i>all</i> available packages in the library trees specified by <code>lib.loc</code> are searched.
lib.loc	a character vector describing the location of R library trees to search through, or <code>NULL</code> . The default value of <code>NULL</code> corresponds to all libraries currently known.
help.db	a character string giving the file path to a previously built and saved help database, or <code>NULL</code> .
verbose	logical; if <code>TRUE</code> , the search process is traced. Integer values are also accepted, with <code>TRUE</code> being equivalent to 2, and 1 being less verbose. On Windows a progress bar is shown during rebuilding, and on Unix a heartbeat is shown for <code>verbose = 1</code> and a package-by-package list for <code>verbose &gt;= 2</code> .



<code>rebuild</code>	a logical indicating whether the help database should be rebuilt. This will be done automatically if <code>lib.loc</code> or the search path is changed, or if <code>package</code> is used and a value is not found.
<code>agrep</code>	if <code>NULL</code> (the default unless <code>keyword</code> is used) and the character string to be matched consists of alphanumeric characters, whitespace or a dash only, approximate (fuzzy) matching via <code>agrep</code> is used unless the string has fewer than 5 characters; otherwise, it is taken to contain a <a href="#">regular expression</a> to be matched via <code>grep</code> . If <code>FALSE</code> , approximate matching is not used. Otherwise, one can give a numeric or a list specifying the maximal distance for the approximate match, see argument <code>max.distance</code> in the documentation for <code>agrep</code> .
<code>use_UTF8</code>	logical: should be results be given in UTF-8 encoding? Also changes the meaning of regexps in <code>agrep</code> to be Perl regexps.
<code>field</code>	a single value of <code>fields</code> to search.

### Details

Upon installation of a package, a pre-built `help.search` index is serialized as `'hsearch.rds'` in the `'Meta'` directory (provided the package has any help pages). These files are used to create the database.

The arguments `apropos` and `whatIs` play a role similar to the Unix commands with the same names.

Searching with `agrep = FALSE` will be several times faster than the default (once the database is built). However, as from R 2.10.0 approximate searches should be fast enough (around a second with 2000 packages installed).

If possible, the help database is saved in memory or (if memory limits have been set: see [mem.limits](#)) to a file in the session temporary directory for use by subsequent calls in the session.

Note that currently the aliases in the matching help files are not displayed.

As with `?`, in `??` the pattern may be prefixed with a package name followed by `::` or `:::` to limit the search to that package.

### Value

The results are returned in a list object of class `"hsearch"`, which has a print method for nicely formatting the results of the query. This mechanism is experimental, and may change in future versions of R.

In R.app on Mac OS X, this will show up a browser with selectable items. On exiting this browser, the help pages for the selected items will be shown in separate help windows.

The internal format of the class is undocumented and subject to change.

### See Also

[help](#); [help.start](#) for starting the hypertext (currently HTML) version of R's online documentation, which offers a similar search mechanism.

[RSiteSearch](#) to access an on-line search of R resources.

[apropos](#) uses regexps and has nice examples.

**Examples**

```

help.search("linear models")      # In case you forgot how to fit linear
                                # models
help.search("non-existent topic")

??utils::help # All the topics matching "help" in the utils package

## Not run:
help.search("print")              # All help pages with topics or title
                                # matching 'print'
help.search(apropos = "print")    # The same

help.search(keyword = "hplot")    # All help pages documenting high-level
                                # plots.
file.show(file.path(R.home("doc"), "KEYWORDS")) # show all keywords

## Help pages with documented topics starting with 'try'.
help.search("\\btry", fields = "alias")

## End(Not run)

```

---

help.start

*Hypertext Documentation*


---

**Description**

Start the hypertext (currently HTML) version of R's online documentation.

**Usage**

```

help.start(update = FALSE, gui = "irrelevant",
           browser = getOption("browser"), remote = NULL)

```

**Arguments**

update	logical: should this attempt to update the package index to reflect the currently available packages. (Not attempted if <code>remote</code> is non-NULL.)
gui	just for compatibility with S-PLUS.
browser	the name of the program to be used as hypertext browser. It should be in the <code>PATH</code> , or a full path specified. Alternatively, it can be an R function which will be called with a URL as its only argument. This option is normally unset on Windows, when the file-association mechanism will be used.
remote	A character string giving a valid URL for the ' <i>R_HOME</i> ' directory on a remote location.

**Details**

Unless `remote` is specified this requires the HTTP server to be available (it will be started if possible: see [startDynamicHelp](#)).

One of the links on the index page is the HTML package index, '`R.home("docs")/html/packages.html`', which can be remade by

`make.packages.html` (`temp = FALSE`). For local operation, the HTTP server will remake a temporary version of this list when the link is first clicked, and each time thereafter check if updating is needed (if `.libPaths` has changed or any of the directories has been changed). This can be slow, and using `update = TRUE` will ensure that the packages list is updated before launching the index page.

Argument `remote` can be used to point to HTML help published by another R installation: it will typically only show packages from the main library of that installation.

### See Also

`help()` for on- and off-line help in other formats.

`browseURL` for how the help file is displayed.

`RSiteSearch` to access an on-line search of R resources.

### Examples

```
help.start()
## Not run:
## the 'remote' arg can be tested by
help.start(remote=paste("file://", R.home(), sep=""))

## End(Not run)
```

---

INSTALL

*Install Add-on Packages*

---

### Description

Utility for installing add-on packages.

### Usage

```
R CMD INSTALL [options] [-l lib] pkgs
```

### Arguments

<code>pkgs</code>	a space-separated list with the path names of the packages to be installed.
<code>lib</code>	the path name of the R library tree to install to. Also accepted in the form <code>'--library=lib'</code> .
<code>options</code>	a space-separated list of options through which in particular the process for building the help files can be controlled. Most options should only be given once, and paths including spaces should be quoted. Use <code>R CMD INSTALL --help</code> for the full current list of options.

## Details

This will stop at the first error, so if you want all the `pkgs` to be tried, call this via a shell loop.

If used as `R CMD INSTALL pkgs` without explicitly specifying `lib`, packages are installed into the library tree rooted at the first directory in the library path which would be used by `R` run in the current environment.

To install into the library tree `lib`, use `R CMD INSTALL -l lib pkgs`. This prepends `lib` to the library path for duration of the install, so required packages in the installation directory will be found (and used in preference to those in other libraries).

Both `lib` and the elements of `pkgs` may be absolute or relative path names of directories. `pkgs` may also contain names of package archive files: these are then extracted to a temporary directory. These are tarballs containing a single directory, optionally compressed by `gzip`, `bzip2`, `xz` or `compress`. Finally, binary package archive files (as created by `R CMD INSTALL --binary`) can be supplied.

Tarballs are by default unpackaged by the internal `tar` function: if needed an external `tar` command can be specified by the environment variable `R_INSTALL_TAR`: please ensure that it can handle the type of compression used on the tarball.

The package sources can be cleaned up prior to installation by `--preclean` or after by `--clean`: cleaning is essential if the sources are to be used with more than one architecture or platform.

Some package sources contain a `configure` script that can be passed arguments or variables via the option `--configure-args` and `--configure-vars`, respectively, if necessary. The latter is useful in particular if libraries or header files needed for the package are in non-system directories. In this case, one can use the configure variables `LIBS` and `CPPFLAGS` to specify these locations (and set these via `--configure-vars`), see section “Configuration variables” in “R Installation and Administration” for more information. (If these are used more than once on the command line they are concatenated.) The configure mechanism can be bypassed using the option `--no-configure`.

If the attempt to install the package fails, leftovers are removed. If the package was already installed, the old version is restored. This happens either if a command encounters an error or if the install is interrupted from the keyboard: after cleaning up the script terminates.

By default the library directory is ‘locked’ by creating a directory `00LOCK` within it. This has two purposes: it prevents any other process installing into that library concurrently, and is used to store any previous version of the package to restore on error. A finer-grained locking is provided by the option `--pkglock` which creates a separate lock for each package: this allows enough freedom for careful parallel installation as done by `install.packages(Ncpus = n)` with  $n > 1$ . Finally locking (and restoration on error) can be suppressed by `--no-lock` or `--unsafe` (two names for the same option).

Some platforms (notably Mac OS X) support sub-architectures in which binaries for different CPUs are installed within the same library tree. For such installations, the default behaviour is to try to build packages for all installed sub-architectures unless the package has a `configure` script or a `src/Makefile`, when only the sub-architecture running `R CMD INSTALL` is used. To use only that sub-architecture, use `--no-multiarch`. To install just the compiled code for another sub-architecture, use `--libs-only`.

Use `R CMD INSTALL --help` for concise usage information, including all the available options

## Packages using the methods package

Packages that require the `methods` package and make use functions such as `setMethod` or `setClass`, should be installed using lazy-loading: use the field `LazyLoad` in the `DESCRIPTION` file to ensure this.

**Note**

Some parts of the operation of `INSTALL` depend on the R temporary directory (see `tempdir`, usually under `'tmp'`) having both write and execution access to the account running R. This is usually the case, but if `'tmp'` has been mounted as `noexec`, environment variable `TMPDIR` may need to be set to a directory from which execution is allowed.

**See Also**

`REMOVE` and `library` for information on using several library trees; `update.packages` for automatic update of packages using the internet (or other R level installation of packages, such as by `install.packages`).

The section on “Add-on packages” in “R Installation and Administration” and the chapter on “Creating R packages” in “Writing R Extensions” `RShowDoc` and the `'doc/manual'` subdirectory of the R source tree).

---

`install.packages`     *Install Packages from CRAN-like Repositories*

---

**Description**

Download and install packages from CRAN-like repositories or from local files.

**Usage**

```
install.packages(pkgs, lib, repos = getOption("repos"),
                 contriburl = contrib.url(repos, type),
                 method, available = NULL, destdir = NULL,
                 dependencies = NA, type = getOption("pkgType"),
                 configure.args = getOption("configure.args"),
                 configure.vars = getOption("configure.vars"),
                 clean = FALSE, Ncpus = getOption("Ncpus"), ...)
```

**Arguments**

<code>pkgs</code>	<p>character vector of the short names of packages whose current versions should be downloaded from the repositories.</p> <p>If <code>repos = NULL</code>, a character vector of file paths of <code>'tar.gz'</code> files. These can be source archives or binary package archive files (as created by R <code>CMD build --binary</code>). Tilde-expansion will be done on the file paths.</p> <p>If this is a zero-length character vector, a listbox of available packages is presented where possible.</p>
<code>lib</code>	<p>character vector giving the library directories where to install the packages. Recycled as needed. If missing, defaults to the first element of <code>.libPaths()</code>.</p>
<code>repos</code>	<p>character vector, the base URL(s) of the repositories to use, i.e., the URL of the CRAN master such as <code>"http://cran.r-project.org"</code> or its Statlib mirror, <code>"http://lib.stat.cmu.edu/R/CRAN"</code>.</p> <p>Can be <code>NULL</code> to install from local files (with extension <code>'tar.gz'</code> for source packages).</p>

<code>contriburl</code>	URL(s) of the contrib sections of the repositories. Use this argument only if your repository mirror is incomplete, e.g., because you burned only the ‘contrib’ section on a CD. Overrides argument <code>repos</code> . As with <code>repos</code> , can also be NULL to install from local files.
<code>method</code>	download method, see <a href="#">download.file</a> .
<code>available</code>	an object as returned by <a href="#">available.packages</a> listing packages available at the repositories, or NULL which makes an internal call to <code>available.packages</code> .
<code>destdir</code>	directory where downloaded packages are stored. If it is NULL (the default) a directory <code>downloaded_packages</code> of the session temporary directory will be used (and the files will be deleted at the end of the session).
<code>dependencies</code>	logical indicating to also install uninstalled packages on which these packages depend/suggest/import (and so on recursively). Not used if <code>repos = NULL</code> . Can also be a character vector, a subset of <code>c("Depends", "Imports", "LinkingTo", "Suggests", "Enhances")</code> . Only supported if <code>lib</code> is of length one (or missing), so it is unambiguous where to install the dependent packages. The default, NA, means <code>c("Depends", "Imports", "LinkingTo")</code> if <code>lib</code> is unambiguous, and FALSE otherwise.
<code>type</code>	character, indicating the type of package to download and install. Possible values are "source", "mac.binary", "mac.binary.leopard", "win.binary" and "win64.binary": the binary types can be listed and downloaded but not installed on other platforms. The default is the appropriate binary type on Windows and on the CRAN binary Mac OS X distribution, otherwise "source".
<code>configure.args</code>	(not used on Windows) a character vector or a named list. If a character vector with no names is supplied, the elements are concatenated into a single string (separated by a space) and used as the value for the ‘--configure-args’ flag in the call to <code>R CMD INSTALL</code> . If the character vector has names these are assumed to identify values for ‘--configure-args’ for individual packages. This allows one to specify settings for an entire collection of packages which will be used if any of those packages are to be installed. (These settings can therefore be re-used and act as default settings.) A named list can be used also to the same effect, and that allows multi-element character strings for each package which are concatenated to a single string to be used as the value for ‘--configure-args’.
<code>configure.vars</code>	(not used on Windows) analogous, for ‘--configure-vars’ which is used to set environment variables for the <code>configure</code> run.
<code>clean</code>	a logical value indicating whether to specify to add the ‘--clean’ flag to the call to <code>R CMD INSTALL</code> . This is sometimes used to perform additional operations at the end of the package installation in addition to removing intermediate files.
<code>Ncpus</code>	The number of parallel processes to use for a parallel install of source packages. Values greater than one are supported only if GNU <code>make</code> is in use (more precisely, if <code>make -j Ncpus</code> works). Defaults to 1 if the option is unset.
<code>...</code>	Arguments to be passed to <a href="#">download.file</a> .

## Details

R packages are primarily distributed as *source* packages, but *binary* packages (a packaging up of the installed package) are also available, and the type most commonly used by Windows and users of the Mac OS X GUI R.app. `install.packages` can install either type, either by downloading a file from a repository or from a local file. The default type is given by `getOption("pkgType")`: this "source" apart from under Windows or a CRAN binary distribution for Mac OS X.

`install.packages` is used to install packages. It takes a vector of names and a destination library, downloads the packages from the repositories and installs them. (If the library is omitted it defaults to the first directory in `.libPaths()`, with a warning if there is more than one.) If `lib` is omitted or is of length one and is not a (group) writable directory, the code offers to create a personal library tree (the first element of `Sys.getenv("R_LIBS_USER")`) and install there.

For source packages from a repository is used an attempt is made to install the packages in an order that respects their dependencies. This does assume that all the entries in `lib` are on the default library path for installs (set by `R_LIBS`).

You are advised to run `update.packages` before `install.packages` to ensure that any already installed dependencies have their latest versions.

## Value

Invisible NULL.

## Note

Some binary distributions of R have `INSTALL` in a separate bundle, e.g. an R-devel RPM. `install.packages` will give an error if called with `type = "source"` on such a system.

Some binary distributions can be installed on a machine without the tools needed to install packages: the remedy is to do a complete install of R which should bring in all those tools as dependencies.

## See Also

[update.packages](#), [available.packages](#), [download.packages](#), [installed.packages](#), [contrib.url](#).

See [download.file](#) for how to handle proxies and other options to monitor file transfers.

`INSTALL`, `REMOVE`, [remove.packages](#), [library](#), [.packages](#), [read.dcf](#)

The 'R Installation and Administration' manual for how to set up a repository.

## Examples

```
## Not run:
install.packages(
  c("XML_0.99-5.tar.gz",
    ".././Interfaces/Perl/RSPerl_0.8-0.tar.gz"),
  repos = NULL,
  configure.args = c(XML = '--with-xml-config=xml-config',
                    RSPerl = "--with-modules='IO Fcntl'"))

## End(Not run)
```

---

installed.packages *Find Installed Packages*

---

### Description

Find (or retrieve) details of all packages installed in the specified libraries.

### Usage

```
installed.packages(lib.loc = NULL, priority = NULL,
                  noCache = FALSE, fields = NULL)
```

### Arguments

<code>lib.loc</code>	character vector describing the location of R library trees to search through, or NULL for all known trees (see <code>.libPaths</code> ).
<code>priority</code>	character vector or NULL (default). If non-null, used to select packages; "high" is equivalent to <code>c("base", "recommended")</code> . To select all packages without an assigned priority use <code>priority = "NA"</code> .
<code>noCache</code>	Do not use cached information.
<code>fields</code>	a character vector giving the fields to extract from each package's DESCRIPTION file in addition to the default ones, or NULL (default). Unavailable fields result in NA values.

### Details

`installed.packages` scans the 'DESCRIPTION' files of each package found along `lib.loc` and returns a matrix of package names, library paths and version numbers.

The information found is cached (by library) for the R session and specified `fields` argument, and updated only if the top-level library directory has been altered, for example by installing or removing a package. If the cached information becomes confused, it can be refreshed by running `installed.packages(noCache = TRUE)`.

### Value

A matrix with one row per package, row names the package names and column names "Package", "LibPath", "Version", "Priority", "Depends", "Imports", "LinkingTo", "Suggests", "Enhances", "OS\_type", "License" and "Built" (the R version the package was built under). Additional columns can be specified using the `fields` argument.

### See Also

[update.packages](#), [install.packages](#), [INSTALL](#), [REMOVE](#).

### Examples

```
str(ip <- installed.packages(priority = "high"))
ip[, c(1,3:5)]
plic <- installed.packages(priority = "high", fields="License")
## what licenses are there:
table( plic[, "License"] )
```



---

 LINK

*Create Executable Programs*


---

**Description**

Front-end for creating executable programs.

**Usage**

```
R CMD LINK [options] linkcmd
```

**Arguments**

linkcmd	a list of commands to link together suitable object files (include library objects) to create the executable program.
options	further options to control the linking, or for obtaining information about usage and version.

**Details**

The linker front-end is useful in particular when linking against the R shared library, in which case linkcmd must contain `-lR` but need not specify its library path.

Currently only works if the C compiler is used for linking, and no C++ code is used.

Use `R CMD LINK --help` for more usage information.

**Note**

Some binary distributions of R have LINK in a separate bundle, e.g. an R-devel RPM.

---

 localeToCharset

*Select a Suitable Encoding Name from a Locale Name*


---

**Description**

This functions aims to find a suitable coding for the locale named, by default the current locale, and if it is a UTF-8 locale a suitable single-byte encoding.

**Usage**

```
localeToCharset(locale = Sys.getlocale("LC_CTYPE"))
```

**Arguments**

locale	character string naming a locale.
--------	-----------------------------------

**Details**

The operation differs by OS. Locale names are normally like `es_MX.iso88591`. If final component indicates an encoding and it is not `utf8` we just need to look up the equivalent encoding name. Otherwise, the language (here `es`) is used to choose a primary or fallback encoding.

In the `C` locale the answer will be `"ASCII"`.

**Value**

A character vector naming an encoding and possibly a fallback single-encoding, `NA` if unknown.

**Note**

The encoding names are those used by `libiconv`, and ought also to work with `glibc` but maybe not with commercial Unixen.

**See Also**

[Sys.getlocale](#), [iconv](#).

**Examples**

```
localeToCharset()
```

---

ls.str

*List Objects and their Structure*

---

**Description**

`ls.str` and `lsf.str` are variations of `ls` applying `str()` to each matched name: see section [Value](#).

**Usage**

```
ls.str(pos = -1, name, envir, all.names = FALSE,
       pattern, mode = "any")
```

```
lsf.str(pos = -1, envir, ...)
```

```
## S3 method for class 'ls_str':
print(x, max.level = 1, give.attr = FALSE, ...,
      digits = max(1, getOption("str")$digits.d))
```

**Arguments**

<code>pos</code>	integer indicating <a href="#">search</a> path position.
<code>name</code>	optional name indicating <a href="#">search</a> path position, see <a href="#">ls</a> .
<code>envir</code>	environment to use, see <a href="#">ls</a> .
<code>all.names</code>	logical indicating if names which begin with a <code>.</code> are omitted; see <a href="#">ls</a> .
<code>pattern</code>	a <a href="#">regular expression</a> passed to <a href="#">ls</a> . Only names matching <code>pattern</code> are considered.

<code>max.level</code>	maximal level of nesting which is applied for displaying nested structures, e.g., a list containing sub lists. Default 1: Display only the first nested level.
<code>give.attr</code>	logical; if TRUE (default), show attributes as sub structures.
<code>mode</code>	character specifying the <code>mode</code> of objects to consider. Passed to <code>exists</code> and <code>get</code> .
<code>x</code>	an object of class "ls_str".
<code>...</code>	further arguments to pass. <code>lsf.str</code> passes them to <code>ls.str</code> which passes them on to <code>ls</code> . The (non-exported) print method <code>print.ls_str</code> passes them to <code>str</code> .
<code>digits</code>	the number of significant digits to use for printing.

### Value

`ls.str` and `lsf.str` return an object of class "ls\_str", basically the character vector of matching names (functions only for `lsf.str`), similarly to `ls`, with a `print()` method that calls `str()` on each object.

### Author(s)

Martin Maechler

### See Also

`str`, `summary`, `args`.

### Examples

```
require(stats)

lsf.str()#- how do the functions look like which I am using?
ls.str(mode = "list") #- what are the structured objects I have defined?

## create a few objects
example(glm, echo = FALSE)
ll <- as.list(LETTERS)
print(ls.str(), max.level = 0)# don't show details

## which base functions have "file" in their name ?
lsf.str(pos = length(search()), pattern = "file")

## demonstrating that ls.str() works inside functions
## ["browser/debug mode"]:
tt <- function(x, y=1) { aa <- 7; r <- x + y; ls.str() }
(nms <- sapply(strsplit(capture.output(tt(2)), " *: *"), `[`, 1))
stopifnot(nms == c("aa", "r", "x", "y"))
```

---

`maintainer`*Show Package Maintainer*

---

**Description**

Show the name and email address of the maintainer of a package.

**Usage**

```
maintainer(pkg)
```

**Arguments**

`pkg`                   Character. The name of a single package.

**Details**

Accesses the package description to return the name and email address of the maintainer.

Questions about contributed packages should often be addressed to the package maintainer; questions about base packages should usually be addressed to the R-help or R-devel mailing lists. Bug reports should be submitted using the [bug.report](#) function.

**Value**

A character string giving the name and email address of the maintainer of the package.

**Author(s)**

David Scott <d.scott@auckland.ac.nz> from code on R-help originally due to Charlie Sharpsteen <source@sharpsteen.net>.

**References**

<http://n4.nabble.com/R-help-question-How-can-we-enable-useRs-to-contribute-corr/html>

**See Also**

[packageDescription](#), [bug.report](#)

**Examples**

```
maintainer("MASS")
```

---

make.packages.html *Update HTML Package List*

---

### Description

Re-create the HTML documentation files to reflect all available packages.

### Usage

```
make.packages.html(lib.loc = .libPaths(), temp = TRUE, verbose = TRUE)
```

### Arguments

<code>lib.loc</code>	character vector. List of libraries to be included.
<code>temp</code>	logical: should the package indices be created in a temporary location for use by the HTTP server?
<code>verbose</code>	logical: should messages and a heartbeat be shown?

### Details

This creates the ‘packages.html’ file, either a temporary copy for use by [help.start](#), or the copy in ‘R.home("doc")/html’ (for which you will need write permission).

It can be very slow, as all the package ‘DESCRIPTION’ files in all the library trees are read.

For `temp = TRUE` there is some caching of information, so the file will only be re-created if `lib.loc` or any of the directories it lists have been changed.

### Value

Invisible logical, with `FALSE` indicating a failure to create the file, probably due to lack of suitable permissions.

### See Also

[help.start](#)

### Examples

```
## Not run:  
# to prefer HTML help, put in your .Rprofile  
options(help_type = "html")  
make.packages.html(temp = FALSE)  
# this can be slow for large numbers of installed packages.  
  
## End(Not run)
```

---

`make.socket`*Create a Socket Connection*

---

### Description

With `server = FALSE` attempts to open a client socket to the specified port and host. With `server = TRUE` listens on the specified port for a connection and then returns a server socket. It is a good idea to use [on.exit](#) to ensure that a socket is closed, as you only get 64 of them.

### Usage

```
make.socket(host = "localhost", port, fail = TRUE, server = FALSE)
```

### Arguments

<code>host</code>	name of remote host
<code>port</code>	port to connect to/listen on
<code>fail</code>	failure to connect is an error?
<code>server</code>	a server socket?

### Value

An object of class `"socket"`.

<code>socket</code>	socket number. This is for internal use
<code>port</code>	port number of the connection
<code>host</code>	name of remote computer

### Warning

I don't know if the connecting host name returned when `server = TRUE` can be trusted. I suspect not.

### Author(s)

Thomas Lumley

### References

Adapted from Luke Tierney's code for `XLISP-Stat`, in turn based on code from Robbins and Robbins "Practical UNIX Programming"

### See Also

[close.socket](#), [read.socket](#)

## Examples

```
daytime <- function(host = "localhost"){
  a <- make.socket(host, 13)
  on.exit(close.socket(a))
  read.socket(a)
}
## Official time (UTC) from US Naval Observatory
## Not run: daytime("tick.usno.navy.mil")
```

---

memory.size

*Report on Memory Allocation*

---

## Description

`memory.size` and `memory.limit` are used to manage the total memory allocation on Windows. On other platforms these are stubs which report infinity with a warning.

## Usage

```
memory.size(max = FALSE)
```

```
memory.limit(size = NA)
```

## Arguments

`max` logical. If true the maximum amount of memory obtained from the OS is reported, otherwise the amount currently in use.

`size` numeric. If NA report the memory size, otherwise request a new limit, in Mb.

## Details

To restrict memory usage on a Unix-alike use the facilities of the shell used to launch R, e.g. `limit` or `ulimit`.

## Value

Size in bytes: always `Inf`.

## See Also

[Memory-limits](#) for other limits.

---

menu

*Menu Interaction Function*

---

### Description

menu presents the user with a menu of choices labelled from 1 to the number of choices. To exit without choosing an item one can select '0'.

### Usage

```
menu(choices, graphics = FALSE, title = NULL)
```

### Arguments

choices	a character vector of choices
graphics	a logical indicating whether a graphics menu should be used if available.
title	a character string to be used as the title of the menu. NULL is also accepted.

### Details

If `graphics = TRUE` and a windowing system is available (Windows, Mac OS X or X11 via Tcl/Tk) a listbox widget is used, otherwise a text menu. It is an error to use menu in a non-interactive session.

Ten or fewer items will be displayed in a single column, more in multiple columns if possible within the current display width.

No title is displayed if `title` is NULL or "".

### Value

The number corresponding to the selected item, or 0 if no choice was made.

### References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

### See Also

[select.list](#), which is used to implement the graphical menu, and allows multiple selections.

### Examples

```
## Not run:
switch(menu(c("List letters", "List LETTERS")) + 1,
        cat("Nothing done\n"), letters, LETTERS)

## End(Not run)
```



---

 methods

*List Methods for S3 Generic Functions or Classes*


---

**Description**

List all available methods for an S3 generic function, or all methods for a class.

**Usage**

```
methods(generic.function, class)
```

**Arguments**

<code>generic.function</code>	a generic function, or a character string naming a generic function.
<code>class</code>	a symbol or character string naming a class: only used if <code>generic.function</code> is not supplied.

**Details**

Function `methods` can be used to find out about the methods for a particular generic function or class. The functions listed are those which *are named like methods* and may not actually be methods (known exceptions are discarded in the code). Note that the listed methods may not be user-visible objects, but often help will be available for them.

If `class` is used, we check that a matching generic can be found for each user-visible object named. If `generic.function` is given, there is a warning if it appears not to be a generic function. (The check for being generic used can be fooled.)

**Value**

An object of class "MethodsFunction", a character vector of function names with an "info" attribute. There is a `print` method which marks with an asterisk any methods which are not visible: such functions can be examined by `getS3method` or `getAnywhere`.

The "info" attribute is a data frame, currently with a logical column, `visible` and a factor column `from` (indicating where the methods were found).

**Note**

This scheme is called *S3* (S version 3). For new projects, it is recommended to use the more flexible and robust *S4* scheme provided in the **methods** package. Functions can have both S3 and S4 methods, and function `showMethods` will list the S4 methods (possibly none).

The original `methods` function was written by Martin Maechler.

**References**

Chambers, J. M. (1992) *Classes and methods: object-oriented programming in S*. Appendix A of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

[S3Methods](#), [class](#), [getS3method](#).

For S4, [showMethods](#), [Methods](#).

**Examples**

```
require(stats)

methods(summary)
methods(class = "aov")
methods("[") # uses C-internal dispatching
methods("$")
methods("$<-") # replacement function
methods("+") # binary operator
methods("Math") # group generic
require(graphics)
methods("axis") # looks like it has methods, but not generic
## Not run:
methods(print) # over 100

## End(Not run)
## --> help(showMethods) for related examples
```

---

 mirrorAdmin

*Managing Repository Mirrors*


---

**Description**

Functions helping to maintain CRAN, some of them may also be useful for administrators of other repository networks.

**Usage**

```
mirror2html(mirrors = NULL, file = "mirrors.html",
            head = "mirrors-head.html", foot = "mirrors-foot.html")
checkCRAN(method)
```

**Arguments**

mirrors	A data frame, by default the CRAN list of mirrors is used.
file	A connection object or a character string.
head	Name of optional header file.
foot	Name of optional footer file.
method	Download method, see <code>download.file</code> .

**Details**

`mirror2html` creates the HTML file for the CRAN list of mirrors and invisibly returns the HTML text.

`checkCRAN` performs a sanity checks on all CRAN mirrors.

---

`modifyList`*Recursively Modify Elements of a List*

---

**Description**

Modifies a possibly nested list recursively by changing a subset of elements at each level to match a second list.

**Usage**

```
modifyList(x, val)
```

**Arguments**

`x` a named `list`, possibly empty.  
`val` a named list with components to replace corresponding components in `x`.

**Value**

A modified version of `x`, with the modifications determined as follows (here, list elements are identified by their names). Elements in `val` which are missing from `x` are added to `x`. For elements that are common to both but are not both lists themselves, the component in `x` is replaced by the one in `val`. For common elements that are both lists, `x[[name]]` is replaced by `modifyList(x[[name]], val[[name]])`.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**Examples**

```
foo <- list(a = 1, b = list(c = "a", d = FALSE))
bar <- modifyList(foo, list(e = 2, b = list(d = TRUE)))
str(foo)
str(bar)
```

---

`news`*Build and Query R or Package News Information*

---

**Description**

Build and query the news for R or add-on packages.

**Usage**

```
news(query, package = "R", lib.loc = NULL, format = NULL,
      reader = NULL, db = NULL)
```

## Arguments

<code>query</code>	an expression for selecting news entries
<code>package</code>	a character string giving the name of an installed add-on package, or "R".
<code>lib.loc</code>	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known.
<code>format</code>	Not yet used.
<code>reader</code>	Not yet used.
<code>db</code>	a news db obtained from <code>news()</code> .

## Details

If `package` is "R" (default), `readNEWS` in package `tools` is used to build a news db from the R 'NEWS' file. Otherwise, if the given add-on package can be found in the given libraries and has a 'NEWS' file, it is attempted to read the package news in structured form. The 'NEWS' files in add-on packages use a variety of different formats; the default news reader should be capable to extract individual news entries from a majority of packages from the standard repositories, which use (slight variations of) the following format:

- Entries are grouped according to version, with version header 'Changes in version' at the beginning of a line, followed by a version number, optionally followed by an ISO 8601 (%Y-%m-%d, see `strptime`) format date, possibly parenthesized.
- Entries may be grouped according to category, with a category header (different from a version header) starting at the beginning of a line.
- Entries are written as itemize-type lists, using one of 'o', '\*', '-' or '+' as item tag. Entries must be indented, and ideally use a common indentation for the item texts.

Additional formats and readers may be supported in the future.

The news db built is a character data frame inheriting from "news\_db" with variables `Version`, `Category`, `Date` and `Text`, where the last contains the entry texts read, and the other variables may be NA if they were missing or could not be determined.

Using `query`, one can select news entries from the db. If missing or NULL, the complete db is returned. Otherwise, `query` should be an expression involving (a subset of) the variables `Version`, `Category`, `Date` and `Text`, and when evaluated within the db returning a logical vector with length the number of entries in the db. The entries for which evaluation gave TRUE are selected. When evaluating, `Version` and `Date` are coerced to `numeric_version` and `Date` objects, respectively, so that the comparison operators for these classes can be employed.

## Value

An data frame inheriting from class "news\_db".

## Examples

```
## Build a db of all R news entries.
db <- news()
## Bug fixes with PR number in 2.9.0.
news(Version == "2.9.0" & grepl("^BUG", Category) & grepl("PR#", Text),
     db = db)
## Entries with version >= 2.8.1 (including "2.8.1 patched"):
table(news(Version >= "2.8.1", db = db)$Version)
```

normalizePath

*Express File Paths in Canonical Form*

---

**Description**

Convert file paths to canonical form for the platform, to display them in a user-understandable form.

**Usage**

```
normalizePath(path)
```

**Arguments**

path                    character vector of file paths.

**Details**

Where the Unix-alike platform supports it this turns paths into absolute paths in their canonical form (no '.', '..', nor symbolic links).

On Windows it converts relative paths to absolute paths, and converts short names to long names. It will always use backslashes as the path separator.

**Value**

A character vector.

If a path is not a real path the result is undefined. On Unix-alikes, this will likely be the corresponding input element. On Windows, it will likely result in an error being signalled.

**Examples**

```
cat(normalizePath(c(R.home(), tempdir())), sep = "\n")
```

---

nsl*Look up the IP Address by Hostname*

---

**Description**

Interface to gethostbyname.

**Usage**

```
nsl(hostname)
```

**Arguments**

hostname                the name of the host.

**Value**

The IP address, as a character string, or NULL if the call fails.

**Note**

This was included as a test of internet connectivity, to fail if the node running R is not connected. It will also return `NULL` if BSD networking is not supported, including the header file ‘arpa/inet.h’.

**Examples**

```
## Not run: nsl("www.r-project.org")
```

---

object.size	<i>Report the Space Allocated for an Object</i>
-------------	---

---

**Description**

Provides an estimate of the memory that is being used to store an R object.

**Usage**

```
object.size(x)

## S3 method for class 'object_size':
print(x, quote = FALSE,
      units = c("b", "auto", "Kb", "Mb", "Gb"), ...)
```

**Arguments**

<code>x</code>	An R object.
<code>quote</code>	logical, indicating whether or not the result should be printed with surrounding quotes.
<code>units</code>	The units to be used in printing the size.
<code>...</code>	Arguments to be passed to or from other methods.

**Details**

Exactly which parts of the memory allocation should be attributed to which object is not clear-cut. This function merely provides a rough indication: it should be reasonably accurate for atomic vectors, but does not detect if elements of a list are shared, for example. (Sharing amongst elements of a character vector is taken into account, but not that between character vectors in a single object.)

The calculation is of the size of the object, and excludes the space needed to store its name in the symbol table.

Associated space (e.g. the environment of a function and what the pointer in a `EXTPTRSXP` points to) is not included in the calculation.

Object sizes are larger on 64-bit builds than 32-bit ones, but will very likely be the same on different platforms with the same word length and pointer size.

**Value**

An object of class "object.size" with a length-one double value, an estimate of the memory allocation attributable to the object in bytes.

**See Also**

[Memory-limits](#) for the design limitations on object size.

**Examples**

```
object.size(letters)
object.size(ls)
print(object.size(library), units = "auto")
## find the 10 largest objects in the base package
z <- sapply(ls("package:base"), function(x)
            object.size(get(x, envir = baseenv())))
as.matrix(rev(sort(z)) [1:10])
```

---

package.skeleton    *Create a Skeleton for a New Source Package*

---

**Description**

`package.skeleton` automates some of the setup for a new source package. It creates directories, saves functions, data, and R code files to appropriate places, and creates skeleton help files and a ‘Read-and-delete-me’ file describing further steps in packaging.

**Usage**

```
package.skeleton(name = "anRpackage", list,
                 environment = .GlobalEnv,
                 path = ".", force = FALSE, namespace = FALSE,
                 code_files = character())
```

**Arguments**

<code>name</code>	character string: the package name and directory name for your package.
<code>list</code>	character vector naming the R objects to put in the package. Usually, at most one of <code>list</code> , <code>environment</code> , or <code>code_files</code> will be supplied. See ‘Details’.
<code>environment</code>	an environment where objects are looked for. See ‘Details’.
<code>path</code>	path to put the package directory in.
<code>force</code>	If <code>FALSE</code> will not overwrite an existing directory.
<code>namespace</code>	a logical indicating whether to add a name space for the package. If <code>TRUE</code> , a <code>NAMESPACE</code> file is created to export all objects whose names begin with a letter, plus all S4 methods and classes.
<code>code_files</code>	a character vector with the paths to R code files to build the package around. See ‘Details’.

## Details

The arguments `list`, `environment`, and `code_files` provide alternative ways to initialize the package. If `code_files` is supplied, the files so named will be sourced to form the environment, then used to generate the package skeleton. Otherwise `list` defaults to the non-hidden files in `environment` (those whose name does not start with `.`), but can be supplied to select a subset of the objects in that environment.

Stubs of help files are generated for functions, data objects, and S4 classes and methods, using the `prompt`, `promptClass`, and `promptMethods` functions.

The package sources are placed in subdirectory `name` of `path`. If `code_files` is supplied, these files are copied; otherwise, objects will be dumped into individual source files. The file names in `code_files` should have suffix `".R"` and be in the current working directory.

The filenames created for source and documentation try to be valid for all OSes known to run R. Invalid characters are replaced by `'_'`, invalid names are preceded by `'zz'`, names are converted to lower case (to avoid case collisions on case-insensitive file systems) and finally the converted names are made unique by `make.unique` (`sep = "_"`). This can be done for code and help files but not data files (which are looked for by name). Also, the code and help files should have names starting with an ASCII letter or digit, and this is checked and if necessary `z` prepended.

When you are done, delete the `'Read-and-delete-me'` file, as it should not be distributed.

## Value

Used for its side-effects.

## References

Read the *Writing R Extensions* manual for more details.

Once you have created a *source* package you need to install it: see the *R Installation and Administration* manual, `INSTALL` and `install.packages`.

## See Also

`prompt`, `promptClass`, and `promptMethods`.

## Examples

```
require(stats)
## two functions and two "data sets" :
f <- function(x,y) x+y
g <- function(x,y) x-y
d <- data.frame(a=1, b=2)
e <- rnorm(1000)

package.skeleton(list=c("f", "g", "d", "e"), name="mypkg")
```



packageDescription *Package Description*

---

### Description

Parses and returns the ‘DESCRIPTION’ file of a package.

### Usage

```
packageDescription(pkg, lib.loc = NULL, fields = NULL,  
                  drop = TRUE, encoding = "")
```

### Arguments

pkg	a character string with the package name.
lib.loc	a character vector of directory names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries.
fields	a character vector giving the tags of fields to return (if other fields occur in the file they are ignored).
drop	If TRUE and the length of fields is 1, then a single character string with the value of the respective field is returned instead of an object of class "packageDescription".
encoding	If there is an Encoding field, to what encoding should re-encoding be attempted? If NA, no re-encoding. The other values are as used by <a href="#">iconv</a> , so the default "" indicates the encoding of the current locale.

### Details

A package will not be ‘found’ unless it has a ‘DESCRIPTION’ file which contains a valid Version field. Different warnings are given when no package directory is found and when there is a suitable directory but no valid ‘DESCRIPTION’ file.

An [attached](#) environment named to look like a package (e.g. `package:utils2`) will be ignored.

### Value

If a ‘DESCRIPTION’ file for the given package is found and can successfully be read, `packageDescription` returns an object of class "packageDescription", which is a named list with the values of the (given) fields as elements and the tags as names, unless `drop = TRUE`.

If parsing the ‘DESCRIPTION’ file was not successful, it returns a named list of NAs with the field tags as names if `fields` is not null, and NA otherwise.

### See Also

[read.dcf](#)

**Examples**

```

packageDescription("stats")
packageDescription("stats", fields = c("Package", "Version"))

packageDescription("stats", fields = "Version")
packageDescription("stats", fields = "Version", drop = FALSE)

```

---

packageStatus	<i>Package Management Tools</i>
---------------	---------------------------------

---

**Description**

Summarize information about installed packages and packages available at various repositories, and automatically upgrade outdated packages.

**Usage**

```

packageStatus(lib.loc = NULL, repositories = NULL, method,
              type = getOption("pkgType"))

## S3 method for class 'packageStatus':
summary(object, ...)

## S3 method for class 'packageStatus':
update(object, lib.loc = levels(object$inst$LibPath),
        repositories = levels(object$avail$Repository), ...)

## S3 method for class 'packageStatus':
upgrade(object, ask = TRUE, ...)

```

**Arguments**

lib.loc	a character vector describing the location of R library trees to search through, or NULL. The default value of NULL corresponds to all libraries currently known.
repositories	a character vector of URLs describing the location of R package repositories on the Internet or on the local machine.
method	Download method, see <a href="#">download.file</a> .
type	type of package distribution: see <a href="#">install.packages</a> .
object	an object of class "packageStatus" as returned by packageStatus.
ask	if TRUE, the user is prompted which packages should be upgraded and which not.
...	currently not used.

**Details**

The URLs in `repositories` should be full paths to the appropriate contrib sections of the repositories. The default is `contrib.url(getOption("repos"))`.

There are `print` and `summary` methods for the "packageStatus" objects: the `print` method gives a brief tabular summary and the `summary` method prints the results.

The `update` method updates the `"packageStatus"` object. The `upgrade` method is similar to `update.packages`: it offers to install the current versions of those packages which are not currently up-to-date.

### Value

An object of class `"packageStatus"`. This is a list with two components

<code>inst</code>	a data frame with columns as the <i>matrix</i> returned by <code>installed.packages</code> plus <code>"Status"</code> , a factor with levels <code>c("ok", "upgrade")</code> . Only the newest version of each package is reported, in the first repository in which it appears.
<code>avail</code>	a data frame with columns as the <i>matrix</i> returned by <code>available.packages</code> plus <code>"Status"</code> , a factor with levels <code>c("installed", "not installed", "unavailable")</code> ..

### See Also

[installed.packages](#), [available.packages](#)

### Examples

```
## Not run:
x <- packageStatus()
print(x)
summary(x)
upgrade(x)
x <- update(x)
print(x)

## End(Not run)
```

---

page

*Invoke a Pager on an R Object*

---

### Description

Displays a representation of the object named by `x` in a pager *via* `file.show`.

### Usage

```
page(x, method = c("dput", "print"), ...)
```

### Arguments

<code>x</code>	An R object, or a character string naming an object.
<code>method</code>	The default method is to dump the object <i>via</i> <code>dput</code> . An alternative is to use <code>print</code> and capture the output to be shown in the pager.
<code>...</code>	additional arguments for <code>dput</code> , <code>print</code> or <code>file.show</code> (such as <code>title</code> ).

**Details**

If `x` is a length-one character vector, it is used as the name of an object to look up in the environment from which `page` is called. All other objects are displayed directly.

A default value of `title` is passed to `file.show` if one is not supplied in . . . .

**See Also**

[file.show](#), [edit](#), [fix](#).

To go to a new page when graphing, see [frame](#).

**Examples**

```
## Not run: ## four ways to look at the code of 'page'
page(page)           # as an object
page("page")        # a character string
v <- "page"; page(v) # a length-one character vector
page(utils::page)    # a call

## End(Not run)
```

---

person

*Person Names and Contact Information*

---

**Description**

A class and utility methods for holding information about persons like name and email address.

**Usage**

```
person(first = "", last = "", middle = "", email = "")
personList(...)
as.person(x)
as.personList(x)

## S3 method for class 'person':
as.character(x, ...)
## S3 method for class 'personList':
as.character(x, ...)

## S3 method for class 'person':
toBibtex(object, ...)
## S3 method for class 'personList':
toBibtex(object, ...)
```

**Arguments**

<code>first</code>	character string, first name
<code>middle</code>	character string, middle name(s)
<code>last</code>	character string, last name
<code>email</code>	character string, email address

```

...           for personList an arbitrary number of person objects
x             a character string or an object of class person or personList
object       an object of class person or personList

```

### Examples

```

## create a person object directly
p1 <- person("Karl", "Pearson", email = "pearson@stats.heaven")
p1

## convert a string
p2 <- as.person("Ronald Aylmer Fisher")
p2

## create one object holding both
p <- personList(p1, p2)
ps <- as.character(p)
ps
as.personList(ps)

## convert to BibTeX author field
toBibtex(p)

```

---

PkgUtils

*Utilities for Building and Checking Add-on Packages*


---

### Description

Utilities for checking whether the sources of an R add-on package work correctly, and for building a source or binary package from them.

### Usage

```

R CMD build [options] pkgdirs
R CMD check [options] pkgdirs

```

### Arguments

```

pkgdirs       a list of names of directories with sources of R add-on packages. For check this
               can also be the filename of a compressed tar archive with extension ‘.tar.gz’
               or ‘.tgz’ or ‘.tar.bz2’.
options       further options to control the processing, or for obtaining information about us-
               age and version of the utility.

```

### Details

R CMD check checks R add-on packages from their sources, performing a wide variety of diagnostic checks.

R CMD build builds R source or binary packages from their sources. The name(s) of the packages are taken from the ‘DESCRIPTION’ files and not from the directory names.

Use R CMD foo --help to obtain usage information on utility foo.

Several of the options to build --binary are passed to [INSTALL](#) so consult its help for the details.

**See Also**

The sections on “Checking and building packages” and “Processing Rd format” in “Writing R Extensions” (see the ‘doc/manual’ subdirectory of the R source tree).

`INSTALL` is called by `build --binary`.

prompt

*Produce Prototype of an R Documentation File***Description**

Facilitate the constructing of files documenting R objects.

**Usage**

```
prompt(object, filename = NULL, name = NULL, ...)

## Default S3 method:
prompt(object, filename = NULL, name = NULL,
       force.function = FALSE, ...)

## S3 method for class 'data.frame':
prompt(object, filename = NULL, name = NULL, ...)
```

**Arguments**

<code>object</code>	an R object, typically a function for the default method. Can be <code>missing</code> when name is specified.
<code>filename</code>	usually, a connection or a character string giving the name of the file to which the documentation shell should be written. The default corresponds to a file whose name is <code>name</code> followed by <code>".Rd"</code> . Can also be <code>NA</code> (see below).
<code>name</code>	a character string specifying the name of the object.
<code>force.function</code>	a logical. If <code>TRUE</code> , treat <code>object</code> as function in any case.
<code>...</code>	further arguments passed to or from other methods.

**Details**

Unless `filename` is `NA`, a documentation shell for `object` is written to the file specified by `filename`, and a message about this is given. For function objects, this shell contains the proper function and argument names. R documentation files thus created still need to be edited and moved into the ‘man’ subdirectory of the package containing the object to be documented.

If `filename` is `NA`, a list-style representation of the documentation shell is created and returned. Writing the shell to a file amounts to `cat(unlist(x), file = filename, sep = "\n")`, where `x` is the list-style representation.

When `prompt` is used in `for` loops or scripts, the explicit name specification will be useful.

**Value**

If `filename` is `NA`, a list-style representation of the documentation shell. Otherwise, the name of the file written to is returned invisibly.

**Warning**

The default filename may not be a valid filename under limited file systems (e.g. those on Windows).

Currently, calling `prompt` on a non-function object assumes that the object is in fact a data set and hence documents it as such. This may change in future versions of R. Use `promptData` to create documentation skeletons for data sets.

**Note**

The documentation file produced by `prompt.data.frame` does not have the same format as many of the data frame documentation files in the **base** package. We are trying to settle on a preferred format for the documentation.

**Author(s)**

Douglas Bates for `prompt.data.frame`

**References**

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

**See Also**

`promptData`, `help` and the chapter on “Writing R documentation” in “Writing R Extensions” (see the ‘doc/manual’ subdirectory of the R source tree).

For creation of many help pages (for a package), see `package.skeleton`.

To prompt the user for input, see `readline`.

**Examples**

```
require(graphics)
prompt(plot.default)
prompt(interactive, force.function = TRUE)
unlink("plot.default.Rd")
unlink("interactive.Rd")

prompt(women) # data.frame
unlink("women.Rd")

prompt(sunspots) # non-data.frame data
unlink("sunspots.Rd")

## Not run:
## Create a help file for each function in the .GlobalEnv:
for(f in ls()) if(is.function(get(f))) prompt(name = f)

## End(Not run)
```

---

`promptData`*Generate a Shell for Documentation of Data Sets*

---

### Description

Generates a shell of documentation for a data set.

### Usage

```
promptData(object, filename = NULL, name = NULL)
```

### Arguments

<code>object</code>	an R object to be documented as a data set.
<code>filename</code>	usually, a connection or a character string giving the name of the file to which the documentation shell should be written. The default corresponds to a file whose name is <code>name</code> followed by ".Rd". Can also be NA (see below).
<code>name</code>	a character string specifying the name of the object.

### Details

Unless `filename` is NA, a documentation shell for `object` is written to the file specified by `filename`, and a message about this is given.

If `filename` is NA, a list-style representation of the documentation shell is created and returned. Writing the shell to a file amounts to `cat(unlist(x), file = filename, sep = "\n")`, where `x` is the list-style representation.

Currently, only data frames are handled explicitly by the code.

### Value

If `filename` is NA, a list-style representation of the documentation shell. Otherwise, the name of the file written to is returned invisibly.

### Warning

This function is still experimental. Both interface and value might change in future versions. In particular, it may be preferable to use a character string naming the data set and optionally a specification of where to look for it instead of using `object/name` as we currently do. This would be different from `prompt`, but consistent with other `prompt`-style functions in package **methods**, and also allow prompting for data set documentation without explicitly having to load the data set.

### See Also

[prompt](#)

### Examples

```
promptData(sunspots)
unlink("sunspots.Rd")
```



---

`promptPackage`*Generate a Shell for Documentation of a Package*

---

### Description

Generates a shell of documentation for an installed or source package.

### Usage

```
promptPackage(package, lib.loc = NULL, filename = NULL,  
              name = NULL, final = FALSE)
```

### Arguments

<code>package</code>	the name of an <i>installed</i> or <i>source</i> package to be documented.
<code>lib.loc</code>	a character vector describing the location of R library trees to search through, or NULL. The default value of NULL corresponds to all libraries currently known. For a source package this should specify the parent directory of the package's sources.
<code>filename</code>	usually, a connection or a character string giving the name of the file to which the documentation shell should be written. The default corresponds to a file whose name is <code>name</code> followed by ".Rd". Can also be NA (see below).
<code>name</code>	a character string specifying the name of the help topic, typically of the form ' <code>&lt;pkg&gt;-package</code> '.
<code>final</code>	a logical value indicating whether to attempt to create a usable version of the help topic, rather than just a shell.

### Details

Unless `filename` is NA, a documentation shell for `package` is written to the file specified by `filename`, and a message about this is given.

If `filename` is NA, a list-style representation of the documentation shell is created and returned. Writing the shell to a file amounts to `cat(unlist(x), file = filename, sep = "\n")`, where `x` is the list-style representation.

If `final` is TRUE, the generated documentation will not include the place-holder slots for manual editing, it will be usable as-is. In most cases a manually edited file is preferable (but `final = TRUE` is certainly less work).

### Value

If `filename` is NA, a list-style representation of the documentation shell. Otherwise, the name of the file written to is returned invisibly.

### See Also

[prompt](#)

**Examples**

```
filename <- tempfile()
promptPackage("utils", filename = filename)
file.show(filename)
unlink(filename)
```

---

 Question

*Documentation Shortcuts*


---

**Description**

These functions provide access to documentation. Documentation on a topic with name `name` (typically, an R object or a data set) can be displayed by either `help("name")` or `?name`.

**Usage**

```
?topic
type?topic
```

**Arguments**

<code>topic</code>	Usually, a <a href="#">name</a> or character string specifying the topic for which help is sought. Alternatively, a function call to ask for documentation on a corresponding S4 method: see the section on S4 method documentation. The calls <code>pkg::topic</code> and <code>pkg:::topic</code> are treated specially, and look for help on <code>topic</code> in package <code>pkg</code> .
<code>type</code>	the special type of documentation to use for this topic; for example, if the type is <code>class</code> , documentation is provided for the class with name <code>topic</code> . See the Section ‘S4 Method Documentation’ for the uses of <code>type</code> to get help on formal methods, including <code>methods?function</code> and <code>method?call</code> .

**Details**

This is a shortcut to [help](#) and uses its default type of help.

Some topics need to be quoted (by [backticks](#)) or given as a character string. There include those which cannot syntactically appear on their own such as unary and binary operators, `function` and control-flow [reserved](#) words (including `if`, `else`, `for`, `in`, `repeat`, `while`, `break` and `next`). The other reserved words can be used as if they were names, for example `TRUE`, `NA` and `Inf`.

**S4 Method Documentation**

Authors of formal (‘S4’) methods can provide documentation on specific methods, as well as overall documentation on the methods of a particular function. The “?” operator allows access to this documentation in three ways.

The expression `methods?f` will look for the overall documentation methods for the function `f`. Currently, this means the documentation file containing the alias `f-methods`.

There are two different ways to look for documentation on a particular method. The first is to supply the `topic` argument in the form of a function call, omitting the `type` argument. The effect is to look for documentation on the method that would be used if this function call were actually

evaluated. See the examples below. If the function is not a generic (no S4 methods are defined for it), the help reverts to documentation on the function name.

The "?" operator can also be called with `doc_type` supplied as `method`; in this case also, the `topic` argument is a function call, but the arguments are now interpreted as specifying the class of the argument, not the actual expression that will appear in a real call to the function. See the examples below.

The first approach will be tedious if the actual call involves complicated expressions, and may be slow if the arguments take a long time to evaluate. The second approach avoids these issues, but you do have to know what the classes of the actual arguments will be when they are evaluated.

Both approaches make use of any inherited methods; the signature of the method to be looked up is found by using `selectMethod` (see the documentation for `getMethod`).

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

## See Also

[help](#)

?? for finding help pages on a vague topic.

## Examples

```
?lapply

?"for"          # but quotes/backticks are needed
?"+"

?women          # information about data set "women"

## Not run:
require(methods)
## define a S4 generic function and some methods
combo <- function(x, y) c(x, y)
setGeneric("combo")
setMethod("combo", c("numeric", "numeric"), function(x, y) x+y)

## assume we have written some documentation
## for combo, and its methods ....

?combo # produces the function documentation

methods?combo # looks for the overall methods documentation

method?combo("numeric", "numeric") # documentation for the method above

?combo(1:10, rnorm(10)) # ... the same method, selected according to
                        # the arguments (one integer, the other numeric)

?combo(1:10, letters) # documentation for the default method

## End(Not run)
```

## Description

This package provides a mechanism to generate relevant completions from a partially completed command line. It is not intended to be useful by itself, but rather in conjunction with other mechanisms that use it as a backend. The functions listed in the usage section provide a simple control and query mechanism. The actual interface consists of a few unexported functions described further down.

## Usage

```
rc.settings(ops, ns, args, func, ipck, S3, data, help,
            argdb, files)

rc.status()
rc.getOption(name)
rc.options(...)

.DollarNames(x, pattern)

## Default S3 method:
.DollarNames(x, pattern = "")
## S3 method for class 'list':
.DollarNames(x, pattern = "")
## S3 method for class 'environment':
.DollarNames(x, pattern = "")
```

## Arguments

`ops`, `ns`, `args`, `func`, `ipck`, `S3`, `data`, `help`, `argdb`, `files`  
logical, turning some optional completion features on and off.

`ops`: activates completion after the `$` and `@` operators

`ns`: controls name space related completions

`args`: enables completion of function arguments

`func`: enables detection of functions. If enabled, a customizable extension ("`"` by default) is appended to function names. The process of determining whether a potential completion is a function requires evaluation, including for lazy loaded symbols. This is extremely undesirable for large objects, because of potentially wasteful use of memory in addition to the time overhead associated with loading. For this reason, this feature is disabled by default.

`S3`: when `args=TRUE`, activates completion on arguments of all S3 methods (otherwise just the generic, which usually has very few arguments)

`ipck`: enables completion of installed package names inside `library` and `require`

`data`: enables completion of data sets (including those already visible) inside `data`

	<b>help:</b> enables completion of help requests starting with a question mark, by looking inside help index files
	<b>argdb:</b> when <code>args=TRUE</code> , completion is attempted on function arguments. Generally, the list of valid arguments is determined by dynamic calls to <code>args</code> . While this gives results that are technically correct, the use of the <code>...</code> argument often hides some useful arguments. To give more flexibility in this regard, an optional table of valid arguments names for specific functions is retained internally. Setting <code>argdb=TRUE</code> enables preferential lookup in this internal data base for functions with an entry in it. Of course, this is useful only when the data base contains information about the function of interest. Some functions are included in the package (the maintainer is happy to add more upon request), and more can be added by the user through the unexported function <code>.addFunctionInfo</code> (see below).
	<b>files:</b> enables filename completion in R code. This is initially set to <code>FALSE</code> , in which case the underlying completion front-end can take over (and hopefully do a better job than we would have done). For systems where no such facilities exist, this can be set to <code>TRUE</code> if file name completion is desired. This is used on Windows (where file paths including spaces do work): on Unix-alikes <code>readline</code> 's filename completion is normally used.
	All settings are turned on by default except <code>ipck</code> , <code>func</code> and <code>files</code> . Turn more off if your CPU cycles are valuable; you will still retain basic completion on names of objects in the search list. See below for additional details.
name, ...	user-settable options. Currently valid names are <b>function.suffix:</b> default " <code>(</code> " <b>funarg.suffix:</b> default " <code>=</code> " <b>package.suffix:</b> default " <code>::</code> " See <a href="#">options</a> for detailed usage description.
x	An R object for which valid names after " <code>\$</code> " are computed and returned.
pattern	A regular expression. Only matching names are returned.

## Details

There are several types of completion, some of which can be disabled using `rc.settings`. The most basic level, which can not be turned off once the package is loaded, provides completion on names visible on the search path, along with a few special keywords (e.g. `TRUE`). This type of completion is not attempted if the partial 'word' (a.k.a. token) being completed is empty (since there would be too many completions). The more advanced types of completion are described below.

**Completion after extractors `$` and `@`:** When the `ops` setting is turned on, completion after `$` and `@` is attempted. This requires the prefix to be evaluated, which is attempted unless it involves an explicit function call (implicit function calls involving the use of `[`, `$`, etc *do not* inhibit evaluation).

Valid completions after the `$` extractor are determined by the generic function `.DollarNames`. Some basic methods are provided, and more can be written for custom classes.

**Completion inside name spaces:** When the `ns` setting is turned on, completion inside name spaces is attempted when a token is preceded by the `::` or `:::` operators. Additionally, the basic completion mechanism is extended to include attached name spaces, or more precisely, `foopkg::` becomes a valid completion of `foo` if the return value of `search()` includes the string `"package:foopkg"`.

The completion of package name spaces applies only to attached packages, i.e. if `MASS` is not attached (whether or not it is loaded), `MAS` will not complete to `MASS : .`. However, attempted completion *inside* an apparent name space will attempt to load the name space if it is not already loaded, e.g. trying to complete on `MASS : : fr` will load `MASS` (but not necessarily attach it) even if it is not already loaded.

**Completion of function arguments:** When the `args` setting is turned on, completion on function arguments is attempted whenever deemed appropriate. The mechanism used will currently fail if the relevant function (at the point where completion is requested) was entered on a previous prompt (which implies in particular that the current line is being typed in response to a continuation prompt, usually `+`). Note that separation by newlines is fine.

The list of possible argument completions that is generated can be misleading. There is no problem for non-generic functions (except that `...` is listed as a completion; this is intentional as it signals the fact that the function can accept further arguments). However, for generic functions, it is practically impossible to give a reliable argument list without evaluating arguments (and not even then, in some cases), which is risky (in addition to being difficult to code, which is the real reason it hasn't even been tried), especially when that argument is itself an inline function call. Our compromise is to consider arguments of *all* currently available methods of that generic. This has two drawbacks. First, not all listed completions may be appropriate in the call currently being constructed. Second, for generics with many methods (like `print` and `plot`), many matches will need to be considered, which may take a noticeable amount of time. Despite these drawbacks, we believe this behaviour to be more useful than the only other practical alternative, which is to list arguments of the generic only.

Only S3 methods are currently supported in this fashion, and that can be turned off using the `S3` setting.

Since arguments can be unnamed in R function calls, other types of completion are also appropriate whenever argument completion is. Since there are usually many many more visible objects than formal arguments of any particular function, possible argument completions are often buried in a bunch of other possibilities. However, recall that basic completion is suppressed for blank tokens. This can be useful to list possible arguments of a function. For example, trying to complete `seq([TAB]` and `seq(from = 1, [TAB])` will both list only the arguments of `seq` (or any of its methods), whereas trying to complete `seq(length[TAB]` will list both the `length.out` argument and the `length()` function as possible completions. Note that no attempt is made to remove arguments already supplied, as that would incur a further speed penalty.

**Special functions:** For a few special functions (`library`, `data`, etc), the first argument is treated specially, in the sense that normal completion is suppressed, and some function specific completions are enabled if so requested by the settings. The `ipck` setting, which controls whether `library` and `require` will complete on *installed packages*, is disabled by default because the first call to `installed.packages` is potentially time consuming (e.g. when packages are installed on a remote network file server). Note, however, that the results of a call to `installed.packages` is cached, so subsequent calls are usually fast, so turning this option on is not particularly onerous even in such situations.

## Value

`rc.status` returns, as a list, the contents of an internal (unexported) environment that is used to record the results of the last completion attempt. This can be useful for debugging. For such use, one must resist the temptation to use completion when typing the call to `rc.status` itself, as that then becomes the last attempt by the time the call is executed.

The items of primary interest in the returned list are:

<code>comps</code>	the possible completions generated by the last call to <code>.completeToken</code> , as a character vector
<code>token</code>	the token that was (or, is to be) completed, as set by the last call to <code>.assignToken</code> (possibly inside a call to <code>.guessTokenFromLine</code> )
<code>linebuffer</code>	the full line, as set by the last call to <code>.assignLinebuffer</code>
<code>start</code>	the start position of the token in the line buffer, as set by the last call to <code>.assignStart</code>
<code>end</code>	the end position of the token in the line buffer, as set by the last call to <code>.assignEnd</code>
<code>fileName</code>	logical, indicating whether the cursor is currently inside quotes. If so, no completion is attempted. A reasonable default behaviour for the backend in that case is to fall back to filename completion.
<code>fguess</code>	the name of the function <code>rcompgen</code> thinks the cursor is currently inside
<code>isFirstArg</code>	logical. If cursor is inside a function, is it the first argument?

In addition, the components `settings` and `options` give the current values of settings and options respectively.

`rc.getOption` and `rc.options` behave much like `getOption` and `options` respectively.

### Unexported API

There are several unexported functions in the package. Of these, a few are special because they provide the API through which other mechanisms can make use of the facilities provided by this package (they are unexported because they are not meant to be called directly by users). The usage of these functions are:

```
.assignToken(text)
.assignLinebuffer(line)
.assignStart(start)
.assignEnd(end)

.completeToken()
.retrieveCompletions()
.getFileComp()

.guessTokenFromLine()
.win32consoleCompletion(linebuffer, cursorPosition,
                        check.repeat = TRUE,
                        minlength = -1)

.addFunctionInfo(...)
```

The first four functions set up a completion attempt by specifying the token to be completed (`text`), and indicating where (`start` and `end`, which should be integers) the token is placed within the complete line typed so far (`line`).

Potential completions of the token are generated by `.completeToken`, and the completions can be retrieved as an R character vector using `.retrieveCompletions`.

If the cursor is inside quotes, no completion is attempted. The function `.getFileComp` can be used after a call to `.completeToken` to determine if this is the case (returns `TRUE`), and alternative completions generated as deemed useful. In most cases, filename completion is a reasonable fallback.

The `.guessTokenFromLine` function is provided for use with backends that do not already break a line into tokens. It requires the `linebuffer` and `endpoint` (cursor position) to be already set, and itself sets the token and the start position. It returns the token as a character string. (This is used by the ESS completion hook example given in the `examples/altesscomp.el` file.)

The `.win32consoleCompletion` is similar in spirit, but is more geared towards the Windows GUI (or rather, any front-end that has no completion facilities of its own). It requires the `linebuffer` and cursor position as arguments, and returns a list with three components, `addition`, `possible` and `comps`. If there is an unambiguous extension at the current position, `addition` contains the additional text that should be inserted at the cursor. If there is more than one possibility, these are available either as a character vector of preformatted strings in `possible`, or as a single string in `comps`. `possible` consists of lines formatted using the current `width` option, so that printing them on the console one line at a time will be a reasonable way to list them. `comps` is a space separated (collapsed) list of the same completions, in case the front-end wishes to display it in some other fashion.

The `minlength` argument can be used to suppress completion when the token is too short (which can be useful if the front-end is set up to try completion on every keypress). If `check.repeat` is `TRUE`, it is detected if the same completion is being requested more than once in a row, and ambiguous completions are returned only in that case. This is an attempt to emulate GNU Readline behaviour, where a single TAB completes up to any unambiguous part, and multiple possibilities are reported only on two consecutive TABs.

As the various front-end interfaces evolve, the details of these functions are likely to change as well.

The function `.addFunctionInfo` can be used to add information about the permitted argument names for specific functions. Multiple named arguments are allowed in calls to it, where the tags are names of functions and values are character vectors representing valid arguments. When the `argdb` setting is `TRUE`, these are used as a source of valid argument names for the relevant functions.

### Note

If you are uncomfortable with unsolicited evaluation of pieces of code, you should set `ops = FALSE`. Otherwise, trying to complete `foo@ba` will evaluate `foo`, trying to complete `foo[i,1:10]$ba` will evaluate `foo[i,1:10]`, etc. This should not be too bad, as explicit function calls (involving parentheses) are not evaluated in this manner. However, this *will* affect lazy loaded symbols (and presumably other promise type thingies).

### Author(s)

Deepayan Sarkar, <deepayan.sarkar@r-project.org>

---

read.DIF

*Data Input from Spreadsheet*

---

### Description

Reads a file in Data Interchange Format (DIF) and creates a data frame from it. DIF is a format for data matrices such as single spreadsheets.



**Usage**

```
read.DIF(file, header = FALSE,
         dec = ".", row.names, col.names,
         as.is = !stringsAsFactors,
         na.strings = "NA", colClasses = NA, nrows = -1,
         skip = 0, check.names = TRUE,
         blank.lines.skip = TRUE,
         stringsAsFactors = default.stringsAsFactors(),
         transpose = FALSE)
```

**Arguments**

- |            |   |
|------------|---|
| file       | the name of the file which the data are to be read from, or a connection, or a complete URL.<br>The name "clipboard" may also be used on Windows, in which case <code>read.DIF("clipboard")</code> will look for a DIF format entry in the Windows clipboard.   |
| header     | a logical value indicating whether the spreadsheet contains the names of the variables as its first line. If missing, the value is determined from the file format: <code>header</code> is set to <code>TRUE</code> if and only if the first row contains only character values and the top left cell is empty.   |
| dec        | the character used in the file for decimal points.  |
| row.names  | a vector of row names. This can be a vector giving the actual row names, or a single number giving the column of the table which contains the row names, or character string giving the name of the table column containing the row names.<br>If there is a header and the first row contains one fewer field than the number of columns, the first column in the input is used for the row names. Otherwise if <code>row.names</code> is missing, the rows are numbered.<br>Using <code>row.names = NULL</code> forces row numbering.  |
| col.names  | a vector of optional names for the variables. The default is to use "V" followed by the column number.  |
| as.is      | the default behavior of <code>read.DIF</code> is to convert character variables (which are not converted to logical, numeric or complex) to factors. The variable <code>as.is</code> controls the conversion of columns not otherwise specified by <code>colClasses</code> . Its value is either a vector of logicals (values are recycled if necessary), or a vector of numeric or character indices which specify which columns should not be converted to factors.<br>Note: to suppress all conversions including those of numeric columns, set <code>colClasses = "character"</code> .<br>Note that <code>as.is</code> is specified per column (not per variable) and so includes the column of row names (if any) and any columns to be skipped. |
| na.strings | a character vector of strings which are to be interpreted as NA values. Blank fields are also considered to be missing values in logical, integer, numeric and complex fields.  |
| colClasses | character. A vector of classes to be assumed for the columns. Recycled as necessary, or if the character vector is named, unspecified values are taken to be NA.<br>Possible values are NA (when <code>type.convert</code> is used), "NULL" (when the column is skipped), one of the atomic vector classes (logical, integer, numeric,  |

complex, character, raw), or "factor", "Date" or "POSIXct". Otherwise there needs to be an `as` method (from package **methods**) for conversion from "character" to the specified formal class.

Note that `colClasses` is specified per column (not per variable) and so includes the column of row names (if any).

<code>nrows</code>	the maximum number of rows to read in. Negative values are ignored.
<code>skip</code>	the number of lines of the data file to skip before beginning to read data.
<code>check.names</code>	logical. If TRUE then the names of the variables in the data frame are checked to ensure that they are syntactically valid variable names. If necessary they are adjusted (by <code>make.names</code> ) so that they are, and also to ensure that there are no duplicates.
<code>blank.lines.skip</code>	logical: if TRUE blank lines in the input are ignored.
<code>stringsAsFactors</code>	logical: should character vectors be converted to factors?
<code>transpose</code>	logical, indicating if the row and column interpretation should be transposed. Microsoft's Excel has been known to produce (non-standard conforming) DIF files which would need <code>transpose = TRUE</code> to be read correctly.

### Value

A data frame (`data.frame`) containing a representation of the data in the file. Empty input is an error unless `col.names` is specified, when a 0-row data frame is returned: similarly giving just a header line if `header = TRUE` results in a 0-row data frame.

### Note

The columns referred to in `as.is` and `colClasses` include the column of row names (if any).  
Less memory will be used if `colClasses` is specified as one of the six atomic vector classes.

### Author(s)

R Core; `transpose` option by Christoph Buser, ETH Zurich

### References

The DIF format specification can be found by searching on <http://www.wotsit.org/>; the optional header fields are ignored. See also [http://en.wikipedia.org/wiki/Data\\_Interchange\\_Format](http://en.wikipedia.org/wiki/Data_Interchange_Format).

The term is likely to lead to confusion: Windows will have a 'Windows Data Interchange Format (DIF) data format' as part of its WinFX system, which may or may not be compatible.

### See Also

The *R Data Import/Export* manual.

`scan`, `type.convert`, `read.fwf` for reading fixed width formatted input; `read.table`; `data.frame`.

**Examples**

```
## read.DIF() needs transpose=TRUE for file exported from Excel
udir <- system.file("misc", package="utils")
dd <- read.DIF(file.path(udir, "exDIF.dif"), header= TRUE, transpose=TRUE)
dc <- read.csv(file.path(udir, "exDIF.csv"), header= TRUE)
stopifnot(identical(dd,dc), dim(dd) == c(4,2))
```

---

read.fortran	<i>Read Fixed-Format Data</i>
--------------	-------------------------------

---

**Description**

Read fixed-format data files using Fortran-style format specifications.

**Usage**

```
read.fortran(file, format, ..., as.is = TRUE, colClasses = NA)
```

**Arguments**

file	File or connection to read from
format	Character vector or list of vectors. See ‘Details’ below.
...	Other arguments for <a href="#">read.fwf</a>
as.is	Keep characters as characters?
colClasses	Variable classes to override defaults. See <a href="#">read.table</a> for details.

**Details**

The format for a field is of one of the following forms: `rFl.d`, `rDl.d`, `rXl`, `rAl`, `rIl`, where `l` is the number of columns, `d` is the number of decimal places, and `r` is the number of repeats. `F` and `D` are numeric formats, `A` is character, `I` is integer, and `X` indicates columns to be skipped. The repeat code `r` and decimal place code `d` are always optional. The length code `l` is required except for `X` formats when `r` is present.

For a single-line record, `format` should be a character vector. For a multiline record it should be a list with a character vector for each line.

Skipped (`X`) columns are not passed to `read.fwf`, so `colClasses`, `col.names`, and similar arguments passed to `read.fwf` should not reference these columns.

**Value**

A data frame

**Note**

`read.fortran` does not use actual Fortran input routines, so the formats are at best rough approximations to the Fortran ones. In particular, specifying `d > 0` in the `F` or `D` format will shift the decimal `d` places to the left, even if it is explicitly specified in the input file.

**See Also**

[read.fwf](#), [read.table](#), [read.csv](#)

**Examples**

```
ff <- tempfile()
cat(file=ff, "123456", "987654", sep="\n")
read.fortran(ff, c("F2.1", "F2.0", "I2"))
read.fortran(ff, c("2F1.0", "2X", "2A1"))
unlink(ff)
cat(file=ff, "123456AB", "987654CD", sep="\n")
read.fortran(ff, list(c("2F3.1", "A2"), c("3I2", "2X")))
unlink(ff)
# Note that the first number is read differently than Fortran would
# read it:
cat(file=ff, "12.3456", "1234567", sep="\n")
read.fortran(ff, "F7.4")
unlink(ff)
```

read.fwf

*Read Fixed Width Format Files***Description**

Read a table of fixed width formatted data into a [data.frame](#).

**Usage**

```
read.fwf(file, widths, header = FALSE, sep = "\t",
         skip = 0, row.names, col.names, n = -1,
         buffersize = 2000, ...)
```

**Arguments**

<code>file</code>	the name of the file which the data are to be read from. Alternatively, <code>file</code> can be a <a href="#">connection</a> , which will be opened if necessary, and if so closed at the end of the function call.
<code>widths</code>	integer vector, giving the widths of the fixed-width fields (of one line), or list of integer vectors giving widths for multiline records.
<code>header</code>	a logical value indicating whether the file contains the names of the variables as its first line. If present, the names must be delimited by <code>sep</code> .
<code>sep</code>	character; the separator used internally; should be a character that does not occur in the file (except in the header).
<code>skip</code>	number of initial lines to skip; see <a href="#">read.table</a> .
<code>row.names</code>	see <a href="#">read.table</a> .
<code>col.names</code>	see <a href="#">read.table</a> .
<code>n</code>	the maximum number of records (lines) to be read, defaulting to no limit.
<code>buffersize</code>	Maximum number of lines to read at one time
<code>...</code>	further arguments to be passed to <a href="#">read.table</a> . Useful further arguments include <code>as.is</code> , <code>na.strings</code> , <code>colClasses</code> and <code>strip.white</code> .

**Details**

Multiline records are concatenated to a single line before processing. Fields that are of zero-width or are wholly beyond the end of the line in `file` are replaced by NA.

Negative-width fields are used to indicate columns to be skipped, eg `-5` to skip 5 columns. These fields are not seen by `read.table` and so should not be included in a `col.names` or `colClasses` argument (nor in the header line, if present).

Reducing the `buffer.size` argument may reduce memory use when reading large files with long lines. Increasing `buffer.size` may result in faster processing when enough memory is available.

**Value**

A `data.frame` as produced by `read.table` which is called internally.

**Author(s)**

Brian Ripley for R version: original Perl by Kurt Hornik.

**See Also**

`scan` and `read.table`.

**Examples**

```
ff <- tempfile()
cat(file=ff, "123456", "987654", sep="\n")
read.fwf(ff, widths=c(1,2,3)) #> 1 23 456 \ 9 87 654
read.fwf(ff, widths=c(1,-2,3)) #> 1 456 \ 9 654
unlink(ff)
cat(file=ff, "123", "987654", sep="\n")
read.fwf(ff, widths=c(1,0, 2,3)) #> 1 NA 23 NA \ 9 NA 87 654
unlink(ff)
cat(file=ff, "123456", "987654", sep="\n")
read.fwf(ff, widths=list(c(1,0, 2,3), c(2,2,2))) #> 1 NA 23 456 98 76 54
unlink(ff)
```

---

read.socket

*Read from or Write to a Socket*

---

**Description**

`read.socket` reads a string from the specified socket, `write.socket` writes to the specified socket. There is very little error checking done by either.

**Usage**

```
read.socket(socket, maxlen = 256, loop = FALSE)
write.socket(socket, string)
```

**Arguments**

socket	a socket object
maxlen	maximum length of string to read
loop	wait for ever if there is nothing to read?
string	string to write to socket

**Value**

read.socket returns the string read.

**Author(s)**

Thomas Lumley

**See Also**

[close.socket](#), [make.socket](#)

**Examples**

```
finger <- function(user, host = "localhost", port = 79, print = TRUE)
{
  if (!is.character(user))
    stop("user name must be a string")
  user <- paste(user, "\r\n")
  socket <- make.socket(host, port)
  on.exit(close.socket(socket))
  write.socket(socket, user)
  output <- character(0)
  repeat{
    ss <- read.socket(socket)
    if (ss == "") break
    output <- paste(output, ss)
  }
  close.socket(socket)
  if (print) cat(output)
  invisible(output)
}
## Not run:
finger("root") ## only works if your site provides a finger daemon
## End(Not run)
```

---

read.table

*Data Input*

---

**Description**

Reads a file in table format and creates a data frame from it, with cases corresponding to lines and variables to fields in the file.

**Usage**

```

read.table(file, header = FALSE, sep = " ", quote = "\"'",
           dec = ".", row.names, col.names,
           as.is = !stringsAsFactors,
           na.strings = "NA", colClasses = NA, nrow = -1,
           skip = 0, check.names = TRUE, fill = !blank.lines.skip,
           strip.white = FALSE, blank.lines.skip = TRUE,
           comment.char = "#",
           allowEscapes = FALSE, flush = FALSE,
           stringsAsFactors = default.stringsAsFactors(),
           fileEncoding = "", encoding = "unknown")

read.csv(file, header = TRUE, sep = ",", quote="\"", dec=".",
         fill = TRUE, comment.char=" ", ...)

read.csv2(file, header = TRUE, sep = ";", quote="\"", dec=" ",
          fill = TRUE, comment.char=" ", ...)

read.delim(file, header = TRUE, sep = "\t", quote="\"", dec=".",
           fill = TRUE, comment.char=" ", ...)

read.delim2(file, header = TRUE, sep = "\t", quote="\"", dec=" ",
            fill = TRUE, comment.char=" ", ...)

```

**Arguments**

**file** the name of the file which the data are to be read from. Each row of the table appears as one line of the file. If it does not contain an *absolute* path, the file name is *relative* to the current working directory, `getwd()`. Tilde-expansion is performed where supported. As from R 2.10.0 this can be a compressed file (see [file](#)).

Alternatively, `file` can be a readable text-mode [connection](#) (which will be opened for reading if necessary, and if so `closed` (and hence destroyed) at the end of the function call). (If `stdin()` is used, the prompts for lines may be somewhat confusing. Terminate input with a blank line or an EOF signal, `Ctrl-D` on Unix and `Ctrl-Z` on Windows. Any pushback on `stdin()` will be cleared before return.)

`file` can also be a complete URL.

**header** a logical value indicating whether the file contains the names of the variables as its first line. If missing, the value is determined from the file format: `header` is set to `TRUE` if and only if the first row contains one fewer field than the number of columns.

**sep** the field separator character. Values on each line of the file are separated by this character. If `sep = " "` (the default for `read.table`) the separator is ‘white space’, that is one or more spaces, tabs, newlines or carriage returns.

**quote** the set of quoting characters. To disable quoting altogether, use `quote = ""`. See [scan](#) for the behaviour on quotes embedded in quotes. Quoting is only considered for columns read as character, which is all of them unless `colClasses` is specified.

**dec** the character used in the file for decimal points.

row.names	<p>a vector of row names. This can be a vector giving the actual row names, or a single number giving the column of the table which contains the row names, or character string giving the name of the table column containing the row names. If there is a header and the first row contains one fewer field than the number of columns, the first column in the input is used for the row names. Otherwise if row.names is missing, the rows are numbered.</p> <p>Using row.names = NULL forces row numbering. Missing or NULL row.names generate row names that are considered to be ‘automatic’ (and not preserved by <code>as.matrix</code>).</p>
col.names	<p>a vector of optional names for the variables. The default is to use "V" followed by the column number.</p>
as.is	<p>the default behavior of <code>read.table</code> is to convert character variables (which are not converted to logical, numeric or complex) to factors. The variable <code>as.is</code> controls the conversion of columns not otherwise specified by <code>colClasses</code>. Its value is either a vector of logicals (values are recycled if necessary), or a vector of numeric or character indices which specify which columns should not be converted to factors.</p> <p>Note: to suppress all conversions including those of numeric columns, set <code>colClasses = "character"</code>.</p> <p>Note that <code>as.is</code> is specified per column (not per variable) and so includes the column of row names (if any) and any columns to be skipped.</p>
na.strings	<p>a character vector of strings which are to be interpreted as NA values. Blank fields are also considered to be missing values in logical, integer, numeric and complex fields.</p>
colClasses	<p>character. A vector of classes to be assumed for the columns. Recycled as necessary, or if the character vector is named, unspecified values are taken to be NA.</p> <p>Possible values are NA (the default, when <code>type.convert</code> is used), "NULL" (when the column is skipped), one of the atomic vector classes (logical, integer, numeric, complex, character, raw), or "factor", "Date" or "POSIXct". Otherwise there needs to be an <code>as</code> method (from package <b>methods</b>) for conversion from "character" to the specified formal class.</p> <p>Note that <code>colClasses</code> is specified per column (not per variable) and so includes the column of row names (if any).</p>
nrows	<p>integer: the maximum number of rows to read in. Negative and other invalid values are ignored.</p>
skip	<p>integer: the number of lines of the data file to skip before beginning to read data.</p>
check.names	<p>logical. If TRUE then the names of the variables in the data frame are checked to ensure that they are syntactically valid variable names. If necessary they are adjusted (by <code>make.names</code>) so that they are, and also to ensure that there are no duplicates.</p>
fill	<p>logical. If TRUE then in case the rows have unequal length, blank fields are implicitly added. See ‘Details’.</p>
strip.white	<p>logical. Used only when <code>sep</code> has been specified, and allows the stripping of leading and trailing white space from character fields (numeric fields are always stripped). See <code>scan</code> for further details, remembering that the columns may include the row names.</p>
blank.lines.skip	<p>logical: if TRUE blank lines in the input are ignored.</p>



<code>comment.char</code>	character: a character vector of length one containing a single character or an empty string. Use "" to turn off the interpretation of comments altogether.
<code>allowEscapes</code>	logical. Should C-style escapes such as ‘\n’ be processed or read verbatim (the default)? Note that if not within quotes these could be interpreted as a delimiter (but not as a comment character). For more details see <a href="#">scan</a> .
<code>flush</code>	logical: if TRUE, <code>scan</code> will flush to the end of the line after reading the last of the fields requested. This allows putting comments after the last field.
<code>stringsAsFactors</code>	logical: should character vectors be converted to factors? Note that this is overridden by <code>as.is</code> and <code>colClasses</code> , both of which allow finer control.
<code>fileEncoding</code>	character string: if non-empty declares the encoding used on a file (not a connection) so the character data can be re-encoded. See <a href="#">file</a> and ‘Note’.
<code>encoding</code>	encoding to be assumed for input strings. It is used to mark character strings as known to be in Latin-1 or UTF-8 (see <a href="#">Encoding</a> ): it is not used to re-encode the input, but allows R to handle encoded strings in their native encoding (if one of those two). See ‘Value’.
...	Further arguments to be passed to <code>read.table</code> .

## Details

This function is the principal means of reading tabular data into R.

Unless `colClasses` is specified, all columns are read as character columns and then converted using `type.convert` to logical, integer, numeric, complex or (depending on `as.is`) factor as appropriate. Quotes are (by default) interpreted in all fields, so a column of values like "42" will result in an integer column.

A field or line is ‘blank’ if it contains nothing (except whitespace if no separator is specified) before a comment character or the end of the field or line.

If `row.names` is not specified and the header line has one less entry than the number of columns, the first column is taken to be the row names. This allows data frames to be read in from the format in which they are printed. If `row.names` is specified and does not refer to the first column, that column is discarded from such files.

The number of data columns is determined by looking at the first five lines of input (or the whole file if it has less than five lines), or from the length of `col.names` if it is specified and is longer. This could conceivably be wrong if `fill` or `blank.lines.skip` are true, so specify `col.names` if necessary.

`read.csv` and `read.csv2` are identical to `read.table` except for the defaults. They are intended for reading ‘comma separated value’ files (‘.CSV’) or (`read.csv2`) the variant used in countries that use a comma as decimal point and a semicolon as field separator. Similarly, `read.delim` and `read.delim2` are for reading delimited files, defaulting to the TAB character for the delimiter. Notice that `header = TRUE` and `fill = TRUE` in these variants, and that the comment character is disabled.

The rest of the line after a comment character is skipped; quotes are not processed in comments. Complete comment lines are allowed provided `blank.lines.skip = TRUE`; however, comment lines prior to the header must have the comment character in the first non-blank column.

Quoted fields with embedded newlines are supported except after a comment character.

**Value**

A data frame (`data.frame`) containing a representation of the data in the file.

Empty input is an error unless `col.names` is specified, when a 0-row data frame is returned: similarly giving just a header line if `header = TRUE` results in a 0-row data frame. Note that in either case the columns will be logical unless `colClasses` was supplied.

Character strings in the result (including factor levels) will have a declared encoding if `encoding` is "latin1" or "UTF-8".

**Note**

The columns referred to in `as.is` and `colClasses` include the column of row names (if any).

Less memory will be used if `colClasses` is specified as one of the six [atomic](#) vector classes. This can be particularly so when reading a column that takes many distinct numeric values, as storing each distinct value as a character string can take up to 14 times as much memory as storing it as an integer.

Using `nrows`, even as a mild over-estimate, will help memory usage.

Using `comment.char = ""` will be appreciably faster than the `read.table` default.

`read.table` is not the right tool for reading large matrices, especially those with many columns: it is designed to read *data frames* which may have columns of very different classes. Use [scan](#) instead.

Because this function uses [pushBack](#) it can only handle character strings which can be represented in the current locale. So although `fileEncoding` can be used to specify the encoding of the input file (or a connection can be specified which re-encodes), the implied re-encoding must be possible. This is not a problem in UTF-8 locales, but it can be on Windows—other tools such as [readLines](#) and [scan](#) be used to avoid this limitation.

**References**

Chambers, J. M. (1992) *Data for models*. Chapter 3 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

The *R Data Import/Export* manual.

[scan](#), [type.convert](#), [read.fwf](#) for reading *fixed width formatted* input; [write.table](#); [data.frame](#).

[count.fields](#) can be useful to determine problems with reading files which result in reports of incorrect record lengths.

<http://tools.ietf.org/html/rfc4180> for the IANA definition of CSV files (which requires comma as separator and CRLF line endings).

recover

*Browsing after an Error*

---

**Description**

This function allows the user to browse directly on any of the currently active function calls, and is suitable as an error option. The expression `options(error=recover)` will make this the error option.

**Usage**

```
recover()
```

**Details**

When called, `recover` prints the list of current calls, and prompts the user to select one of them. The standard R `browser` is then invoked from the corresponding environment; the user can type ordinary S language expressions to be evaluated in that environment.

When finished browsing in this call, type `c` to return to `recover` from the browser. Type another frame number to browse some more, or type `0` to exit `recover`.

The use of `recover` largely supersedes `dump.frames` as an error option, unless you really want to wait to look at the error. If `recover` is called in non-interactive mode, it behaves like `dump.frames`. For computations involving large amounts of data, `recover` has the advantage that it does not need to copy out all the environments in order to browse in them. If you do decide to quit interactive debugging, call `dump.frames` directly while browsing in any frame (see the examples).

**Value**

Nothing useful is returned. However, you *can* invoke `recover` directly from a function, rather than through the error option shown in the examples. In this case, execution continues after you type `0` to exit `recover`.

**Compatibility Note**

The R `recover` function can be used in the same way as the S function of the same name; therefore, the error option shown is a compatible way to specify the error action. However, the actual functions are essentially unrelated and interact quite differently with the user. The navigating commands `up` and `down` do not exist in the R version; instead, exit the browser and select another frame.

**References**

John M. Chambers (1998). *Programming with Data*; Springer.  
See the compatibility note above, however.

**See Also**

`browser` for details about the interactive computations; `options` for setting the error option; `dump.frames` to save the current environments for later debugging.

**Examples**

```
## Not run:

options(error = recover) # setting the error option

### Example of interaction

> myFit <- lm(y ~ x, data = xy, weights = w)
Error in lm.wfit(x, y, w, offset = offset, ...) :
  missing or negative weights not allowed

Enter a frame number, or 0 to exit
1:lm(y ~ x, data = xy, weights = w)
2:lm.wfit(x, y, w, offset = offset, ...)
Selection: 2
Called from: eval(expr, envir, enclos)
Browse[1]> objects() # all the objects in this frame
[1] "method" "n"      "ny"      "offset" "tol"    "w"
[7] "x"      "y"
Browse[1]> w
[1] -0.5013844  1.3112515  0.2939348 -0.8983705 -0.1538642
[6] -0.9772989  0.7888790 -0.1919154 -0.3026882
Browse[1]> dump.frames() # save for offline debugging
Browse[1]> c # exit the browser

Enter a frame number, or 0 to exit
1:lm(y ~ x, data = xy, weights = w)
2:lm.wfit(x, y, w, offset = offset, ...)
Selection: 0 # exit recover
>

## End(Not run)
```

relist

*Allow Re-Listing an unlist()ed Object***Description**

`relist()` is an S3 generic function with a few methods in order to allow easy inversion of `unlist(obj)` when that is used with an object `obj` of (S3) class "relistable".

**Usage**

```
relist(flesh, skeleton)
## Default S3 method:
relist(flesh, skeleton = attr(flesh, "skeleton"))
## S3 method for class 'factor':
relist(flesh, skeleton = attr(flesh, "skeleton"))
## S3 method for class 'list':
relist(flesh, skeleton = attr(flesh, "skeleton"))
## S3 method for class 'matrix':
relist(flesh, skeleton = attr(flesh, "skeleton"))
```

```

as.relistable(x)
is.relistable(x)

## S3 method for class 'relistable':
unlist(x, recursive = TRUE, use.names = TRUE)

```

### Arguments

<code>flesh</code>	a vector to be relisted
<code>skeleton</code>	a list, the structure of which determines the structure of the result
<code>x</code>	an R object, typically a list (or vector).
<code>recursive</code>	logical. Should unlisting be applied to list components of <code>x</code> ?
<code>use.names</code>	logical. Should names be preserved?

### Details

Some functions need many parameters, which are most easily represented in complex structures, e.g., nested lists. Unfortunately, many mathematical functions in R, including `optim` and `nlm` can only operate on functions whose domain is a vector. R has `unlist()` to convert nested list objects into a vector representation. `relist()`, its methods and the functionality mentioned here provide the inverse operation to convert vectors back to the convenient structural representation. This allows structured functions (such as `optim()`) to have simple mathematical interfaces.

For example, a likelihood function for a multivariate normal model needs a variance-covariance matrix and a mean vector. It would be most convenient to represent it as a list containing a vector and a matrix. A typical parameter might look like

```
list(mean=c(0, 1), vcov=cbind(c(1, 1), c(1, 0))).
```

However, `optim` cannot operate on functions that take lists as input; it only likes numeric vectors. The solution is conversion. Given a function `mvdnorm(x, mean, vcov, log=FALSE)` which computes the required probability density, then

```

ipar <- list(mean=c(0, 1), vcov=cbind(c(1, 1), c(1, 0)))
initial.param <- as.relistable(ipar)

ll <- function(param.vector)
{
  param <- relist(param.vector, skeleton=ipar)
  -sum(mvdnorm(x, mean = param$mean, vcov = param$vcov,
              log = TRUE))
}

optim(unlist(initial.param), ll)

```

`relist` takes two parameters: `skeleton` and `flesh`. `Skeleton` is a sample object that has the right shape but the wrong content. `flesh` is a vector with the right content but the wrong shape. Invoking

```
relist(flesh, skeleton)
```

will put the content of `flesh` on the skeleton. You don't need to specify `skeleton` explicitly if the skeleton is stored as an attribute inside `flesh`. In particular, if `flesh` was created from some object `obj` with `unlist(as.relistable(obj))` then the `skeleton` attribute is automatically set. (Note that this does not apply to the example here, as `optim` is creating a new vector to pass to `ll` and not its `par` argument.)

As long as `skeleton` has the right shape, it should be a precise inverse of `unlist`. These equalities hold:

```
relist(unlist(x), x) == x
unlist(relist(y, skeleton)) == y

x <- as.relistable(x)
relist(unlist(x)) == x
```

### Value

an object of (S3) class "relistable" (and "list").

### Author(s)

R Core, based on a code proposal by Andrew Clausen.

### See Also

[unlist](#)

### Examples

```
ipar <- list(mean=c(0, 1), vcov=cbind(c(1, 1), c(1, 0)))
initial.param <- as.relistable(ipar)
ul <- unlist(initial.param)
relist(ul)
stopifnot(identical(relist(ul), initial.param))
```

---

REMOVE

*Remove Add-on Packages*

---

### Description

Utility for removing add-on packages.

### Usage

```
R CMD REMOVE [options] [-l lib] pkgs
```

### Arguments

<code>pkgs</code>	a space-separated list with the names of the packages to be removed.
<code>lib</code>	the path name of the R library tree to remove from. May be absolute or relative. Also accepted in the form <code>'--library=lib'</code> .
<code>options</code>	further options for help or version.

**Details**

If used as `R CMD REMOVE pkgs` without explicitly specifying `lib`, packages are removed from the library tree rooted at the first directory in the library path which would be used by `R` run in the current environment.

To remove from the library tree `lib` instead of the default one, use `R CMD REMOVE -l lib pkgs`.

Use `R CMD REMOVE --help` for more usage information.

**Note**

Some binary distributions of `R` have `REMOVE` in a separate bundle, e.g. an `R-devel RPM`.

**See Also**

[INSTALL](#), [remove.packages](#)

---

<code>remove.packages</code>	<i>Remove Installed Packages</i>
------------------------------	----------------------------------

---

**Description**

Removes installed packages/bundles and updates index information as necessary.

**Usage**

```
remove.packages(pkgs, lib)
```

**Arguments**

<code>pkgs</code>	a character vector with the names of the packages to be removed.
<code>lib</code>	a character vector giving the library directories to remove the packages from. If missing, defaults to the first element in <code>.libPaths()</code> .

**See Also**

[REMOVE](#) for a command line version; [install.packages](#) for installing packages.

---

<code>RHOME</code>	<i>R Home Directory</i>
--------------------	-------------------------

---

**Description**

Returns the location of the `R` home directory, which is the root of the installed `R` tree.

**Usage**

```
R RHOME
```

---

`roman`*Roman Numerals*

---

**Description**

Manipulate integers as roman numerals.

**Usage**

```
as.roman(x)
```

**Arguments**

`x` a numeric vector, or a character vector of arabic or roman numerals.

**Details**

`as.roman` creates objects of class "roman" which are internally represented as integers, and have suitable methods for printing, formatting, subsetting, and coercion to character.

Only numbers between 1 and 3899 have a unique representation as roman numbers.

**References**

Wikipedia contributors (2006). Roman numerals. Wikipedia, The Free Encyclopedia. [http://en.wikipedia.org/w/index.php?title=Roman\\_numerals&oldid=78252134](http://en.wikipedia.org/w/index.php?title=Roman_numerals&oldid=78252134). Accessed September 29, 2006.

**Examples**

```
## First five roman 'numbers'.
(y <- as.roman(1 : 5))
## Middle one.
y[3]
## Current year as a roman number.
(y <- as.roman(format(Sys.Date(), "%Y")))
## 10 years ago ...
y - 10
```

---

`Rprof`*Enable Profiling of R's Execution*

---

**Description**

Enable or disable profiling of the execution of R expressions.

**Usage**

```
Rprof(filename = "Rprof.out", append = FALSE, interval = 0.02,
       memory.profiling=FALSE)
```



**Arguments**

filename	The file to be used for recording the profiling results. Set to NULL or "" to disable profiling.
append	logical: should the file be over-written or appended to?
interval	real: time interval between samples.
memory.profiling	logical: write memory use information to the file?

**Details**

Enabling profiling automatically disables any existing profiling to another or the same file.

Profiling works by writing out the call stack every `interval` seconds, to the file specified. Either the `summaryRprof` function or the Perl script `R CMD Rprof` can be used to process the output file to produce a summary of the usage; use `R CMD Rprof --help` for usage information.

How time is measured varies by platform: on a Unix-alike it is the CPU time of the R process, so for example excludes time when R is waiting for input or for processes run by `system` to return.

Note that the timing interval cannot usefully be too small: once the timer goes off, the information is not recorded until the next timing click (probably in the range 1–10msecs).

Functions will only be recorded in the profile log if they put a context on the call stack (see `sys.calls`). Some `primitive` functions do not do so: specifically those which are of `type "special"` (see the ‘R Internals’ manual for more details).

**Note**

Profiling is not available on all platforms. By default, it is attempted to compile support for profiling. Configure R with ‘`--disable-R-profiling`’ to change this.

As R profiling uses the same mechanisms as C profiling, the two cannot be used together, so do not use `Rprof` in an executable built for profiling.

**See Also**

The chapter on “Tidying and profiling R code” in “Writing R Extensions” (see the ‘doc/manual’ subdirectory of the R source tree).

`summaryRprof`

`tracemem`, `Rprofmem` for other ways to track memory use.

**Examples**

```
## Not run: Rprof()
## some code to be profiled
Rprof(NULL)
## some code NOT to be profiled
Rprof(append=TRUE)
## some code to be profiled
Rprof(NULL)
...
## Now post-process the output as described in Details

## End(Not run)
```

---

`Rprofmem`*Enable Profiling of R's Memory Use*

---

**Description**

Enable or disable reporting of memory allocation in R.

**Usage**

```
Rprofmem(filename = "Rprofmem.out", append = FALSE, threshold = 0)
```

**Arguments**

<code>filename</code>	The file to be used for recording the memory allocations. Set to <code>NULL</code> or <code>" "</code> to disable reporting.
<code>append</code>	logical: should the file be over-written or appended to?
<code>threshold</code>	numeric: allocations on R's "large vector" heap larger than this number of bytes will be reported.

**Details**

Enabling profiling automatically disables any existing profiling to another or the same file.

Profiling writes the call stack to the specified file every time `malloc` is called to allocate a large vector object or to allocate a page of memory for small objects. The size of a page of memory and the size above which `malloc` is used for vectors are compile-time constants, by default 2000 and 128 bytes respectively.

The profiler tracks allocations, some of which will be to previously used memory and will not increase the total memory use of R.

**Value**

None

**Note**

The memory profiler slows down R even when not in use, and so is a compile-time option. The memory profiler can be used at the same time as other R and C profilers.

**See Also**

The R sampling profiler, [Rprof](#) also collects memory information.

[tracemem](#) traces duplications of specific objects.

The "Writing R Extensions" manual section on "Tidying and profiling R code"

**Examples**

```
## Not run:
## not supported unless R is compiled to support it.
Rprofmem("Rprofmem.out", threshold=1000)
example(glm)
Rprofmem(NULL)
noquote(readLines("Rprofmem.out", n=5))

## End(Not run)
```

---

Rscript

*Scripting Front-End for R*


---

**Description**

This is an alternative front end for use in ‘#!’ scripts and other scripting applications.

**Usage**

```
Rscript [options] [-e expression] file [args]
```

**Arguments**

options	A list of options beginning with ‘--’. These can be any of the options of the standard R front-end, and also those described in the details.
expression	a R expression.
file	The name of a file containing R commands. ‘-’ indicates ‘stdin’.
args	Arguments to be passed to the script in file.

**Details**

Rscript --help gives details of usage, and Rscript --version gives the version of Rscript.

Other invocations invoke the R front-end with selected options. This front-end is convenient for writing ‘#!’ scripts since it is an executable and takes file directly as an argument. Options ‘--slave --no-restore’ are always supplied: these imply ‘--no-save’. (The standard Windows command line has no concept of ‘#!’ scripts, but Cygwin shells do.)

Either one or more ‘-e’ options or file should be supplied. When using ‘-e’ options be aware of the quoting rules in the shell used: see the examples.

Additional options accepted (before file or args) are

‘-verbose’ gives details of what Rscript is doing. Also passed on to R.

‘-default-packages=list’ where list is a comma-separated list of package names or NULL. Sets the environment variable R\_DEFAULT\_PACKAGES which determines the packages loaded on startup. The default for Rscript omits **methods** as it takes about 60% of the startup time.

Normally the version of R is determined at installation, but this can be overridden by setting the environment variable RHOME.

stdin() refers to the input file, and file("stdin") to the stdin file stream of the process.

**Note**

Rscript is only supported on systems with the `execv` system call.

**Examples**

```
## Not run:
Rscript -e 'date()' -e 'format(Sys.time(), "%a %b %d %X %Y")'

## example #! script for a Unix-alike

#! /path/to/Rscript --vanilla --default-packages=utils
args <- commandArgs(TRUE)
res <- try(install.packages(args))
if(inherits(res, "try-error")) q(status=1) else q()

## End(Not run)
```

---

RShowDoc

*Show R Manuals and Other Documentation*


---

**Description**

Utility function to find and display R documentation.

**Usage**

```
RShowDoc(what, type = c("pdf", "html", "txt"), package)
```

**Arguments**

<code>what</code>	a character string: see ‘Details’.
<code>type</code>	an optional character string giving the preferred format.
<code>package</code>	an optional character string specifying the name of a package within which to look for documentation.

**Details**

`what` can specify one of several different sources of documentation, including the R manuals (R-admin, R-data, R-exts, R-intro, R-ints, R-lang), NEWS, COPYING (the GPL licence), FAQ (also available as R-FAQ), and the files in ‘[R\\_HOME/doc](#)’.

If `package` is supplied, documentation is looked for in the ‘doc’ and top-level directories of an installed package of that name.

If `what` is missing a brief usage message is printed.

The documentation types are tried in turn starting with the first specified in `type` (or “pdf” if none is specified).

**Value**

A invisible character string given the path to the file found.

**Examples**

```
## Not run:
RShowDoc("R-lang")
RShowDoc("FAQ", type="html")
RShowDoc("frame", package="grid")
RShowDoc("changes.txt", package="grid")
RShowDoc("NEWS", package="MASS")

## End(Not run)
```

---

RSiteSearch	<i>Search for Key Words or Phrases in the R-help Mailing List Archives or Documentation</i>
-------------	---

---

**Description**

Search for key words or phrases in the R-help mailing list archives, help pages, vignettes or task views, using the search engine at <http://search.r-project.org> and view them in a web browser.

**Usage**

```
RSiteSearch(string,
             restrict = c("functions", "vignettes", "views"),
             format = c("normal", "short"),
             sortby = c("score", "date:late", "date:early",
                       "subject", "subject:descending",
                       "from", "from:descending",
                       "size", "size:descending"),
             matchesPerPage = 20)
```

**Arguments**

string	A character string specifying word(s) or a phrase to search. If the words are to be searched as one entity, enclose all words in braces (see the first example).
restrict	a character vector, typically of length greater than one. Possible areas to search in: Rhelp10 for R-help mailing list archive starting January 2010, Rhelp08 for mailing list archive 2008–2009, Rhelp02 for mailing list archive 2002–2007, Rhelp01 for mailing list archive before 2002, R-devel for R-devel mailing list, R-sig-mix for R-sig-mix mailing list, functions for help pages, views for task views and vignettes for package vignettes.
format	normal or short (no excerpts); can be abbreviated.
sortby	character string (can be abbreviated) indicating how to sort the search results: (score, date:late for sorting by date with latest results first, date:early for earliest first, subject for subject in alphabetical order, subject:descending for reverse alphabetical order, from or from:descending for sender (when applicable), size or size:descending for size.)
matchesPerPage	How many items to show per page.

**Details**

This function is designed to work with the search site at <http://search.r-project.org>, and depends on that site continuing to be made available (thanks to Jonathan Baron and the School of Arts and Sciences of the University of Pennsylvania).

Unique partial matches will work for all arguments. Each new browser window will stay open unless you close it.

**Value**

(Invisibly) the complete URL passed to the browser, including the query string.

**Author(s)**

Andy Liaw and Jonathan Baron

**See Also**

[help.search](#), [help.start](#) for local searches.

[browseURL](#) for how the help file is displayed.

**Examples**

```
# need Internet connection
RSiteSearch("{logistic regression}") # matches exact phrase
Sys.sleep(5) # allow browser to open, take a quick look
RSiteSearch("Baron Liaw", restrict = "Rhelp02")
## Search in R-devel archive and recent R-help (and store the query-string):
Sys.sleep(5)
fullquery <- RSiteSearch("S4", restrict = c("R-dev", "Rhelp10", "Rhelp08"))
fullquery # a string of ~ 116 characters
## the latest purported bug reports, responses ...

Sys.sleep(5)
RSiteSearch("bug", restrict = "R-devel", sortby = "date:late")
```

---

rtags

*An Etags-like Tagging Utility for R*


---

**Description**

rtags provides etags-like indexing capabilities for R code, using R's own parser.

**Usage**

```
rtags(path = ".", pattern = "\\.[RrSs]$",
      recursive = FALSE,
      src = list.files(path = path, pattern = pattern,
                      full.names = TRUE,
                      recursive = recursive),
      keep.re = NULL,
      ofile = "", append = FALSE,
      verbose = getOption("verbose"))
```

**Arguments**

<code>path, pattern, recursive</code>	Arguments passed on to <code>list.files</code> to determine the files to be tagged. By default, these are all files with extension <code>.R</code> , <code>.r</code> , <code>.S</code> , and <code>.s</code> in the current directory. These arguments are ignored if <code>src</code> is specified.
<code>src</code>	A vector of file names to be indexed.
<code>keep.re</code>	A regular expression further restricting <code>src</code> (the files to be indexed). For example, specifying <code>keep.re="/R/[^/]*\\.R\$"</code> will only retain files with extension <code>.R</code> inside a directory named <code>R</code> .
<code>ofile</code>	Passed on to <code>cat</code> as the <code>file</code> argument; typically the output file where the tags will be written (" <code>TAGS</code> " by convention). By default, the output is written to the R console (unless redirected).
<code>append</code>	Logical, indicating whether the output should overwrite an existing file, or append to it.
<code>verbose</code>	Logical. If <code>TRUE</code> , file names are echoed to the R console as they are processed.

**Details**

Many text editors allow definitions of functions and other language objects to be quickly and easily located in source files through a tagging utility. This functionality requires the relevant source files to be preprocessed, producing an index (or tag) file containing the names and their corresponding locations. There are multiple tag file formats, the most popular being the vi-style `ctags` format and the emacs-style `etags` format. Tag files in these formats are usually generated by the `ctags` and `etags` utilities respectively. Unfortunately, these programs do not recognize R code syntax. They do allow tagging of arbitrary language files through regular expressions, but this too is insufficient.

The `rtags` function is intended to be a tagging utility for R code. It parses R code files (using R's parser) and produces tags in Emacs' `etags` format. Support for vi-style tags is currently absent, but should not be difficult to add.

**Author(s)**

Deepayan Sarkar

**References**

<http://en.wikipedia.org/wiki/Ctags>, [http://www.gnu.org/software/emacs/emacs-lisp-intro/html\\_node/emacs.html#Tags](http://www.gnu.org/software/emacs/emacs-lisp-intro/html_node/emacs.html#Tags)

**See Also**

`list.files`, `cat`

**Examples**

```
## Not run:
rtags("/path/to/src/repository",
      pattern = "[.]*\\. [RrSs]$",
      keep.re = "/R/",
      verbose = TRUE,
      ofile = "TAGS",
      append = FALSE,
      recursive = TRUE)
```

```
## End(Not run)
```

---

Rtangle

*R Driver for Stangle*

---

## Description

A driver for [Stangle](#) that extracts R code chunks.

## Usage

```
Rtangle()  
RtangleSetup(file, syntax, output = NULL, annotate = TRUE,  
             split = FALSE, prefix = TRUE, quiet = FALSE)
```

## Arguments

<code>file</code>	Name of Sweave source file.
<code>syntax</code>	An object of class <code>SweaveSyntax</code> .
<code>output</code>	Name of output file, default is to remove extension <code>‘.nw’</code> , <code>‘.Rnw’</code> or <code>‘.Snw’</code> and to add extension <code>‘.R’</code> . Any directory names in <code>file</code> are also removed such that the output is created in the current working directory.
<code>annotate</code>	By default, code chunks are separated by comment lines specifying the names and numbers of the code chunks. If <code>FALSE</code> , only the code chunks without any decorating comments are extracted.
<code>split</code>	Split output in single files per code chunk?
<code>prefix</code>	If <code>split = TRUE</code> , prefix the chunk labels by the basename of the input file to get output file names?
<code>quiet</code>	If <code>TRUE</code> all progress messages are suppressed.

## Author(s)

Friedrich Leisch

## References

Friedrich Leisch: Sweave User Manual, 2008  
<http://www.stat.uni-muenchen.de/~leisch/Sweave>

## See Also

[Sweave](#), [RweaveLatex](#)



RweaveLatex

*R/LaTeX Driver for Sweave***Description**

A driver for [Sweave](#) that translates R code chunks in LaTeX files.

**Usage**

```
RweaveLatex()
```

```
RweaveLatexSetup(file, syntax, output = NULL, quiet = FALSE,
                  debug = FALSE, stylepath, ...)
```

**Arguments**

<code>file</code>	Name of Sweave source file.
<code>syntax</code>	An object of class <code>SweaveSyntax</code> .
<code>output</code>	Name of output file, default is to remove extension <code>.nw</code> , <code>.Rnw</code> or <code>.Snw</code> and to add extension <code>.tex</code> . Any directory names in <code>file</code> are also removed such that the output is created in the current working directory.
<code>quiet</code>	If <code>TRUE</code> all progress messages are suppressed.
<code>debug</code>	If <code>TRUE</code> , input and output of all code chunks is copied to the console.
<code>stylepath</code>	See ‘Details’.
<code>...</code>	named values for the options listed in ‘Supported Options’.

**Details**

The LaTeX file generated needs to contain `\usepackage{Sweave}`, and if this is not present in the Sweave source file, it is inserted by the `RweaveLatex` driver. If `stylepath = TRUE`, a hard-coded path to the file `Sweave.sty` in the R installation is set in place of `Sweave`. The hard-coded path makes the TeX file less portable, but avoids the problem of installing the current version of `Sweave.sty` to some place in your TeX input path. However, TeX may not be able to process the hard-coded path if it contains spaces (as it often will under Windows) or TeX special characters.

The default in R prior to 2.7.0 was `stylepath = TRUE`. It is now taken from the environment variable `SWEAVE_STYLEPATH_DEFAULT`, or is `FALSE` if that is unset or empty. If set, it should be exactly `TRUE` or `FALSE`: any other values are taken as `FALSE`.

By default, `Sweave.sty` sets the width of all included graphics to:

```
\setkeys{Gin}{width=0.8\textwidth}
```

This setting affects the width size option passed to the `\includegraphics{}` directive for each plot file and in turn impacts the scaling of your plot files as they will appear in your final document.

Thus, for example, you may set `width=3` in your figure chunk and the runtime generated EPS and PDF files will be set to 3 inches in width. However, the width of your graphic in your final document, will be set to `0.8\textwidth` and the height dimension will be scaled accordingly. Fonts and symbols will be similarly scaled in the final document.

You can adjust the default value by including the `\setkeys{Gin}{width=...}` directive in your `.Rnw` file after the `\begin{document}` directive and changing the `width` option value as you prefer, using standard LaTeX measurement values.

If you wish to override this default behavior entirely, you can add a `\usepackage[nogin]{Sweave}` directive in your preamble. In this case, no size/scaling options will be passed to the `\includegraphics{}` directive and the `height` and `width` options will determine both the runtime generated graphic file sizes and the size of the graphics in your final document.

`'Sweave.sty'` also supports the `'[noae]'` option, which suppresses the use of the `'ae'` package, the use of which may interfere with certain encoding and typeface selections. If you have problems in the rendering of certain character sets, try this option.

The use of fancy quotes (see [sQuote](#)) can cause problems when setting R output. Either set `options(useFancyQuotes = FALSE)` or arrange that LaTeX is aware of the encoding used (by a `\usepackage[utf8]{inputenc}` declaration: Windows users will need to replace `'utf8'` by `'cp1252'` or similar) and ensure that typewriter fonts containing directional quotes are used.

## Supported Options

RweaveLatex supports the following options for code chunks (the values in parentheses show the default values):

**echo:** logical (TRUE). Include S code in the output file?

**keep.source:** logical (FALSE). When echoing, if `keep.source == TRUE` the original source is copied to the file. Otherwise, deparsed source is echoed.

**eval:** logical (TRUE). If FALSE, the code chunk is not evaluated, and hence no text or graphical output produced.

**results:** character string (`verbatim`). If `verbatim`, the output of S commands is included in the verbatim-like `Soutput` environment. If `tex`, the output is taken to be already proper latex markup and included as is. If `hide` then all output is completely suppressed (but the code executed during the weave).

**print:** logical (FALSE). If TRUE, each expression in the code chunk is wrapped into a `print()` statement before evaluation, such that the values of all expressions become visible.

**term:** logical (TRUE). If TRUE, visibility of values emulates an interactive R session: values of assignments are not printed, values of single objects are printed. If FALSE, output comes only from explicit `print` or `cat` statements.

**split:** logical (FALSE). If TRUE, text output is written to separate files for each code chunk.

**strip.white:** character string (`false`). If `true`, blank lines at the beginning and end of output are removed. If `all`, then all blank lines are removed from the output.

**prefix:** logical (TRUE). If TRUE generated filenames of figures and output have a common prefix.

**prefix.string:** a character string, default is the name of the `'Snw'` source file.

**include:** logical (TRUE), indicating whether input statements for text output and `includegraphics` statements for figures should be auto-generated. Use `include = FALSE` if the output should appear in a different place than the code chunk (by placing the input line manually).

**fig:** logical (FALSE), indicating whether the code chunk produces graphical output. Note that only one figure per code chunk can be processed this way.

**eps:** logical (TRUE), indicating whether EPS figures should be generated. Ignored if `fig = FALSE`.

**pdf:** logical (TRUE), indicating whether PDF figures should be generated. Ignored if `fig = FALSE`.

**pdf.version, pdf.encoding:** passed to `pdf` to set the version and encoding. Defaults taken from `pdf.options()`.

**width:** numeric (6), width of figures in inches. See ‘Details’.

**height:** numeric (6), height of figures in inches. See ‘Details’.

**expand:** logical (TRUE). Expand references to other chunks so that only R code appears in the output file. If FALSE, the chunk reference (e.g. `<<chunkname>>`) will appear. The `expand=FALSE` option requires `keep.source = TRUE` or it will have no effect.

**concordance:** logical (FALSE). Write a concordance file to link the input line numbers to the output line numbers. This is an experimental feature; see the source code for the output format, which is subject to change in future releases.

### Author(s)

Friedrich Leisch

### References

Friedrich Leisch: Sweave User Manual, 2008  
<http://www.stat.uni-muenchen.de/~leisch/Sweave>

### See Also

[Sweave](#), [Rtangle](#)

---

savehistory

*Load or Save or Display the Commands History*

---

### Description

Load or save or display the commands history.

### Usage

```
loadhistory(file = ".Rhistory")
savehistory(file = ".Rhistory")

history(max.show = 25, reverse = FALSE, pattern, ...)

timestamp(stamp = date(),
           prefix = "##----- ", suffix = " -----##",
           quiet = FALSE)
```

**Arguments**

<code>file</code>	The name of the file in which to save the history, or from which to load it. The path is relative to the current working directory.
<code>max.show</code>	The maximum number of lines to show. <code>Inf</code> will give all of the currently available history.
<code>reverse</code>	logical. If true, the lines are shown in reverse order. Note: this is not useful when there are continuation lines.
<code>pattern</code>	A character string to be matched against the lines of the history
<code>...</code>	Arguments to be passed to <code>grep</code> when doing the matching.
<code>stamp</code>	A value or vector of values to be written into the history.
<code>prefix</code>	A prefix to apply to each line.
<code>suffix</code>	A suffix to apply to each line.
<code>quiet</code>	If TRUE, suppress printing timestamp to the console.

**Details**

There are several history mechanisms available for the different R consoles, which work in similar but not identical ways. Other uses of R, in particular embedded uses, may have no history. This works under the `readline` command-line interface but not otherwise (for example, in batch use or in an embedded application, nor currently in R.app).

The `readline` history mechanism is controlled by two environment variables: `R_HISTSIZE` controls the number of lines that are saved (default 512), and `R_HISTFILE` sets the filename used for the loading/saving of history if requested at the beginning/end of a session (but not the default for these functions). There is no limit on the number of lines of history retained during a session, so setting `R_HISTSIZE` to a large value has no penalty unless a large file is actually generated.

These variables are read at the time of saving, so can be altered within a session by the use of `Sys.setenv`.

Note that `readline` history library saves files with permission `0600`, that is with read/write permission for the user and not even read permission for any other account.

`history` shows only unique matching lines if `pattern` is supplied.

The `timestamp` function writes a timestamp (or other message) into the history and echos it to the console. On platforms that do not support a history mechanism (where the mechanism does not support timestamps) only the console message is printed.

**Note**

If you want to save the history at the end of (almost) every interactive session (even those in which you do not save the workspace), you can put a call to `savehistory()` in `.Last`. See the examples.

**Examples**

```
## Not run:
.Last <- function()
  if(interactive()) try(savehistory("~/Rhistory"))

## End(Not run)
```

---

select.list	<i>Select Items from a List</i>
-------------	---------------------------------

---

### Description

Select item(s) from a character vector.

### Usage

```
select.list(choices, preselect = NULL, multiple = FALSE, title = NULL,  
            graphics = getOption("menu.graphics"))
```

### Arguments

choices	a character vector of items.
preselect	a character vector, or NULL. If non-null and if the string(s) appear in the list, the item(s) are selected initially.
multiple	logical: can more than one item be selected?
title	optional character string for window title, or NULL for no title.
graphics	logical: should a graphical widget be used?

### Details

The normal default is `graphics = TRUE`. Under the Mac OS X GUI this brings up a modal dialog box with a (scrollable) list of items, which can be selected by the mouse. On other Unix-like platforms it will use a Tcl/Tk listbox widget if possible.

If `graphics` is `FALSE` or no graphical widget is available it displays a text list from which the user can choose by number(s). The `multiple = FALSE` case uses `menu`. Preselection is only supported for `multiple = TRUE`, where it is indicated by a "+" preceding the item.

It is an error to use `select.list` in a non-interactive session.

### Value

A character vector of selected items. If `multiple` is false and no item was selected (or Cancel was used), "" is returned. If `multiple` is true and no item was selected (or Cancel was used) then a character vector of length 0 is returned.

### See Also

[menu](#), [tk\\_select.list](#) for a graphical version using Tcl/Tk.

### Examples

```
## Not run:  
select.list(sort(.packages(all.available = TRUE)))  
  
## End(Not run)
```

---

sessionInfo                    *Collect Information About the Current R Session*

---

### Description

Print version information about R and attached or loaded packages.

### Usage

```
sessionInfo(package=NULL)
## S3 method for class 'sessionInfo':
print(x, locale=TRUE, ...)
## S3 method for class 'sessionInfo':
toLatex(object, locale=TRUE, ...)
```

### Arguments

package	a character vector naming installed packages. By default all attached packages are used.
x	an object of class "sessionInfo".
object	an object of class "sessionInfo".
locale	show locale information?
...	currently not used.

### See Also

[R.version](#)

### Examples

```
sessionInfo()
toLatex(sessionInfo(), locale=FALSE)
```

---

setRepositories                *Select Package Repositories*

---

### Description

Interact with the user to choose the package repositories to be used.

### Usage

```
setRepositories(graphics = getOption("menu.graphics"), ind = NULL)
```

### Arguments

graphics	Logical. If true, use a graphical list: on Windows or Mac OS X GUI use a list box, and on a Unix-alike if <b>tk</b> and an X server are available, use Tk widget. Otherwise use a text <a href="#">menu</a> .
ind	NULL or a vector of integer indices, which have the same effect as if they were entered at the prompt for graphics=FALSE.

**Details**

The default list of known repositories is stored in the file '`R_HOME/etc/repositories`'. That file can be edited for a site, or a user can have a personal copy in '`HOME/.R/repositories`' which will take precedence.

A Bioconductor mirror can be selected by setting `options("BioC_mirror")`: the default value is '`"http://www.bioconductor.org"`'.

The items that are preselected are those that are currently in `options("repos")` plus those marked as default in the list of known repositories.

The list of repositories offered depends on the setting of option `"pkgType"` as some repositories only offer a subset of types (e.g. only source packages or not Mac OS X binary packages). Further, for binary packages some repositories (notably R-Forge) only offer packages for the current or recent versions of R.

Repository 'CRAN' is treated specially: the value is taken from the current setting of `getOption("repos")` if this has an element "CRAN": this ensures mirror selection is sticky.

This function requires the R session to be interactive unless `ind` is supplied.

**Value**

This function is invoked mainly for its side effect of updating `options("repos")`. It returns (invisibly) the previous `repos` options setting (as a `list` with component `repos`) or `NULL` if no changes were applied.

**Note**

This does **not** set the list of repositories at startup: to do so set `options(repos=)` in a start up file (see help topic [Startup](#)).

**See Also**

`chooseCRANmirror`, `install.packages`.

---

 SHLIB

*Build Shared Object/DLL for Dynamic Loading*


---

**Description**

Compile the given source files and then link all specified object files into a shared library aka DLL which can be loaded into R using `dyn.load` or `library.dynam`.

**Usage**

```
R CMD SHLIB [options] [-o dllname] files
```

**Arguments**

<code>files</code>	a list specifying the object files to be included in the shared object/DLL. You can also include the name of source files (for which the object files are automatically made from their sources) and library linking commands.
<code>dllname</code>	the full name of the shared object/DLL to be built, including the extension (typically <code>.so</code> on Unix systems, and <code>.dll</code> on Windows). If not given, the basename of the object is taken from the basename of the first file.
<code>options</code>	Further options to control the processing. Use <code>R CMD SHLIB --help</code> for a current list.

**Details**

`R CMD SHLIB` is the mechanism used by `INSTALL` to compile source code in packages. It will generate suitable compilation commands for C, C++, ObjC(++) and Fortran sources: Fortran 90/95 sources can also be used but it may not be possible to mix these with other languages (on most platforms it is possible to mix with C, but mixing with C++ rarely works).

Please consult section ‘Creating shared objects’ in the manual ‘Writing R Extensions’ for how to customize it (for example to add `cpp` flags and to add libraries to the link step) and for details of some of its quirks.

Items in `files` with extensions `.c`, `.cpp`, `.cc`, `.C`, `.f`, `.f90`, `.f95`, `.m` (ObjC), `.M` and `.mm` (ObjC++) are regarded as source files, and those with extension `.o` as object files. All other items are passed to the linker.

Option `-n` (also known as `--dry-run`) will show the commands that would be run without actually executing them.

**Note**

Some binary distributions of R have SHLIB in a separate bundle, e.g., an R-devel RPM.

**See Also**

`COMPILE`, `dyn.load`, `library.dynam`.

The section on “Customizing compilation” in the “R Administration and Installation” manual (see the `doc/manual` subdirectory of the R source tree).

The ‘R Installation and Administration’ and ‘Writing R Extensions’ manuals.

**Examples**

```
## Not run:
R CMD SHLIB -o mylib.so a.f b.f -L/opt/acml3.5.0/gnu64/lib -lacml

## End(Not run)
```



---

stack

*Stack or Unstack Vectors from a Data Frame or List*


---

### Description

Stacking vectors concatenates multiple vectors into a single vector along with a factor indicating where each observation originated. Unstacking reverses this operation.

### Usage

```
stack(x, ...)
## Default S3 method:
stack(x, ...)
## S3 method for class 'data.frame':
stack(x, select, ...)

unstack(x, ...)
## Default S3 method:
unstack(x, form, ...)
## S3 method for class 'data.frame':
unstack(x, form, ...)
```

### Arguments

<code>x</code>	object to be stacked or unstacked
<code>select</code>	expression, indicating variables to select from a data frame
<code>form</code>	a two-sided formula whose left side evaluates to the vector to be unstacked and whose right side evaluates to the indicator of the groups to create. Defaults to <code>formula(x)</code> in <code>unstack.data.frame</code> .
<code>...</code>	further arguments passed to or from other methods.

### Details

The `stack` function is used to transform data available as separate columns in a data frame or list into a single column that can be used in an analysis of variance model or other linear model. The `unstack` function reverses this operation.

### Value

`unstack` produces a list of columns according to the formula `form`. If all the columns have the same length, the resulting list is coerced to a data frame.

`stack` produces a data frame with two columns

<code>values</code>	the result of concatenating the selected vectors in <code>x</code>
<code>ind</code>	a factor indicating from which vector in <code>x</code> the observation originated

### Author(s)

Douglas Bates

**See Also**

[lm](#), [reshape](#)

**Examples**

```
require(stats)
formula(PlantGrowth)      # check the default formula
pg <- unstack(PlantGrowth) # unstack according to this formula
pg
stack(pg)                  # now put it back together
stack(pg, select = -ctrl)  # omitting one vector
```

---

str

*Compactly Display the Structure of an Arbitrary R Object*


---

**Description**

Compactly display the internal **structure** of an R object, a diagnostic function and an alternative to [summary](#) (and to some extent, [dput](#)). Ideally, only one line for each ‘basic’ structure is displayed. It is especially well suited to compactly display the (abbreviated) contents of (possibly nested) lists. The idea is to give reasonable output for **any** R object. It calls [args](#) for (non-primitive) function objects.

`strOptions()` is a convenience function for setting [options](#) (`str = .`), see the examples.

**Usage**

```
str(object, ...)
```

## S3 method for class 'data.frame':

```
str(object, ...)
```

## Default S3 method:

```
str(object, max.level = NA,
     vec.len = strO$vec.len, digits.d = strO$digits.d,
     nchar.max = 128, give.attr = TRUE,
     give.head = TRUE, give.length = give.head,
     width = getOption("width"), nest.lev = 0,
     indent.str = paste(rep.int(" ", max(0, nest.lev + 1)),
                       collapse = ".."),
     comp.str="$ ", no.list = FALSE, envir = baseenv(),
     strict.width = strO$strict.width,
     formatNum = strO$formatNum, list.len = 99, ...)
```

```
strOptions(strict.width = "no", digits.d = 3, vec.len = 4,
          formatNum = function(x, ...)
            format(x, trim=TRUE, drop0trailing=TRUE, ...))
```

**Arguments**

<code>object</code>	any R object about which you want to have some information.
<code>max.level</code>	maximal level of nesting which is applied for displaying nested structures, e.g., a list containing sub lists. Default NA: Display all nesting levels.
<code>vec.len</code>	numeric ( $\geq 0$ ) indicating how many ‘first few’ elements are displayed of each vector. The number is multiplied by different factors (from .5 to 3) depending on the kind of vector. Defaults to the <code>vec.len</code> component of option "str" (see <a href="#">options</a> ) which defaults to 4.
<code>digits.d</code>	number of digits for numerical components (as for <a href="#">print</a> ). Defaults to the <code>digits.d</code> component of option "str" which defaults to 3.
<code>nchar.max</code>	maximal number of characters to show for <a href="#">character</a> strings. Longer strings are truncated, see <code>longch</code> example below.
<code>give.attr</code>	logical; if TRUE (default), show attributes as sub structures.
<code>give.length</code>	logical; if TRUE (default), indicate length (as <code>[1:...] </code> ).
<code>give.head</code>	logical; if TRUE (default), give (possibly abbreviated) mode/class and length (as <code>&lt;type&gt;[1:...] </code> ).
<code>width</code>	the page width to be used. The default is the currently active <code>options("width")</code> ; note that this has only a weak effect, unless <code>strict.width</code> is not "no".
<code>nest.lev</code>	current nesting level in the recursive calls to <code>str</code> .
<code>indent.str</code>	the indentation string to use.
<code>comp.str</code>	string to be used for separating list components.
<code>no.list</code>	logical; if true, no ‘list of ...’ nor the class are printed.
<code>envir</code>	the environment to be used for <i>promise</i> (see <a href="#">delayedAssign</a> ) objects only.
<code>strict.width</code>	string indicating if the <code>width</code> argument’s specification should be followed strictly, one of the values <code>c("no", "cut", "wrap")</code> . Defaults to the <code>strict.width</code> component of option "str" (see <a href="#">options</a> ) which defaults to "no" for back compatibility reasons; "wrap" uses <code>strwrap</code> ( <code>*</code> , <code>width=width</code> ) whereas "cut" cuts directly to width. Note that a small <code>vec.length</code> may be better than setting <code>strict.width = "wrap"</code> .
<code>formatNum</code>	a function such as <code>format</code> for formatting numeric vectors. It defaults to the <code>formatNum</code> component of option "str", see “Usage” of <code>strOptions()</code> above, which is almost back compatible to R $\leq 2.7.x$ , however, using <code>formatC</code> may be slightly better.
<code>list.len</code>	numeric; maximum number of list elements to display within a level.
<code>...</code>	potential further arguments (required for Method/Generic reasons).

**Value**

`str` does not return anything, for efficiency reasons. The obvious side effect is output to the terminal.

**Author(s)**

Martin Maechler <maechler@stat.math.ethz.ch> since 1990.

**See Also**

`ls.str` for *listing* objects with their structure; [summary](#), [args](#).

**Examples**

```
require(stats); require(grDevices); require(graphics)
## The following examples show some of 'str' capabilities
str(1:12)
str(ls)
str(args) #- more useful than args(args) !
str(freeny)
str(str)
str(.Machine, digits.d = 20)
str( lsfit(1:9,1:9) )
str( lsfit(1:9,1:9), max.level = 1)
str( lsfit(1:9,1:9), width = 60, strict.width = "cut")
str( lsfit(1:9,1:9), width = 60, strict.width = "wrap")
op <- options(); str(op) # save first;
                        # otherwise internal options() is used.
need.dev <-
  !exists(".Device") || is.null(.Device) || .Device == "null device"
{ if(need.dev) postscript()
  str(par())
  if(need.dev) graphics.off()
}
ch <- letters[1:12]; is.na(ch) <- 3:5
str(ch) # character NA's

str(list(a="A", L = as.list(1:100)), list.len = 9)
nchar(longch <- paste(rep(letters,100), collapse=""))
str(longch)
str(longch, nchar.max = 52)

str(longch, strict.width = "wrap")

## Settings for narrow transcript :
op <- options(width = 60,
              str = strOptions(strict.width = "wrap"))
str(lsfit(1:9,1:9))
str(options())
## reset to previous:
options(op)

str(quote( { A+B; list(C,D) } ))

## S4 classes :
require(stats4)
x <- 0:10; y <- c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8)
ll <- function(ymax=15, xh=6)
  -sum(dpois(y, lambda=ymax/(1+x/xh), log=TRUE))
fit <- mle(ll)
str(fit)
```

summaryRprof

*Summarise Output of R Sampling Profiler***Description**

Summarise the output of the `Rprof` function to show the amount of time used by different R functions.

**Usage**

```
summaryRprof(filename = "Rprof.out", chunksize = 5000,
             memory=c("none", "both", "tseries", "stats"),
             index=2, diff=TRUE, exclude=NULL)
```

**Arguments**

<code>filename</code>	Name of a file produced by <code>Rprof()</code>
<code>chunksize</code>	Number of lines to read at a time
<code>memory</code>	Summaries for memory information. See ‘Details’ below
<code>index</code>	How to summarize the stack trace for memory information. See ‘Details’ below.
<code>diff</code>	If <code>TRUE</code> memory summaries use change in memory rather than current memory
<code>exclude</code>	Functions to exclude when summarizing the stack trace for memory summaries

**Details**

This function is an alternative to R CMD `Rprof`. It provides the convenience of an all-R implementation but will be slower for large files.

As the profiling output file could be larger than available memory, it is read in blocks of `chunksize` lines. Increasing `chunksize` will make the function run faster if sufficient memory is available.

When called with `memory.profiling=TRUE`, the profiler writes information on three aspects of memory use: vector memory in small blocks on the R heap, vector memory in large blocks (from `malloc`), memory in nodes on the R heap. It also records the number of calls to the internal function `duplicate` in the time interval. `duplicate` is called by C code when arguments need to be copied. Note that the profiler does not track which function actually allocated the memory.

With `memory="both"` the change in total memory (truncated at zero) is reported in addition to timing data.

With `memory="tseries"` or `memory="stats"` the `index` argument specifies how to summarize the stack trace. A positive number specifies that many calls from the bottom of the stack; a negative number specifies the number of calls from the top of the stack. With `memory="tseries"` the `index` is used to construct labels and may be a vector to give multiple sets of labels. With `memory="stats"` the `index` must be a single number and specifies how to aggregate the data to the maximum and average of the memory statistics. With both `memory="tseries"` and `memory="stats"` the argument `diff=TRUE` asks for summaries of the increase in memory use over the sampling interval and `diff=FALSE` asks for the memory use at the end of the interval.

**Value**

If `memory="none"`, a list with components

<code>by.self</code>	Timings sorted by ‘self’ time
<code>by.total</code>	Timings sorted by ‘total’ time
<code>sampling.time</code>	
	Total length of profiling run

If `memory="both"` the same list but with memory consumption in Mb in addition to the timings.

If `memory="tseries"` a data frame giving memory statistics over time

If `memory="stats"` a by object giving memory statistics by function.

**See Also**

The chapter on “Tidying and profiling R code” in “Writing R Extensions” (see the ‘doc/manual’ subdirectory of the R source tree).

[Rprof](#)

[tracemem](#) traces copying of an object via the C function `duplicate`.

[Rprofmem](#) is a non-sampling memory use profiler.

<http://developer.r-project.org/memory-profiling.html>

**Examples**

```
## Not run:
## Rprof() is not available on all platforms
Rprof(tmp <- tempfile())
example(glm)
Rprof()
summaryRprof(tmp)
unlink(tmp)

## End(Not run)
```

**Description**

Sweave provides a flexible framework for mixing text and S code for automatic report generation. The basic idea is to replace the S code with its output, such that the final document only contains the text and the output of the statistical analysis.

**Usage**

```
Sweave(file, driver = RweaveLatex(),
       syntax = getOption("SweaveSyntax"), ...)

Stangle(file, driver = Rtangle(),
       syntax = getOption("SweaveSyntax"), ...)
```

**Arguments**

<code>file</code>	Name of Sweave source file.
<code>driver</code>	The actual workhorse, see details below.
<code>syntax</code>	An object of class <code>SweaveSyntax</code> or a character string with its name. The default installation provides <code>SweaveSyntaxNoweb</code> and <code>SweaveSyntaxLatex</code> .
<code>...</code>	Further arguments passed to the driver's setup function.

**Details**

Automatic generation of reports by mixing word processing markup (like latex) and S code. The S code gets replaced by its output (text or graphs) in the final markup file. This allows a report to be re-generated if the input data change and documents the code to reproduce the analysis in the same file that also produces the report.

Sweave combines the documentation and code chunks together (or their output) into a single document. `Stangle` extracts only the code from the Sweave file creating a valid S source file (that can be run using `source`). Code inside `\Sexpr{ }` statements is ignored by `Stangle`.

`Stangle` is just a frontend to `Sweave` using a simple driver by default, which discards the documentation and concatenates all code chunks the current S engine understands.

**Hook Functions**

Before each code chunk is evaluated, a number of hook functions can be executed. If `getOption("SweaveHooks")` is set, it is taken to be a collection of hook functions. For each logical option of a code chunk (`echo`, `print`, ...) a hook can be specified, which is executed if and only if the respective option is `TRUE`. Hooks must be named elements of the list returned by `getOption("SweaveHooks")` and be functions taking no arguments. E.g., if option "SweaveHooks" is defined as `list(fig = foo)`, and `foo` is a function, then it would be executed before the code in each figure chunk. This is especially useful to set defaults for the graphical parameters in a series of figure chunks.

Note that the user is free to define new Sweave options and associate arbitrary hooks with them. E.g., one could define a hook function for option `clean` that removes all objects in the global environment. Then all code chunks with `clean = TRUE` would start operating on an empty workspace.

**Syntax Definition**

Sweave allows a very flexible syntax framework for marking documentation and text chunks. The default is a noweb-style syntax, as alternative a latex-style syntax can be used. See the user manual for details.

**Author(s)**

Friedrich Leisch

**References**

Friedrich Leisch: Dynamic generation of statistical reports using literate data analysis. In W. Härdle and B. Rönz, editors, *Compstat 2002 - Proceedings in Computational Statistics*, pages 575–580. Physika Verlag, Heidelberg, Germany, 2002. ISBN 3-7908-1517-9.

Friedrich Leisch: *Sweave User Manual*, 2008

<http://www.stat.uni-muenchen.de/~leisch/Sweave>

**See Also**

[RweaveLatex](#), [Rtangle](#)

**Examples**

```
testfile <- system.file("Sweave", "Sweave-test-1.Rnw", package = "utils")

## enforce par(ask=FALSE)
options(device.ask.default=FALSE)

## create a LaTeX file
Sweave(testfile)

## This can be compiled to PDF by
## Not run: tools::texi2dvi("Sweave-test-1.tex", pdf=TRUE)
## or outside R by
## R CMD texi2dvi Sweave-test-1.tex
## which sets the appropriate TEXINPUTS path.

## create an S source file from the code chunks
Stangle(testfile)
## which can be sourced, e.g.
source("Sweave-test-1.R")
```

---

SweaveSyntConv      *Convert Sweave Syntax*

---

**Description**

This function converts the syntax of files in [Sweave](#) format to another Sweave syntax definition.

**Usage**

```
SweaveSyntConv(file, syntax, output = NULL)
```

**Arguments**

<code>file</code>	Name of Sweave source file.
<code>syntax</code>	An object of class <code>SweaveSyntax</code> or a character string with its name giving the target syntax to which the file is converted.
<code>output</code>	Name of output file, default is to remove the extension from the input file and to add the default extension of the target syntax. Any directory names in <code>file</code> are also removed such that the output is created in the current working directory.

**Author(s)**

Friedrich Leisch



## References

Friedrich Leisch: Sweave User Manual, 2008  
<http://www.stat.uni-muenchen.de/~leisch/Sweave>

## See Also

[RweaveLatex](#), [Rtangle](#)

## Examples

```
testfile <- system.file("Sweave", "Sweave-test-1.Rnw", package = "utils")

## convert the file to latex syntax
SweaveSyntConv(testfile, SweaveSyntaxLatex)

## and run it through Sweave
Sweave("Sweave-test-1.Stex")
```

---

tar	<i>Create a Tar Archive</i>
-----	-----------------------------

---

## Description

Create a tar archive.

## Usage

```
tar(tarfile, files = NULL,
    compression = c("none", "gzip", "bzip2", "xz"),
    compression_level = 6, tar = Sys.getenv("tar"))
```

## Arguments

tarfile	The pathname of the tar file: tilde expansion (see <a href="#">path.expand</a> ) will be performed. Alternatively, a connection that can be used for binary writes.
files	A character vector of filepaths to be archived: the default is to archive all files under the current directory.
compression	logical or character. The type of compression to be used. Can be abbreviated.
compression_level	integer: the level of compression. Only used for the internal method.
tar	character string: the path to the command to be used.

## Details

This is either a wrapper for a `tar` command or uses an internal implementation in R. The latter is used if `tarfile` is a connection or if the argument `tar` is `"internal"` or `"`.

Beware of portability considerations: the ‘tar’ format no longer has an agreed standard (‘Unix Standard Tar’ was part of POSIX 1003.1:1998 but has been removed in favour of `pax`), and in any case many common implementations diverged from the former standard. Known problems arise from

- The handling of file names of more than 100 bytes. These were unsupported in early versions of `tar`, and supported in one way by POSIX `tar` and in another by GNU `tar`. The internal implementation uses the POSIX way which supports up to 255 bytes (depending on the path), and warns on paths of more than 100 bytes.
- (File) links. `tar` was developed on an OS that used hard links, and physical files that were referred to more than one in the list of files to be included were included only once, the remaining instance being added as links. Later a means to include symbolic links was added. The internal implementation supports symbolic links (on OSes that support them), only. Of course, the question arises as to how links should be unpacked on OSes that do not support them: for files at least file copies can be used.
- Header fields, in particular the padding to be used when fields are not full or not used. POSIX did define the correct behaviour but commonly used implementations did (and still do) not comply.

For portability, avoid file paths of more than 100 bytes, and links (or at least, hard links and symbolic links to directories).

The internal implementation writes only the blocks of 512 bytes required, unlike GNU `tar` which by default pads with 'nul' to a multiple of 20 blocks (10KB). Implementations differ to whether the block padding should occur before or after compression (or both).

The internal implementation currently skips empty directories.

### Value

The return code from `system`, invisibly.

### See Also

[http://en.wikipedia.org/wiki/Tar\\_\(file\\_format\)](http://en.wikipedia.org/wiki/Tar_(file_format)), [http://www.opengroup.org/onlinepubs/009695399/utilities/pax.html#tag\\_04\\_100\\_13\\_06](http://www.opengroup.org/onlinepubs/009695399/utilities/pax.html#tag_04_100_13_06) for the way the POSIX utility `pax` handles `tar` formats.  
`untar`.

### Description

These methods convert R objects to character vectors with BibTeX or LaTeX markup.

### Usage

```
toBibtex(object, ...)
toLatex(object, ...)
## S3 method for class 'Bibtex':
print(x, prefix="", ...)
## S3 method for class 'Latex':
print(x, prefix="", ...)
```

**Arguments**

object	object of a class for which a <code>toBibtex</code> or <code>toLatex</code> method exists.
x	object of class "Bibtex" or "Latex".
prefix	a character string which is printed at the beginning of each line, mostly used to insert whitespace for indentation.
...	currently not used in the print methods.

**Details**

Objects of class "Bibtex" or "Latex" are simply character vectors where each element holds one line of the corresponding BibTeX or LaTeX file.

**See Also**

`citEntry` and `sessionInfo` for examples

---

txtProgressBar	<i>Text Progress Bar</i>
----------------	--------------------------

---

**Description**

Text progress bar in the R console.

**Usage**

```
txtProgressBar(min = 0, max = 1, initial = 0, char = "=",
              width = NA, title, label, style = 1)

getTxtProgressBar(pb)
setTxtProgressBar(pb, value, title = NULL, label = NULL)
## S3 method for class 'txtProgressBar':
close(con, ...)
```

**Arguments**

min, max	(finite) numeric values for the extremes of the progress bar. Must have <code>min &lt; max</code> .
initial, value	initial or new value for the progress bar.
char	the character (or character string) to form the progress bar.
width	the width of the progress bar, as a multiple of the width of <code>char</code> . If <code>NA</code> , the default, the number of characters is that which fits into <code>getOption("width")</code> .
style	the 'style' of the bar – see 'Details'.
pb, con	an object of class "txtProgressBar".
title, label	ignored, for compatibility with other progress bars.
...	for consistency with the generic.

**Details**

`txtProgressBar` will display a progress bar on the R console via a text representation.

`setTxtProgressbar` will update the value. Missing (NA) and out-of-range values of `value` will be (silently) ignored.

The progress bar should be closed when finished with: this outputs the final newline character.

`style = 1` and `style = 2` just shows a line of char. They differ in that `style = 2` redraws the line each time, which is useful if other code might be writing to the R console. `style = 3` marks the end of the range by | and gives a percentage to the right of the bar.

**Value**

For `txtProgressBar` an object of class "txtProgressBar".

For `getTxtProgressBar` and `setTxtProgressBar`, a length-one numeric vector giving the previous value (invisibly for `setTxtProgressBar`).

**Note**

Using `style 2` or `3` or reducing the value with `style = 1` uses '\r' to return to the left margin – the interpretation of carriage return is up to the terminal or console in which R is running.

**See Also**

[tkProgressBar](#).

Windows versions of R also have `winProgressBar`.

**Examples**

```
# slow
testit <- function(x = sort(runif(20)), ...)
{
  pb <- txtProgressBar(...)
  for(i in c(0, x, 1)) {Sys.sleep(0.5); setTxtProgressBar(pb, i)}
  Sys.sleep(1)
  close(pb)
}
testit()
testit(runif(10))
testit(style=3)
```

---

type.convert

*Type Conversion on Character Variables*


---

**Description**

Convert a character vector to logical, integer, numeric, complex or factor as appropriate.

**Usage**

```
type.convert(x, na.strings = "NA", as.is = FALSE, dec = ".")
```

**Arguments**

<code>x</code>	a character vector.
<code>na.strings</code>	a vector of strings which are to be interpreted as <code>NA</code> values. Blank fields are also considered to be missing values in logical, integer, numeric or complex vectors.
<code>as.is</code>	logical. See ‘Details’.
<code>dec</code>	the character to be assumed for decimal points.

**Details**

This is principally a helper function for `read.table`. Given a character vector, it attempts to convert it to logical, integer, numeric or complex, and failing that converts it to factor unless `as.is = TRUE`. The first type that can accept all the non-missing values is chosen.

Vectors which are entirely missing values are converted to logical, since `NA` is primarily logical.

Vectors containing `F`, `T`, `FALSE`, `TRUE` or values from `na.strings` are converted to logical. Vectors containing optional whitespace followed by decimal constants representable as R integers or values from `na.strings` are converted to integer. Other vectors containing optional whitespace followed by other decimal or hexadecimal constants (see [NumericConstants](#)), or `NaN`, `Inf` or `infinity` (ignoring case) or values from `na.strings` are converted to numeric.

Since this is a helper function, the caller should always pass an appropriate value of `as.is`.

**Value**

A vector of the selected class, or a factor.

**See Also**

[read.table](#)

---

untar

*Extract or List Tar Archives*

---

**Description**

Extract files from or list a tar archive.

**Usage**

```
untar(tarfile, files = NULL, list = FALSE, exdir = ".",
      compressed = NA, extras = NULL, verbose = FALSE,
      tar = Sys.getenv("TAR"))
```

**Arguments**

<code>tarfile</code>	The pathname of the tar file: tilde expansion (see <a href="#">path.expand</a> ) will be performed. Alternatively, a connection that can be used for binary reads.
<code>files</code>	A character vector of recorded filepaths to be extracted: the default is to extract all files.
<code>list</code>	If <code>TRUE</code> , just list the files. The equivalent of <code>tar -tf</code> . Otherwise extract the files (the equivalent of <code>tar -xf</code> ).

<code>exdir</code>	The directory to extract files to (the equivalent of <code>tar -C</code> ). It will be created if necessary.
<code>compressed</code>	logical or character. Values "gzip", "bzip2" and "xz" select that form of compression (and may be abbreviated to the first letter). TRUE indicates gzip compression, FALSE no known compression (but the <code>tar</code> command may detect compression automatically), and NA (the default) that the type is inferred from the file header.
<code>extras</code>	NULL or a character string: further command-line flags such as '-p' to be passed to the <code>tar</code> program.
<code>verbose</code>	logical: if true echo the command used.
<code>tar</code>	character string: the path to the command to be used.

### Details

This is either a wrapper for a `tar` command or for an internal implementation written in R. The latter is used if `tarfile` is a connection or if the argument `tar` is "internal" or "" (except on Windows, when `tar.exe` is tried first).

What options are supported will depend on the `tar` used. Modern GNU flavours of `tar` will support compressed archives, and since 1.15 are able to detect the type of compression automatically: version 1.20 added support for `lzma` and version 1.22 for `xz` compression using LZMA2. For other flavours of `tar`, environment variable `R_GZIPCMD` gives the command to decompress `gzip` and `compress` files, and `R_BZIPCMD` for its files. (There is a `bsdtar` command from the 'libarchive' project used by Mac OS 10.6 ('Snow Leopard') which can also detect `gzip` and `bzip2` compression automatically, as can the `tar` from the 'Heirloom Toolchest' project.)

Arguments `compressed`, `extras` and `verbose` are only used when an external `tar` is used.

The internal implementation restores links (hard and soft) as symbolic links on a Unix-alike, and as file copies on Windows (which works only for files, not for directories). Since it uses `gzfile` to read a file it can handle files compressed by any of the methods that function can handle: at least `compress`, `gzip`, `bzip2` and `xz` compression, and some types of `lzma` compression. It does not guard against restoring absolute file paths, as some `tar` implementations do. It will create the parent directories for directories or files in the archive if necessary. It handles both the standard (USTAR/POSIX) and GNU ways of handling file paths of more than 100 bytes.

You may see warnings from the internal implementation such as

```
unsupported entry type 'x'
```

This often indicates an invalid archive: entry types "A-Z" are allowed as extensions, but other types are reserved (this example is from Mac OS 10.6.3). The only thing you can do with such an archive is to find a `tar` program that handles it, and look carefully at the resulting files.

The standards only support ASCII filenames (indeed, only alphanumeric plus period, underscore and hyphen). `untar` makes no attempt to map filenames to those acceptable on the current system, and treats the filenames in the archive as applicable without any re-encoding in the current locale.

### Value

If `list = TRUE`, a character vector of (relative or absolute) paths of files contained in the `tar` archive.

Otherwise the return code from `system`, invisibly.

**See Also**

[tar](#), [unzip](#).

---

unzip

*Extract or List Zip Archives*


---

**Description**

Extract files from or list a zip archive.

**Usage**

```
unzip(zipfile, files = NULL, list = FALSE, overwrite = TRUE,
      junkpaths = FALSE, exdir = ".")
```

**Arguments**

zipfile	The pathname of the zip file: tilde expansion (see <a href="#">path.expand</a> ) will be performed.
files	A character vector of recorded filepaths to be extracted: the default is to extract all files.
list	If TRUE, list the files and extract none. The equivalent of <code>unzip -l</code> .
overwrite	If TRUE, overwrite existing files, otherwise ignore such files. The equivalent of <code>unzip -o</code> .
junkpaths	If TRUE, use only the basename of the stored filepath when extracting. The equivalent of <code>unzip -j</code> .
exdir	The directory to extract files to (the equivalent of <code>unzip -d</code> ). It will be created if necessary.

**Value**

If `list = TRUE`, a data frame with columns `Name`, `Length` (the size of the uncompressed file) and `Date` (of class "`POSIXct`").

Otherwise, a character vector of the filepaths extracted to, invisibly.

**Source**

The C code uses `zlib` and is in particular based on the contributed ‘`minizip`’ application in the `zlib` sources (from [zlib.net](#)) by Gilles Vollant.

**See Also**

[unz](#) and [zip.file.extract](#) to read a single component from a zip file.

---

update.packages      *Compare Installed Packages with CRAN-like Repositories*

---

### Description

`old.packages` indicates packages which have a (suitable) later version on the repositories whereas `update.packages` offers to download and install such packages.

`new.packages` looks for (suitable) packages on the repositories that are not already installed, and optionally offers them for installation.

### Usage

```
update.packages(lib.loc = NULL, repos = getOption("repos"),
               contriburl = contrib.url(repos, type),
               method, instlib = NULL,
               ask = TRUE, available = NULL,
               oldPkgs = NULL, ..., checkBuilt = FALSE,
               type = getOption("pkgType"))
```

```
old.packages(lib.loc = NULL, repos = getOption("repos"),
             contriburl = contrib.url(repos, type),
             instPkgs = installed.packages(lib.loc = lib.loc),
             method, available = NULL, checkBuilt = FALSE,
             type = getOption("pkgType"))
```

```
new.packages(lib.loc = NULL, repos = getOption("repos"),
             contriburl = contrib.url(repos, type),
             instPkgs = installed.packages(lib.loc = lib.loc),
             method, available = NULL, ask = FALSE, ...,
             type = getOption("pkgType"))
```

### Arguments

<code>lib.loc</code>	character vector describing the location of R library trees to search through (and update packages therein), or <code>NULL</code> for all known trees (see <code>.libPaths</code> ).
<code>repos</code>	character vector, the base URL(s) of the repositories to use, i.e., the URL of the CRAN master such as <code>"http://cran.r-project.org"</code> or its Statlib mirror, <code>"http://lib.stat.cmu.edu/R/CRAN"</code> . Can be <code>NULL</code> to install from local files ( <code>'tar.gz'</code> for source packages).
<code>contriburl</code>	URL(s) of the contrib sections of the repositories. Use this argument only if your repository mirror is incomplete, e.g., because you burned only the <code>'contrib'</code> section on a CD. Overrides argument <code>repos</code> . As with <code>repos</code> , can also be <code>NULL</code> to install from local files.
<code>method</code>	Download method, see <a href="#">download.file</a> .
<code>instlib</code>	character string giving the library directory where to install the packages.
<code>ask</code>	logical indicating whether to ask user before packages are actually downloaded and installed, or the character string <code>"graphics"</code> , which brings up a widget to allow the user to (de-)select from the list of packages which could be updated or added. The latter value only works on systems with a GUI version of <a href="#">select.list</a> , and is otherwise equivalent to <code>ask = TRUE</code> .



available	an object as returned by <a href="#">available.packages</a> listing packages available at the repositories, or NULL which makes an internal call to <code>available.packages</code> .
checkBuilt	If TRUE, a package built under an earlier minor version of R is considered to be 'old'.
oldPkgs	if specified as non-NULL, <code>update.packages()</code> only considers these packages for updating.
instPkgs	by default all installed packages, <code>installed.packages(lib.loc=lib.loc)</code> . A subset can be specified; currently this must be in the same (character matrix) format as returned by <code>installed.packages()</code> .
...	Arguments such as <code>destdir</code> and dependencies to be passed to <a href="#">install.packages</a> .
type	character, indicating the type of package to download and install. See <a href="#">install.packages</a> .

### Details

`old.packages` compares the information from [available.packages](#) with that from `instPkgs` (computed by [installed.packages](#) by default) and reports installed packages that have newer versions on the repositories or, if `checkBuilt = TRUE`, that were built under an earlier minor version of R (for example built under 2.8.x when running R 2.9.0). (For binary package types here is no check that the version on the repository was built under the current minor version of R, but it is advertised as being suitable for this version.)

`new.packages` does the same comparison but reports uninstalled packages that are available at the repositories. If `ask != FALSE` it asks which packages should be installed in the first element of `lib.loc`.

The main function of the set is `update.packages`. First a list of all packages found in `lib.loc` is created and compared with those available at the repositories. If `ask = TRUE` (the default) packages with a newer version are reported and for each one the user can specify if it should be updated. If so the packages are downloaded from the repositories and installed in the respective library path (or `instlib` if specified).

For how the list of suitable available packages is determined see [available.packages](#). `available = NULL` make a call to `available.packages(contriburl = contriburl, method = method)` and hence by default filters on R version, OS type and removes duplicates.

### Value

`update.packages` returns NULL invisibly.

For `old.packages`, NULL or a matrix with one row per package, row names the package names and column names "Package", "LibPath", "Installed" (the version), "Built" (the version built under), "ReposVer" and "Repository".

For `new.packages` a character vector of package names, *after* any selected *via* `ask` have been installed.

### Warning

Take care when using dependencies (passed to [install.packages](#)) with `update.packages`, for it is unclear where new dependencies should be installed. The current implementation will only allow it if all the packages to be updated are in a single library, when that library will be used.

**See Also**

[install.packages](#), [available.packages](#), [download.packages](#),  
[installed.packages](#), [contrib.url](#).

See [download.file](#) for how to handle proxies and other options to monitor file transfers.

[INSTALL](#), [REMOVE](#), [remove.packages](#), [library](#), [.packages](#), [read.dcf](#)

The ‘R Installation and Administration’ manual for how to set up a repository.

**Examples**

```
## Not run:
install.packages(
  c("XML_0.99-5.tar.gz",
    "../..//Interfaces/Perl/RSPerl_0.8-0.tar.gz"),
  repos = NULL,
  configure.args = c(XML = '--with-xml-config=xml-config',
                    RSPerl = "--with-modules='IO Fcntl'"))

## End(Not run)
```

---

url.show

*Display a text URL*


---

**Description**

Extension of [file.show](#) to display text files from a remote server.

**Usage**

```
url.show(url, title = url, file = tempfile(),
         delete.file = TRUE, method, ...)
```

**Arguments**

url	The URL to read from.
title	Title for the browser.
file	File to copy to.
delete.file	Delete the file afterwards?
method	File transfer method: see <a href="#">download.file</a>
...	Arguments to pass to <a href="#">file.show</a> .

**See Also**

[url](#), [file.show](#), [download.file](#)

**Examples**

```
## Not run: url.show("http://lib.stat.cmu.edu/datasets/csb/ch3a.txt")
```

---

URLencode

*Encode or Decode a (partial) URL*

---

## Description

Functions to encode or decode characters in URLs.

## Usage

```
URLencode(URL, reserved = FALSE)
URLdecode(URL)
```

## Arguments

URL	A character string.
reserved	should reserved characters be encoded? See ‘Details’.

## Details

Characters in a URL other than the English alphanumeric characters and ‘\$ -\_ . + ! \* ’ ( ) , ’ should be encoded as % plus a two-digit hexadecimal representation, and any single-byte character can be so encoded. (Multi-byte characters are encoded as byte-by-byte.)

In addition, ‘; / ? : @ = &’ are reserved characters, and should be encoded unless used in their reserved sense, which is scheme specific. The default in URLencode is to leave them alone, which is appropriate for ‘file://’ URLs, but probably not for ‘http://’ ones.

## Value

A character string.

## References

RFC1738, <http://www.rfc-editor.org/rfc/rfc1738.txt>

## Examples

```
(y <- URLencode("a url with spaces and / and @"))
URLdecode(y)
(y <- URLencode("a url with spaces and / and @", reserved=TRUE))
URLdecode(y)
URLdecode("ab%20cd")
```

---

utils-deprecated     *Deprecated Functions in Package utils*

---

### Description

These functions are provided for compatibility with older versions of R only, and may be defunct as soon as of the next release.

### Usage

```
CRAN.packages(CRAN = getOption("repos"), method,
              contriburl = contrib.url(CRAN))
```

### Arguments

CRAN	character, an earlier way to specify a repository.
method	Download method, see <a href="#">download.file</a> .
contriburl	URL(s) of the contrib section of the repositories. Use this argument only if your CRAN mirror is incomplete, e.g., because you burned only the ‘contrib’ section on a CD. Overrides argument <code>repos</code> .

### See Also

[Deprecated](#), [Defunct](#)

---

View                     *Invoke a Data Viewer*

---

### Description

Invoke a spreadsheet-style data viewer on a matrix-like R object.

### Usage

```
View(x, title)
```

### Arguments

x	an R object which can be coerced to a data frame with non-zero numbers of rows and columns.
title	title for viewer window. Defaults to name of x prefixed by <code>Data :</code> .

**Details**

Object `x` is coerced (if possible) to a data frame, and all non-numeric columns are then coerced to character. The object is then viewed in a spreadsheet-like data viewer, a read-only version of [data.entry](#).

If there are row names on the data frame that are not `1:nrow`, they are displayed in a separate first column called `row.names`.

Objects with zero columns or zero rows are not accepted.

The array of cells can be navigated by the cursor keys and Home, End, Page Up and Page Down (where supported by X11) as well as Enter and Tab.

**Value**

Invisible `NULL`. The functions puts up a window and returns immediately: the window can be closed via its controls or menus.

**See Also**

[edit.data.frame](#), [data.entry](#).

---

vignette

*View or List Vignettes*

---

**Description**

View a specified vignette, or list the available ones.

**Usage**

```
vignette(topic, package = NULL, lib.loc = NULL, all = TRUE)

## S3 method for class 'vignette':
print(x, ...)
## S3 method for class 'vignette':
edit(name, ...)
```

**Arguments**

<code>topic</code>	a character string giving the (base) name of the vignette to view. If omitted, all vignettes from all installed packages are listed.
<code>package</code>	a character vector with the names of packages to search through, or <code>NULL</code> in which "all" packages (as defined by argument <code>all</code> ) are searched.
<code>lib.loc</code>	a character vector of directory names of R libraries, or <code>NULL</code> . The default value of <code>NULL</code> corresponds to all libraries currently known.
<code>all</code>	logical; if <code>TRUE</code> search all available packages in the library trees specified by <code>lib.loc</code> , and if <code>FALSE</code> , search only attached packages.
<code>x, name</code>	Object of class <code>vignette</code> .
<code>...</code>	Ignored by the <code>print</code> method, passed on to <a href="#">file.edit</a> by the <code>edit</code> method.

## Details

Function `vignette` returns an object of the same class, the `print` method opens a viewer for it. Currently, only PDF versions of vignettes can be viewed. The program specified by the `pdfviewer` option is used for this. If several vignettes have PDF versions with base name identical to `topic`, the first one found is used.

If no topics are given, all available vignettes are listed. The corresponding information is returned in an object of class `"packageIQR"`.

The `edit` method extracts the R code from the vignette to a temporary file and opens the file in an editor (see [edit](#)). This makes it very easy to execute the commands line by line, modify them in any way you want to help you test variants, etc.. An alternative way of extracting the R code from the vignette is to run [Stangle](#) on the source code of the vignette, see the examples below.

## Examples

```
## List vignettes from all *attached* packages
vignette(all = FALSE)

## List vignettes from all *installed* packages (can take a long time!):
vignette(all = TRUE)

## Not run:
## Open the grid intro vignette
vignette("grid")

## The same
v1 <- vignette("grid")
print(v1)

## Now let us have a closer look at the code
edit(v1)

## An alternative way of extracting the code,
## R file is written to current working directory
Stangle(v1$file)

## A package can have more than one vignette (package grid has several):
vignette(package="grid")
vignette("rotated")
## The same, but without searching for it:
vignette("rotated", package="grid")

## End(Not run)
```

---

write.table

*Data Output*

---

## Description

`write.table` prints its required argument `x` (after converting it to a data frame if it is not one nor a matrix) to a file or connection.

**Usage**

```
write.table(x, file = "", append = FALSE, quote = TRUE, sep = " ",
           eol = "\n", na = "NA", dec = ".", row.names = TRUE,
           col.names = TRUE, qmethod = c("escape", "double"))

write.csv(...)
write.csv2(...)
```

**Arguments**

<code>x</code>	the object to be written, preferably a matrix or data frame. If not, it is attempted to coerce <code>x</code> to a data frame.
<code>file</code>	either a character string naming a file or a connection open for writing. "" indicates output to the console.
<code>append</code>	logical. Only relevant if <code>file</code> is a character string. If <code>TRUE</code> , the output is appended to the file. If <code>FALSE</code> , any existing file of the name is destroyed.
<code>quote</code>	a logical value ( <code>TRUE</code> or <code>FALSE</code> ) or a numeric vector. If <code>TRUE</code> , any character or factor columns will be surrounded by double quotes. If a numeric vector, its elements are taken as the indices of columns to quote. In both cases, row and column names are quoted if they are written. If <code>FALSE</code> , nothing is quoted.
<code>sep</code>	the field separator string. Values within each row of <code>x</code> are separated by this string.
<code>eol</code>	the character(s) to print at the end of each line (row). For example, <code>eol="\r\n"</code> will produce Windows' line endings on a Unix-alike OS, and <code>eol="\r"</code> will produce files as expected by Mac OS Excel 2004.
<code>na</code>	the string to use for missing values in the data.
<code>dec</code>	the string to use for decimal points in numeric or complex columns: must be a single character.
<code>row.names</code>	either a logical value indicating whether the row names of <code>x</code> are to be written along with <code>x</code> , or a character vector of row names to be written.
<code>col.names</code>	either a logical value indicating whether the column names of <code>x</code> are to be written along with <code>x</code> , or a character vector of column names to be written. See the section on 'CSV files' for the meaning of <code>col.names = NA</code> .
<code>qmethod</code>	a character string specifying how to deal with embedded double quote characters when quoting strings. Must be one of "escape" (default), in which case the quote character is escaped in C style by a backslash, or "double", in which case it is doubled. You can specify just the initial letter.
<code>...</code>	arguments to <code>write.table</code> : <code>append</code> , <code>col.names</code> , <code>sep</code> , <code>dec</code> and <code>qmethod</code> cannot be altered.

**Details**

If the table has no columns the rownames will be written only if `row.names=TRUE`, and *vice versa*.

Real and complex numbers are written to the maximal possible precision.

If a data frame has matrix-like columns these will be converted to multiple columns in the result (*via* `as.matrix`) and so a character `col.names` or a numeric `quote` should refer to the columns in the result, not the input. Such matrix-like columns are unquoted by default.

Any columns in a data frame which are lists or have a class (e.g. dates) will be converted by the appropriate `as.character` method: such columns are unquoted by default. On the other hand, any class information for a matrix is discarded and non-atomic (e.g. list) matrices are coerced to character.

Only columns which have been converted to character will be quoted if specified by `quote`.

The `dec` argument only applies to columns that are not subject to conversion to character because they have a class or are part of a matrix-like column (or matrix), in particular to columns protected by `I()`. Use `options("OutDec")` to control such conversions.

In almost all cases the conversion of numeric quantities is governed by the option "scipen" (see `options`), but with the internal equivalent of `digits=15`. For finer control, use `format` to make a character matrix/data frame, and call `write.table` on that.

These functions check for a user interrupt every 1000 lines of output.

If `file` is not open for writing, an attempt is made to open it and then close it after use.

To write a Unix-style file on Windows, use a binary connection e.g. `file = file("fn", "wb")`.

### CSV files

By default there is no column name for a column of row names. If `col.names = NA` and `row.names = TRUE` a blank column name is added, which is the convention used for CSV files to be read by spreadsheets.

`write.csv` and `write.csv2` provide convenience wrappers for writing CSV files. They set `sep`, `dec` and `qmethod`, and `col.names` to `NA` if `row.names = TRUE` and `TRUE` otherwise.

`write.csv` uses "." for the decimal point and a comma for the separator.

`write.csv2` uses a comma for the decimal point and a semicolon for the separator, the Excel convention for CSV files in some Western European locales.

These wrappers are deliberately inflexible: they are designed to ensure that the correct conventions are used to write a valid file. Attempts to change `append`, `col.names`, `sep`, `dec` or `qmethod` are ignored, with a warning.

### Note

`write.table` can be slow for data frames with large numbers (hundreds or more) of columns: this is inevitable as each column could be of a different class and so must be handled separately. If they are all of the same class, consider using a matrix instead.

### See Also

The 'R Data Import/Export' manual.

`read.table`, `write`.

`write.matrix` in package **MASS**.

### Examples

```
## Not run:
## To write a CSV file for input to Excel one might use
x <- data.frame(a = I("a \" quote"), b = pi)
write.table(x, file = "foo.csv", sep = ",", col.names = NA,
            qmethod = "double")
## and to read this file back into R one needs
```



```

read.table("foo.csv", header = TRUE, sep = ",", row.names = 1)
## NB: you do need to specify a separator if qmethod = "double".

### Alternatively
write.csv(x, file = "foo.csv")
read.csv("foo.csv", row.names = 1)
## or without row names
write.csv(x, file = "foo.csv", row.names = FALSE)
read.csv("foo.csv")

## End(Not run)

```

---

zip.file.extract     *Extract File from a Zip Archive*

---

### Description

This will extract the file named `file` from the zip archive, if possible, and write it in a temporary location.

### Usage

```

zip.file.extract(file, zipname = "R.zip",
                unzip = getOption("unzip"), dir = tempdir())

```

### Arguments

<code>file</code>	file name. (If a path is given, see ‘Note’.)
<code>zipname</code>	The file name (not path) of a zip archive, including the ".zip" extension if required.
<code>unzip</code>	character string: the method to be used, an empty string indicates "internal".
<code>dir</code>	directory (“folder”) name into which the extraction happens. Must be writable to the caller.

### Details

All platforms support an "internal" unzip: this is the default under Windows and the fall-back under Unix if no unzip program was found during configuration and `R_UNZIPCMD` is not set.

The file will be extracted if it is in the archive and any required unzip utility is available. It will be extracted to the directory given by `dir`, overwriting any existing file of that name.

### Value

The name of the original or extracted file. Success is indicated by returning a different name.

### Note

The "internal" method is very simple, and will not set file dates.

This is a helper function for [help](#), [example](#) and [data](#). As such, it handles file paths in an unusual way. Any path component of `zipname` is ignored, and the path to `file` is used only to determine the directory within which to find `zipname`.

**Source**

The C code uses `zlib` and is in particular based on the contributed 'minizip' application in the `zlib` sources by Gilles Vollant.

**See Also**

[unzip](#)



## **Part II**



## Chapter 10

# The KernSmooth package

---

bkde

*Compute a Binned Kernel Density Estimate*

---

### Description

Returns x and y coordinates of the binned kernel density estimate of the probability density of the data.

### Usage

```
bkde(x, kernel = "normal", canonical = FALSE, bandwidth,  
      gridsize = 401L, range.x, truncate = TRUE)
```

### Arguments

x	vector of observations from the distribution whose density is to be estimated. Missing values are not allowed.
bandwidth	the kernel bandwidth smoothing parameter. Larger values of <code>bandwidth</code> make smoother estimates, smaller values of <code>bandwidth</code> make less smooth estimates. The default is a bandwidth computed from the variance of <code>x</code> , specifically the 'oversmoothed bandwidth selector' of Wand and Jones (1995, page 61).
kernel	character string which determines the smoothing kernel. <code>kernel</code> can be: "normal" - the Gaussian density function (the default). "box" - a rectangular box. "epanech" - the centred beta(2,2) density. "biweight" - the centred beta(3,3) density. "triweight" - the centred beta(4,4) density. This can be abbreviated to any unique abbreviation.
canonical	logical flag: if TRUE, canonically scaled kernels are used.
gridsize	the number of equally spaced points at which to estimate the density.
range.x	vector containing the minimum and maximum values of <code>x</code> at which to compute the estimate. The default is the minimum and maximum data values, extended by the support of the kernel.
truncate	logical flag: if TRUE, data with <code>x</code> values outside the range specified by <code>range.x</code> are ignored.

## Details

This is the binned approximation to the ordinary kernel density estimate. Linear binning is used to obtain the bin counts. For each  $x$  value in the sample, the kernel is centered on that  $x$  and the heights of the kernel at each datapoint are summed. This sum, after a normalization, is the corresponding  $y$  value in the output.

## Value

a list containing the following components:

$x$	vector of sorted $x$ values at which the estimate was computed.
$y$	vector of density estimates at the corresponding $x$ .

## Background

Density estimation is a smoothing operation. Inevitably there is a trade-off between bias in the estimate and the estimate's variability: large bandwidths will produce smooth estimates that may hide local features of the density; small bandwidths may introduce spurious bumps into the estimate.

## References

Wand, M. P. and Jones, M. C. (1995). *Kernel Smoothing*. Chapman and Hall, London.

## See Also

[density](#), [dpik](#), [hist](#), [ksmooth](#).

## Examples

```
data(geyser, package="MASS")
x <- geyser$duration
est <- bkde(x, bandwidth=0.25)
plot(est, type="l")
```

---

bkde2D

*Compute a 2D Binned Kernel Density Estimate*

---

## Description

Returns the set of grid points in each coordinate direction, and the matrix of density estimates over the mesh induced by the grid points. The kernel is the standard bivariate normal density.

## Usage

```
bkde2D(x, bandwidth, gridsize = c(51L, 51L), range.x, truncate = TRUE)
```

**Arguments**

<code>x</code>	a two-column matrix containing the observations from the distribution whose density is to be estimated. Missing values are not allowed.
<code>bandwidth</code>	vector containing the bandwidth to be used in each coordinate direction.
<code>gridsize</code>	vector containing the number of equally spaced points in each direction over which the density is to be estimated.
<code>range.x</code>	a list containing two vectors, where each vector contains the minimum and maximum values of <code>x</code> at which to compute the estimate for each direction. The default minimum in each direction is minimum data value minus 1.5 times the bandwidth for that direction. The default maximum is the maximum data value plus 1.5 times the bandwidth for that direction
<code>truncate</code>	logical flag: if TRUE, data with <code>x</code> values outside the range specified by <code>range.x</code> are ignored.

**Value**

a list containing the following components:

<code>x1</code>	vector of values of the grid points in the first coordinate direction at which the estimate was computed.
<code>x2</code>	vector of values of the grid points in the second coordinate direction at which the estimate was computed.
<code>fhat</code>	matrix of density estimates over the mesh induced by <code>x1</code> and <code>x2</code> .

**Details**

This is the binned approximation to the 2D kernel density estimate. Linear binning is used to obtain the bin counts and the Fast Fourier Transform is used to perform the discrete convolutions. For each `x1,x2` pair the bivariate Gaussian kernel is centered on that location and the heights of the kernel, scaled by the bandwidths, at each datapoint are summed. This sum, after a normalization, is the corresponding `fhat` value in the output.

**References**

- Wand, M. P. (1994). Fast Computation of Multivariate Kernel Estimators. *Journal of Computational and Graphical Statistics*, **3**, 433-445.
- Wand, M. P. and Jones, M. C. (1995). *Kernel Smoothing*. Chapman and Hall, London.

**See Also**

[bkde](#), [density](#), [hist](#).

**Examples**

```
data(geyser, package="MASS")
x <- cbind(geyser$duration, geyser$waiting)
est <- bkde2D(x, bandwidth=c(0.7, 7))
contour(est$x1, est$x2, est$fhat)
persp(est$fhat)
```



bkfe

*Compute a Binned Kernel Functional Estimate***Description**

Returns an estimate of a binned approximation to the kernel estimate of the specified density functional. The kernel is the standard normal density.

**Usage**

```
bkfe(x, drv, bandwidth, gridsize = 401L, range.x, binned = FALSE,
      truncate = TRUE)
```

**Arguments**

<code>x</code>	vector of observations from the distribution whose density is to be estimated. Missing values are not allowed.
<code>drv</code>	order of derivative in the density functional. Must be a non-negative even integer.
<code>bandwidth</code>	the kernel bandwidth smoothing parameter. Must be supplied.
<code>gridsize</code>	the number of equally-spaced points over which binning is performed.
<code>range.x</code>	vector containing the minimum and maximum values of <code>x</code> at which to compute the estimate. The default is the minimum and maximum data values, extended by the support of the kernel.
<code>binned</code>	logical flag: if <code>TRUE</code> , then <code>x</code> and <code>y</code> are taken to be grid counts rather than raw data.
<code>truncate</code>	logical flag: if <code>TRUE</code> , data with <code>x</code> values outside the range specified by <code>range.x</code> are ignored.

**Details**

The density functional of order `drv` is the integral of the product of the density and its `drv`th derivative. The kernel estimates of such quantities are computed using a binned implementation, and the kernel is the standard normal density.

**Value**

the (scalar) estimated functional.

**Background**

Estimates of this type were proposed by Sheather and Jones (1991).

**References**

Sheather, S. J. and Jones, M. C. (1991). A reliable data-based bandwidth selection method for kernel density estimation. *Journal of the Royal Statistical Society, Series B*, **53**, 683–690.

Wand, M. P. and Jones, M. C. (1995). *Kernel Smoothing*. Chapman and Hall, London.

**Examples**

```
data(geyser, package="MASS")
x <- geyser$duration
est <- bkfe(x, drv=4, bandwidth=0.3)
```

dph

*Select a Histogram Bin Width***Description**

Uses direct plug-in methodology to select the bin width of a histogram.

**Usage**

```
dph(x, scalest = "minim", level = 2L, gridsize = 401L,
    range.x = range(x), truncate = TRUE)
```

**Arguments**

<code>x</code>	vector containing the sample on which the histogram is to be constructed.
<code>scalest</code>	estimate of scale. "stdev" - standard deviation is used. "iqr" - inter-quartile range divided by 1.349 is used. "minim" - minimum of "stdev" and "iqr" is used.
<code>level</code>	number of levels of functional estimation used in the plug-in rule.
<code>gridsize</code>	number of grid points used in the binned approximations to functional estimates.
<code>range.x</code>	range over which functional estimates are obtained. The default is the minimum and maximum data values.
<code>truncate</code>	if <code>truncate</code> is TRUE then observations outside of the interval specified by <code>range.x</code> are omitted. Otherwise, they are used to weight the extreme grid points.

**Details**

The direct plug-in approach, where unknown functionals that appear in expressions for the asymptotically optimal bin width and bandwidths are replaced by kernel estimates, is used. The normal distribution is used to provide an initial estimate.

**Value**

the selected bin width.

**Background**

This method for selecting the bin width of a histogram is described in Wand (1995). It is an extension of the normal scale rule of Scott (1979) and uses plug-in ideas from bandwidth selection for kernel density estimation (e.g. Sheather and Jones, 1991).

## References

- Scott, D. W. (1979). On optimal and data-based histograms. *Biometrika*, **66**, 605–610.
- Sheather, S. J. and Jones, M. C. (1991). A reliable data-based bandwidth selection method for kernel density estimation. *Journal of the Royal Statistical Society, Series B*, **53**, 683–690.
- Wand, M. P. (1995). Data-based choice of histogram binwidth. *The American Statistician*, **51**, 59–64.

## See Also

[hist](#)

## Examples

```
data(geyser, package="MASS")
x <- geyser$duration
h <- dpik(x)
bins <- seq(min(x)-h, max(x)+h, by=h)
hist(x, breaks=bins)
```

---

dpik

*Select a Bandwidth for Kernel Density Estimation*

---

## Description

Use direct plug-in methodology to select the bandwidth of a kernel density estimate.

## Usage

```
dpik(x, scalest = "minim", level = 2L, kernel = "normal",
     canonical = FALSE, gridsize = 401L, range.x = range(x),
     truncate = TRUE)
```

## Arguments

<code>x</code>	vector containing the sample on which the kernel density estimate is to be constructed.
<code>scalest</code>	estimate of scale. "stdev" - standard deviation is used. "iqr" - inter-quartile range divided by 1.349 is used. "minim" - minimum of "stdev" and "iqr" is used.
<code>level</code>	number of levels of functional estimation used in the plug-in rule.
<code>kernel</code>	character string which determines the smoothing kernel. <code>kernel</code> can be: "normal" - the Gaussian density function (the default). "box" - a rectangular box. "epanech" - the centred beta(2,2) density. "biweight" - the centred beta(3,3) density. "triweight" - the centred beta(4,4) density. This can be abbreviated to any unique abbreviation.
<code>canonical</code>	logical flag: if TRUE, canonically scaled kernels are used
<code>gridsize</code>	the number of equally-spaced points over which binning is performed to obtain kernel functional approximation.

<code>range.x</code>	vector containing the minimum and maximum values of <code>x</code> at which to compute the estimate. The default is the minimum and maximum data values.
<code>truncate</code>	logical flag: if <code>TRUE</code> , data with <code>x</code> values outside the range specified by <code>range.x</code> are ignored.

### Details

The direct plug-in approach, where unknown functionals that appear in expressions for the asymptotically optimal bandwidths are replaced by kernel estimates, is used. The normal distribution is used to provide an initial estimate.

### Value

the selected bandwidth.

### Background

This method for selecting the bandwidth of a kernel density estimate was proposed by Sheather and Jones (1991) and is described in Section 3.6 of Wand and Jones (1995).

### References

Sheather, S. J. and Jones, M. C. (1991). A reliable data-based bandwidth selection method for kernel density estimation. *Journal of the Royal Statistical Society, Series B*, **53**, 683–690.

Wand, M. P. and Jones, M. C. (1995). *Kernel Smoothing*. Chapman and Hall, London.

### See Also

[bkde](#), [density](#), [ksmooth](#)

### Examples

```
data(geyser, package="MASS")
x <- geyser$duration
h <- dpik(x)
est <- bkde(x, bandwidth=h)
plot(est, type="l")
```

---

dpill

*Select a Bandwidth for Local Linear Regression*

---

### Description

Use direct plug-in methodology to select the bandwidth of a local linear Gaussian kernel regression estimate, as described by Ruppert, Sheather and Wand (1995).

### Usage

```
dpill(x, y, blockmax = 5, divisor = 20, trim = 0.01, proptrun = 0.05,
      gridsize = 401L, range.x, truncate = TRUE)
```

**Arguments**

<code>x</code>	vector of $x$ data. Missing values are not accepted.
<code>y</code>	vector of $y$ data. This must be same length as <code>x</code> , and missing values are not accepted.
<code>blockmax</code>	the maximum number of blocks of the data for construction of an initial parametric estimate.
<code>divisor</code>	the value that the sample size is divided by to determine a lower limit on the number of blocks of the data for construction of an initial parametric estimate.
<code>trim</code>	the proportion of the sample trimmed from each end in the $x$ direction before application of the plug-in methodology.
<code>proptrun</code>	the proportion of the range of $x$ at each end truncated in the functional estimates.
<code>gridsize</code>	number of equally-spaced grid points over which the function is to be estimated.
<code>range.x</code>	vector containing the minimum and maximum values of $x$ at which to compute the estimate. For density estimation the default is the minimum and maximum data values with 5% of the range added to each end. For regression estimation the default is the minimum and maximum data values.
<code>truncate</code>	logical flag: if TRUE, data with $x$ values outside the range specified by <code>range.x</code> are ignored.

**Details**

The direct plug-in approach, where unknown functionals that appear in expressions for the asymptotically optimal bandwidths are replaced by kernel estimates, is used. The kernel is the standard normal density. Least squares quartic fits over blocks of data are used to obtain an initial estimate. Mallows's  $C_p$  is used to select the number of blocks.

**Value**

the selected bandwidth.

**Warning**

If there are severe irregularities (i.e. outliers, sparse regions) in the  $x$  values then the local polynomial smooths required for the bandwidth selection algorithm may become degenerate and the function will crash. Outliers in the  $y$  direction may lead to deterioration of the quality of the selected bandwidth.

**References**

- Ruppert, D., Sheather, S. J. and Wand, M. P. (1995). An effective bandwidth selector for local least squares regression. *Journal of the American Statistical Association*, **90**, 1257–1270.
- Wand, M. P. and Jones, M. C. (1995). *Kernel Smoothing*. Chapman and Hall, London.

**See Also**

[ksmooth](#), [locpoly](#).

**Examples**

```

data(geyser, package = "MASS")
x <- geyser$duration
y <- geyser$waiting
plot(x, y)
h <- dpill(x, y)
fit <- locpoly(x, y, bandwidth = h)
lines(fit)

```

locpoly

*Estimate Functions Using Local Polynomials***Description**

Estimates a probability density function, regression function or their derivatives using local polynomials. A fast binned implementation over an equally-spaced grid is used.

**Usage**

```

locpoly(x, y, drv = 0L, degree, kernel = "normal",
        bandwidth, gridsize = 401L, bwdisc = 25,
        range.x, binned = FALSE, truncate = TRUE)

```

**Arguments**

<code>x</code>	vector of <code>x</code> data. Missing values are not accepted.
<code>bandwidth</code>	the kernel bandwidth smoothing parameter. It may be a single number or an array having length <code>gridsize</code> , representing a bandwidth that varies according to the location of estimation.
<code>y</code>	vector of <code>y</code> data. This must be same length as <code>x</code> , and missing values are not accepted.
<code>drv</code>	order of derivative to be estimated.
<code>degree</code>	degree of local polynomial used. Its value must be greater than or equal to the value of <code>drv</code> . The default value is of degree is <code>drv + 1</code> .
<code>kernel</code>	"normal" - the Gaussian density function. Currently ignored.
<code>gridsize</code>	number of equally-spaced grid points over which the function is to be estimated.
<code>bwdisc</code>	number of logarithmically-equally-spaced bandwidths on which <code>bandwidth</code> is discretised, to speed up computation.
<code>range.x</code>	vector containing the minimum and maximum values of <code>x</code> at which to compute the estimate.
<code>binned</code>	logical flag: if <code>TRUE</code> , then <code>x</code> and <code>y</code> are taken to be grid counts rather than raw data.
<code>truncate</code>	logical flag: if <code>TRUE</code> , data with <code>x</code> values outside the range specified by <code>range.x</code> are ignored.

**Value**

if  $y$  is specified, a local polynomial regression estimate of  $E[Y|X]$  (or its derivative) is computed. If  $y$  is missing, a local polynomial estimate of the density of  $x$  (or its derivative) is computed.

a list containing the following components:

$x$	vector of sorted $x$ values at which the estimate was computed.
$y$	vector of smoothed estimates for either the density or the regression at the corresponding $x$ .

**Details**

Local polynomial fitting with a kernel weight is used to estimate either a density, regression function or their derivatives. In the case of density estimation, the data are binned and the local fitting procedure is applied to the bin counts. In either case, binned approximations over an equally-spaced grid is used for fast computation. The bandwidth may be either scalar or a vector of length `gridsize`.

**References**

Wand, M. P. and Jones, M. C. (1995). *Kernel Smoothing*. Chapman and Hall, London.

**See Also**

[bkde](#), [density](#), [dpill](#), [ksmooth](#), [loess](#), [smooth](#), [supsmu](#).

**Examples**

```
data(geyser, package = "MASS")
# local linear density estimate
x <- geyser$duration
est <- locpoly(x, bandwidth = 0.25)
plot(est, type = "l")

# local linear regression estimate
y <- geyser$waiting
plot(x, y)
fit <- locpoly(x, y, bandwidth = 0.25)
lines(fit)
```

## Chapter 11

# The MASS package

---

abbey

*Determinations of Nickel Content*

---

### Description

A numeric vector of 31 determinations of nickel content (ppm) in a Canadian syenite rock.

### Usage

abbey

### Source

S. Abbey (1988) *Geostandards Newsletter* **12**, 241.

### References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

accdeaths

*Accidental Deaths in the US 1973-1978*

---

### Description

A regular time series giving the monthly totals of accidental deaths in the USA.

### Usage

accdeaths

### Details

The values for first six months of 1979 (p. 326) were 7798 7406 8363 8460 9217 9316.



**Source**

P. J. Brockwell and R. A. Davis (1991) *Time Series: Theory and Methods*. Springer, New York.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

---

 addterm

---

*Try All One-Term Additions to a Model*


---

**Description**

Try fitting all models that differ from the current model by adding a single term from those supplied, maintaining marginality.

This function is generic; there exist methods for classes `lm` and `glm` and the default method will work for many other classes.

**Usage**

```
addterm(object, ...)

## Default S3 method:
addterm(object, scope, scale = 0, test = c("none", "Chisq"),
        k = 2, sorted = FALSE, trace = FALSE, ...)
## S3 method for class 'lm':
addterm(object, scope, scale = 0, test = c("none", "Chisq", "F"),
        k = 2, sorted = FALSE, ...)
## S3 method for class 'glm':
addterm(object, scope, scale = 0, test = c("none", "Chisq", "F"),
        k = 2, sorted = FALSE, trace = FALSE, ...)
```

**Arguments**

<code>object</code>	An object fitted by some model-fitting function.
<code>scope</code>	a formula specifying a maximal model which should include the current one. All additional terms in the maximal model with all marginal terms in the original model are tried.
<code>scale</code>	used in the definition of the AIC statistic for selecting the models, currently only for <code>lm</code> , <code>aov</code> and <code>glm</code> models. Specifying <code>scale</code> asserts that the residual standard error or dispersion is known.
<code>test</code>	should the results include a test statistic relative to the original model? The F test is only appropriate for <code>lm</code> and <code>aov</code> models, and perhaps for some over-dispersed <code>glm</code> models. The Chisq test can be an exact test ( <code>lm</code> models with known scale) or a likelihood-ratio test depending on the method.
<code>k</code>	the multiple of the number of degrees of freedom used for the penalty. Only <code>k=2</code> gives the genuine AIC: <code>k = log(n)</code> is sometimes referred to as BIC or SBC.
<code>sorted</code>	should the results be sorted on the value of AIC?
<code>trace</code>	if TRUE additional information may be given on the fits as they are tried.
<code>...</code>	arguments passed to or from other methods.

**Details**

The definition of AIC is only up to an additive constant: when appropriate (l<sub>m</sub> models with specified scale) the constant is taken to be that used in Mallows' Cp statistic and the results are labelled accordingly.

**Value**

A table of class "anova" containing at least columns for the change in degrees of freedom and AIC (or Cp) for the models. Some methods will give further information, for example sums of squares, deviances, log-likelihoods and test statistics.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[dropterm](#), [stepAIC](#)

**Examples**

```
quine.hi <- aov(log(Days + 2.5) ~ .^4, quine)
quine.lo <- aov(log(Days+2.5) ~ 1, quine)
addterm(quine.lo, quine.hi, test="F")

house.glm0 <- glm(Freq ~ Infl*Type*Cont + Sat, family=poisson,
                 data=housing)
addterm(house.glm0, ~. + Sat:(Infl+Type+Cont), test="Chisq")
house.glm1 <- update(house.glm0, . ~ . + Sat*(Infl+Type+Cont))
addterm(house.glm1, ~. + Sat:(Infl+Type+Cont)^2, test = "Chisq")
```

---

Aids2

*Australian AIDS Survival Data*


---

**Description**

Data on patients diagnosed with AIDS in Australia before 1 July 1991.

**Usage**

```
Aids2
```

**Format**

This data frame contains 2843 rows and the following columns:

state Grouped state of origin: "NSW" includes ACT and "other" is WA, SA, NT and TAS.

sex Sex of patient.

diag (Julian) date of diagnosis.

death (Julian) date of death or end of observation.

status "A" (alive) or "D" (dead) at end of observation.

T.categ Reported transmission category.

age Age (years) at diagnosis.

**Note**

This data set has been slightly jittered as a condition of its release, to ensure patient confidentiality.

**Source**

Dr P. J. Solomon and the Australian National Centre in HIV Epidemiology and Clinical Research.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

Animals

*Brain and Body Weights for 28 Species*

---

**Description**

Average brain and body weights for 28 species of land animals.

**Usage**

Animals

**Format**

body body weight in kg.

brain brain weight in g.

**Note**

The name `Animals` avoids conflicts with a system dataset `animals` in S-PLUS 4.5 and later.

**Source**

P. J. Rousseeuw and A. M. Leroy (1987) *Robust Regression and Outlier Detection*. Wiley, p. 57.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

---

`anorexia`*Anorexia Data on Weight Change*

---

**Description**

The `anorexia` data frame has 72 rows and 3 columns. Weight change data for young female anorexia patients.

**Usage**

```
anorexia
```

**Format**

This data frame contains the following columns:

`Treat` Factor of three levels: "Cont" (control), "CBT" (Cognitive Behavioural treatment) and "FT" (family treatment).

`Prewt` Weight of patient before study period, in lbs.

`Postwt` Weight of patient after study period, in lbs.

**Source**

Hand, D. J., Daly, F., McConway, K., Lunn, D. and Ostrowski, E. eds (1993) *A Handbook of Small Data Sets*. Chapman & Hall, Data set 285 (p. 229)

(Note that the original source mistakenly says that weights are in kg.)

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

`anova.negbin`*Likelihood Ratio Tests for Negative Binomial GLMs*

---

**Description**

Method function to perform sequential likelihood ratio tests for Negative Binomial generalized linear models.

**Usage**

```
## S3 method for class 'negbin':  
anova(object, ..., test = "Chisq")
```

**Arguments**

object	Fitted model object of class "negbin", inheriting from classes "glm" and "lm", specifying a Negative Binomial fitted GLM. Typically the output of <code>glm.nb()</code> .
...	Zero or more additional fitted model objects of class "negbin". They should form a nested sequence of models, but need not be specified in any particular order.
test	Argument to match the <code>test</code> argument of <code>anova.glm</code> . Ignored (with a warning if changed) if a sequence of two or more Negative Binomial fitted model objects is specified, but possibly used if only one object is specified.

**Details**

This function is a method for the generic function `anova()` for class "negbin". It can be invoked by calling `anova(x)` for an object `x` of the appropriate class, or directly by calling `anova.negbin(x)` regardless of the class of the object.

**Note**

If only one fitted model object is specified, a sequential analysis of deviance table is given for the fitted model. The `theta` parameter is kept fixed. If more than one fitted model object is specified they must all be of class "negbin" and likelihood ratio tests are done of each model within the next. In this case `theta` is assumed to have been re-estimated for each model.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

`glm.nb`, `negative.binomial`, `summary.negbin`

**Examples**

```
m1 <- glm.nb(Days ~ Eth*Age*Lrn*Sex, quine, link = log)
m2 <- update(m1, . ~ . - Eth:Age:Lrn:Sex)
anova(m2, m1)
anova(m2)
```

---

area

*Adaptive Numerical Integration*

---

**Description**

Integrate a function of one variable over a finite range using a recursive adaptive method. This function is mainly for demonstration purposes.

**Usage**

```
area(f, a, b, ..., fa = f(a, ...), fb = f(b, ...),
     limit = 10, eps = 1e-05)
```

**Arguments**

f	The integrand as an S function object. The variable of integration must be the first argument.
a	Lower limit of integration.
b	Upper limit of integration.
...	Additional arguments needed by the integrand.
fa	Function value at the lower limit.
fb	Function value at the upper limit.
limit	Limit on the depth to which recursion is allowed to go.
eps	Error tolerance to control the process.

**Details**

The method divides the interval in two and compares the values given by Simpson's rule and the trapezium rule. If these are within eps of each other the Simpson's rule result is given, otherwise the process is applied separately to each half of the interval and the results added together.

**Value**

The integral from a to b of  $f(x)$ .

**References**

Venables, W. N. and Ripley, B. D. (1994) *Modern Applied Statistics with S-Plus*. Springer. pp. 105–110.

**Examples**

```
area(sin, 0, pi) # integrate the sin function from 0 to pi.
```

---

bacteria

*Presence of Bacteria after Drug Treatments*


---

**Description**

Tests of the presence of the bacteria *H. influenzae* in children with otitis media in the Northern Territory of Australia.

**Usage**

```
bacteria
```

## Format

This data frame has 220 rows and the following columns:

**y** presence or absence: a factor with levels n and y.

**ap** active/placebo: a factor with levels a and p.

**hilo** hi/low compliance: a factor with levels hi and lo.

**week** numeric: week of test.

**ID** subject ID: a factor.

**trt** a factor with levels placebo, drug and drug+, a re-coding of ap and hilo.

## Details

Dr A. Leach tested the effects of a drug on 50 children with a history of otitis media in the Northern Territory of Australia. The children were randomized to the drug or the a placebo, and also to receive active encouragement to comply with taking the drug.

The presence of *H. influenzae* was checked at weeks 0, 2, 4, 6 and 11: 30 of the checks were missing and are not included in this data frame.

## Source

Menzies School of Health Research 1999–2000 Annual Report pp. 18–21 (<http://www.menzies.edu.au/publications/anreps/MSHR00.pdf>).

## References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

## Examples

```
contrasts(bacteria$trt) <- structure(contr.sdif(3),
  dimnames = list(NULL, c("drug", "encourage")))
## fixed effects analyses
summary(glm(y ~ trt * week, binomial, data = bacteria))
summary(glm(y ~ trt + week, binomial, data = bacteria))
summary(glm(y ~ trt + I(week > 2), binomial, data = bacteria))

# conditional random-effects analysis
library(survival)
bacteria$Time <- rep(1, nrow(bacteria))
coxph(Surv(Time, unclass(y)) ~ week + strata(ID),
  data = bacteria, method = "exact")
coxph(Surv(Time, unclass(y)) ~ factor(week) + strata(ID),
  data = bacteria, method = "exact")
coxph(Surv(Time, unclass(y)) ~ I(week > 2) + strata(ID),
  data = bacteria, method = "exact")

# PQL glmm analysis
library(nlme)
summary(glmmPQL(y ~ trt + I(week > 2), random = ~ 1 | ID,
  family = binomial, data = bacteria))
```

---

bandwidth.nrd	<i>Bandwidth for density() via Normal Reference Distribution</i>
---------------	--

---

**Description**

A well-supported rule-of-thumb for choosing the bandwidth of a Gaussian kernel density estimator.

**Usage**

```
bandwidth.nrd(x)
```

**Arguments**

x                    A data vector.

**Value**

A bandwidth on a scale suitable for the `width` argument of `density`.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Springer, equation (5.5) on page 130.

**Examples**

```
# The function is currently defined as
function(x)
{
  r <- quantile(x, c(0.25, 0.75))
  h <- (r[2] - r[1])/1.34
  4 * 1.06 * min(sqrt(var(x)), h) * length(x)^(-1/5)
}
```

---

bcv	<i>Biased Cross-Validation for Bandwidth Selection</i>
-----	--

---

**Description**

Uses biased cross-validation to select the bandwidth of a Gaussian kernel density estimator.

**Usage**

```
bcv(x, nb = 1000, lower, upper)
```

**Arguments**

x                    a numeric vector  
nb                    number of bins to use.  
lower, upper        Range over which to minimize. The default is almost always satisfactory.



**Value**

a bandwidth

**References**

Scott, D. W. (1992) *Multivariate Density Estimation: Theory, Practice, and Visualization*. Wiley.  
 Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[ucv](#), [width.SJ](#), [density](#)

**Examples**

```
bcv(geyser$duration)
```

---

 beav1

---

*Body Temperature Series of Beaver 1*


---

**Description**

Reynolds (1994) describes a small part of a study of the long-term temperature dynamics of beaver *Castor canadensis* in north-central Wisconsin. Body temperature was measured by telemetry every 10 minutes for four females, but data from a one period of less than a day for each of two animals is used there.

**Usage**

```
beav1
```

**Format**

The `beav1` data frame has 114 rows and 4 columns. This data frame contains the following columns:

`day` Day of observation (in days since the beginning of 1990), December 12–13.

`time` Time of observation, in the form 0330 for 3.30am.

`temp` Measured body temperature in degrees Celsius.

`activ` Indicator of activity outside the retreat.

**Note**

The observation at 22:20 is missing.

**Source**

P. S. Reynolds (1994) Time-series analyses of beaver body temperatures. Chapter 11 of Lange, N., Ryan, L., Billard, L., Brillinger, D., Conquest, L. and Greenhouse, J. eds (1994) *Case Studies in Biometry*. New York: John Wiley and Sons.

## References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

## See Also

[beav2](#)

## Examples

```
attach(beav1)
beav1$hours <- 24*(day-346) + trunc(time/100) + (time%%100)/60
plot(beav1$hours, beav1$temp, type="l", xlab="time",
     ylab="temperature", main="Beaver 1")
usr <- par("usr"); usr[3:4] <- c(-0.2, 8); par(usr=usr)
lines(beav1$hours, beav1$activ, type="s", lty=2)
temp <- ts(c(beav1$temp[1:82], NA, beav1$temp[83:114]),
          start = 9.5, frequency = 6)
activ <- ts(c(beav1$activ[1:82], NA, beav1$activ[83:114]),
          start = 9.5, frequency = 6)

acf(temp[1:53])
acf(temp[1:53], type = "partial")
ar(temp[1:53])
act <- c(rep(0, 10), activ)
X <- cbind(1, act = act[11:125], act1 = act[10:124],
          act2 = act[9:123], act3 = act[8:122])
alpha <- 0.80
stemp <- as.vector(temp - alpha*lag(temp, -1))
sX <- X[-1, ] - alpha * X[-115,]
beav1.ls <- lm(stemp ~ -1 + sX, na.action = na.omit)
summary(beav1.ls, cor = FALSE)
detach("beav1"); rm(temp, activ)
```

---

beav2

*Body Temperature Series of Beaver 2*

---

## Description

Reynolds (1994) describes a small part of a study of the long-term temperature dynamics of beaver *Castor canadensis* in north-central Wisconsin. Body temperature was measured by telemetry every 10 minutes for four females, but data from a one period of less than a day for each of two animals is used there.

## Usage

```
beav2
```

## Format

The `beav2` data frame has 100 rows and 4 columns. This data frame contains the following columns:

`day` Day of observation (in days since the beginning of 1990), November 3–4.

`time` Time of observation, in the form 0330 for 3.30am.  
`temp` Measured body temperature in degrees Celsius.  
`activ` Indicator of activity outside the retreat.

### Source

P. S. Reynolds (1994) Time-series analyses of beaver body temperatures. Chapter 11 of Lange, N., Ryan, L., Billard, L., Brillinger, D., Conquest, L. and Greenhouse, J. eds (1994) *Case Studies in Biometry*. New York: John Wiley and Sons.

### References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### See Also

[beav1](#)

### Examples

```
attach(beav2)
beav2$hours <- 24*(day-307) + trunc(time/100) + (time%%100)/60
plot(beav2$hours, beav2$temp, type = "l", xlab = "time",
     ylab = "temperature", main = "Beaver 2")
usr <- par("usr"); usr[3:4] <- c(-0.2, 8); par(usr = usr)
lines(beav2$hours, beav2$activ, type = "s", lty = 2)

temp <- ts(temp, start = 8+2/3, frequency = 6)
activ <- ts(activ, start = 8+2/3, frequency = 6)
acf(temp[activ == 0]); acf(temp[activ == 1]) # also look at PACFs
ar(temp[activ == 0]); ar(temp[activ == 1])

arima(temp, order = c(1,0,0), xreg = activ)
dreg <- cbind(sin = sin(2*pi*beav2$hours/24), cos = cos(2*pi*beav2$hours/24))
arima(temp, order = c(1,0,0), xreg = cbind(active=activ, dreg))

library(nlme)
beav2.gls <- gls(temp ~ activ, data = beav2, corr = corAR1(0.8),
               method = "ML")
summary(beav2.gls)
summary(update(beav2.gls, subset = 6:100))
detach("beav2"); rm(temp, activ)
```

---

Belgian-phones

*Belgium Phone Calls 1950-1973*

---

### Description

A list object with the annual numbers of telephone calls, in Belgium. The components are:

`year` last two digits of the year.

`calls` number of telephone calls made (in millions of calls).

**Usage**

```
phones
```

**Source**

P. J. Rousseeuw and A. M. Leroy (1987) *Robust Regression & Outlier Detection*. Wiley.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

```
biopsy
```

*Biopsy Data on Breast Cancer Patients*

---

**Description**

This breast cancer database was obtained from the University of Wisconsin Hospitals, Madison from Dr. William H. Wolberg. He assessed biopsies of breast tumours for 699 patients up to 15 July 1992; each of nine attributes has been scored on a scale of 1 to 10, and the outcome is also known. There are 699 rows and 11 columns.

**Usage**

```
biopsy
```

**Format**

This data frame contains the following columns:

- ID sample code number (not unique).
- V1 clump thickness.
- V2 uniformity of cell size.
- V3 uniformity of cell shape.
- V4 marginal adhesion.
- V5 single epithelial cell size.
- V6 bare nuclei (16 values are missing).
- V7 bland chromatin.
- V8 normal nucleoli.
- V9 mitoses.
- class "benign" or "malignant".

**Source**

P. M. Murphy and D. W. Aha (1992). UCI Repository of machine learning databases. [Machine-readable data repository]. Irvine, CA: University of California, Department of Information and Computer Science.

O. L. Mangasarian and W. H. Wolberg (1990) Cancer diagnosis via linear programming. *SIAM News* **23**, pp 1 & 18.

William H. Wolberg and O.L. Mangasarian (1990) Multisurface method of pattern separation for medical diagnosis applied to breast cytology. *Proceedings of the National Academy of Sciences, U.S.A.* **87**, pp. 9193–9196.

O. L. Mangasarian, R. Setiono and W.H. Wolberg (1990) Pattern recognition via linear programming: Theory and application to medical diagnosis. In *Large-scale Numerical Optimization* eds Thomas F. Coleman and Yuying Li, SIAM Publications, Philadelphia, pp 22–30.

K. P. Bennett and O. L. Mangasarian (1992) Robust linear programming discrimination of two linearly inseparable sets. *Optimization Methods and Software* **1**, pp. 23–34 (Gordon & Breach Science Publishers).

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

---

 birthwt

---

*Risk Factors Associated with Low Infant Birth Weight*


---

**Description**

The `birthwt` data frame has 189 rows and 10 columns. The data were collected at Baystate Medical Center, Springfield, Mass during 1986.

**Usage**

```
birthwt
```

**Format**

This data frame contains the following columns:

`low` indicator of birth weight less than 2.5 kg.  
`age` mother's age in years.  
`lwt` mother's weight in pounds at last menstrual period.  
`race` mother's race (1 = white, 2 = black, 3 = other).  
`smoke` smoking status during pregnancy.  
`ptl` number of previous premature labours.  
`ht` history of hypertension.  
`ui` presence of uterine irritability.  
`ftv` number of physician visits during the first trimester.  
`bwt` birth weight in grams.

**Source**

Hosmer, D.W. and Lemeshow, S. (1989) *Applied Logistic Regression*. New York: Wiley

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```
attach(birthwt)
race <- factor(race, labels = c("white", "black", "other"))
ptd <- factor(ptl > 0)
ftv <- factor(ftv)
levels(ftv)[-1:2] <- "2+"
bwt <- data.frame(low = factor(low), age, lwt, race,
  smoke = (smoke > 0), ptd, ht = (ht > 0), ui = (ui > 0), ftv)
detach("birthwt")
options(contrasts = c("contr.treatment", "contr.poly"))
glm(low ~ ., binomial, bwt)
```

---

 Boston

*Housing Values in Suburbs of Boston*


---

**Description**

The Boston data frame has 506 rows and 14 columns.

**Usage**

Boston

**Format**

This data frame contains the following columns:

*crim* per capita crime rate by town.

*zn* proportion of residential land zoned for lots over 25,000 sq.ft.

*indus* proportion of non-retail business acres per town.

*chas* Charles River dummy variable (= 1 if tract bounds river; 0 otherwise).

*nox* nitrogen oxides concentration (parts per 10 million).

*rm* average number of rooms per dwelling.

*age* proportion of owner-occupied units built prior to 1940.

*dis* weighted mean of distances to five Boston employment centres.

*rad* index of accessibility to radial highways.

*tax* full-value property-tax rate per \$10,000.

*ptratio* pupil-teacher ratio by town.

*black*  $1000(Bk - 0.63)^2$  where *Bk* is the proportion of blacks by town.

*lstat* lower status of the population (percent).

*medv* median value of owner-occupied homes in \$1000s.

**Source**

Harrison, D. and Rubinfeld, D.L. (1978) Hedonic prices and the demand for clean air. *J. Environ. Economics and Management* **5**, 81–102.

Belsley D.A., Kuh, E. and Welsch, R.E. (1980) *Regression Diagnostics. Identifying Influential Data and Sources of Collinearity*. New York: Wiley.

---

 boxcox

*Box-Cox Transformations for Linear Models*


---

**Description**

Computes and optionally plots profile log-likelihoods for the parameter of the Box-Cox power transformation.

**Usage**

```
boxcox(object, ...)
```

```
## Default S3 method:
boxcox(object, lambda = seq(-2, 2, 1/10), plotit = TRUE,
        interp, eps = 1/50, xlab = expression(lambda),
        ylab = "log-Likelihood", ...)
```

```
## S3 method for class 'formula':
boxcox(object, lambda = seq(-2, 2, 1/10), plotit = TRUE,
        interp, eps = 1/50, xlab = expression(lambda),
        ylab = "log-Likelihood", ...)
```

```
## S3 method for class 'lm':
boxcox(object, lambda = seq(-2, 2, 1/10), plotit = TRUE,
        interp, eps = 1/50, xlab = expression(lambda),
        ylab = "log-Likelihood", ...)
```

**Arguments**

object	a formula or fitted model object. Currently only <code>lm</code> and <code>aov</code> objects are handled.
lambda	vector of values of <code>lambda</code> – default $(-2, 2)$ in steps of 0.1.
plotit	logical which controls whether the result should be plotted.
interp	logical which controls whether spline interpolation is used. Default to <code>TRUE</code> if plotting with <code>lambda</code> of length less than 100.
eps	Tolerance for <code>lambda = 0</code> ; defaults to 0.02.
xlab	defaults to <code>"lambda"</code> .
ylab	defaults to <code>"log-Likelihood"</code> .
...	additional parameters to be used in the model fitting.

**Value**

A list of the `lambda` vector and the computed profile log-likelihood vector, invisibly if the result is plotted.

**Side Effects**

If `plotit = TRUE` plots log-likelihood vs lambda and indicates a 95% confidence interval about the maximum observed value of lambda. If `interp = TRUE`, spline interpolation is used to give a smoother plot.

**References**

Box, G. E. P. and Cox, D. R. (1964) An analysis of transformations (with discussion). *Journal of the Royal Statistical Society B*, **26**, 211–252.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```
boxcox(Volume ~ log(Height) + log(Girth), data = trees,
       lambda = seq(-0.25, 0.25, length = 10))
```

```
boxcox(Days+1 ~ Eth*Sex*Age*Lrn, data = quine,
       lambda = seq(-0.05, 0.45, len = 20))
```

---

cabbages

*Data from a cabbage field trial*


---

**Description**

The cabbages data set has 60 observations and 4 variables

**Usage**

```
cabbages
```

**Format**

This data frame contains the following columns:

`Cult` Factor giving the cultivar of the cabbage, two levels: `c39` and `c52`.

`Date` Factor specifying one of three planting dates: `d16`, `d20` or `d21`.

`HeadWt` Weight of the cabbage head, presumably in kg.

`VitC` Ascorbic acid content, in undefined units.

**Source**

Rawlings, J. O. (1988) *Applied Regression Analysis: A Research Tool*. Wadsworth and Brooks/Cole. Example 8.4, page 219. (Rawlings cites the original source as the files of the late Dr Gertrude M Cox.)

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.



---

 caith

*Colours of Eyes and Hair of People in Caithness*


---

**Description**

Data on the cross-classification of people in Caithness, Scotland, by eye and hair colour. The region of the UK is particularly interesting as there is a mixture of people of Nordic, Celtic and Anglo-Saxon origin.

**Usage**

```
caith
```

**Format**

A 4 by 5 table with rows the eye colours (blue, light, medium, dark) and columns the hair colours (fair, red, medium, dark, black).

**Source**

Fisher, R.A. (1940) The precision of discriminant functions. *Annals of Eugenics (London)* **10**, 422–429.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```
corresp(caith)
dimnames(caith)[[2]] <- c("F", "R", "M", "D", "B")
par(mfcol=c(1,3))
plot(corresp(caith, nf=2)); title("symmetric")
plot(corresp(caith, nf=2), type="rows"); title("rows")
plot(corresp(caith, nf=2), type="col"); title("columns")
par(mfrow=c(1,1))
```

---

 Cars93

*Data from 93 Cars on Sale in the USA in 1993*


---

**Description**

The Cars93 data frame has 93 rows and 27 columns.

**Usage**

```
Cars93
```

**Format**

This data frame contains the following columns:

Manufacturer Manufacturer.

Model Model.

Type Type: a factor with levels "Small", "Sporty", "Compact", "Midsize", "Large" and "Van".

Min.Price Minimum Price (in \\$/1,000): price for a basic version.

Price Midrange Price (in \\$/1,000): average of Min.Price and Max.Price.

Max.Price Maximum Price (in \\$/1,000): price for "a premium version".

MPG.city City MPG (miles per US gallon by EPA rating).

MPG.highway Highway MPG.

AirBags Air Bags standard. Factor: none, driver only, or driver & passenger.

DriveTrain Drive train type: rear wheel, front wheel or 4WD; (factor).

Cylinders Number of cylinders (missing for Mazda RX-7, which has a rotary engine).

EngineSize Engine size (litres).

Horsepower Horsepower (maximum).

RPM RPM (revs per minute at maximum horsepower).

Rev.per.mile Engine revolutions per mile (in highest gear).

Man.trans.avail Is a manual transmission version available? (yes or no, Factor).

Fuel.tank.capacity Fuel tank capacity (US gallons).

Passengers Passenger capacity (persons)

Length Length (inches).

Wheelbase Wheelbase (inches).

Width Width (inches).

Turn.circle U-turn space (feet).

Rear.seat.room Rear seat room (inches) (missing for 2-seater vehicles).

Luggage.room Luggage capacity (cubic feet) (missing for vans).

Weight Weight (pounds).

Origin Of non-USA or USA company origins? (factor).

Make Combination of Manufacturer and Model (character).

**Details**

Cars were selected at random from among 1993 passenger car models that were listed in both the *Consumer Reports* issue and the *PACE Buying Guide*. Pickup trucks and Sport/Utility vehicles were eliminated due to incomplete information in the *Consumer Reports* source. Duplicate models (e.g., Dodge Shadow and Plymouth Sundance) were listed at most once.

Further description can be found in Lock (1993).

**Source**

Lock, R. H. (1993) 1993 New Car Data. *Journal of Statistics Education* 1(1). <http://www.amstat.org/publications/jse/v1n1/datasets.lock.html>.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

---

 cats

*Anatomical Data from Domestic Cats*


---

**Description**

The heart and body weights of samples of male and female cats used for *digitalis* experiments. The cats were all adult, over 2 kg body weight.

**Usage**

cats

**Format**

This data frame contains the following columns:

Sex sex: Factor with evels "F" and "M".

Bwt body weight in kg.

Hwt heart weight in g.

**Source**

R. A. Fisher (1947) The analysis of covariance method for the relation between a part and the whole, *Biometrics* **3**, 65–68.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

 cement

*Heat Evolved by Setting Cements*


---

**Description**

Experiment on the heat evolved in the setting of each of 13 cements.

**Usage**

cement

**Format**

x1, x2, x3, x4 Proportions (%) of active ingredients.

y heat evolved in cal/gm.

**Details**

Thirteen samples of Portland cement were set. For each sample, the percentages of the four main chemical ingredients was accurately measured. While the cement was setting the amount of heat evolved was also measured.

**Source**

Woods, H., Steinour, H.H. and Starke, H.R. (1932) Effect of composition of Portland cement on heat evolved during hardening. *Industrial Engineering and Chemistry*, **24**, 1207–1214.

**References**

Hald, A. (1957) *Statistical Theory with Engineering Applications*. Wiley, New York.

**Examples**

```
lm(y ~ x1 + x2 + x3 + x4, cement)
```

---

chem

*Copper in Wholemeal Flour*

---

**Description**

A numeric vector of 24 determinations of copper in wholemeal flour, in parts per million.

**Usage**

```
chem
```

**Source**

Analytical Methods Committee (1989) Robust statistics – how not to reject outliers. *The Analyst* **114**, 1693–1702.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

`con2tr`*Convert Lists to Data Frames for use by Lattice*

---

**Description**

Convert lists to data frames for use by lattice.

**Usage**

```
con2tr(obj)
```

**Arguments**

`obj` A list of components `x`, `y` and `z` as passed to `contour`.

**Details**

`con2tr` repeats the `x` and `y` components suitably to match the vector `z`.

**Value**

A data frame suitable for passing to lattice (formerly trellis) functions.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

`confint-MASS`*Confidence Intervals for Model Parameters*

---

**Description**

Computes confidence intervals for one or more parameters in a fitted model. Package **MASS** adds methods for `glm` and `nls` fits.

**Usage**

```
## S3 method for class 'glm':
confint(object, parm, level = 0.95, trace = FALSE, ...)

## S3 method for class 'nls':
confint(object, parm, level = 0.95, ...)
```

**Arguments**

object	a fitted model object. Methods currently exist for the classes "glm", "nls" and for profile objects from these classes.
parm	a specification of which parameters are to be given confidence intervals, either a vector of numbers or a vector of names. If missing, all parameters are considered.
level	the confidence level required.
trace	logical. Should profiling be traced?
...	additional argument(s) for methods.

**Details**

`confint` is a generic function in package `stats`.

These `confint` methods calls the appropriate profile method, then finds the confidence intervals by interpolation in the profile traces. If the profile object is already available it should be used as the main argument rather than the fitted model object itself.

**Value**

A matrix (or vector) with columns giving lower and upper confidence limits for each parameter. These will be labelled as  $(1 - \text{level})/2$  and  $1 - (1 - \text{level})/2$  in % (by default 2.5% and 97.5%).

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

`confint` (the generic and "lm" method), `profile`

**Examples**

```
expn1 <- deriv(y ~ b0 + b1 * 2^(-x/th), c("b0", "b1", "th"),
              function(b0, b1, th, x) {})

wtloss.gr <- nls(Weight ~ expn1(b0, b1, th, Days),
               data = wtloss, start = c(b0=90, b1=95, th=120))

expn2 <- deriv(~b0 + b1*((w0 - b0)/b1)^(x/d0),
              c("b0", "b1", "d0"), function(b0, b1, d0, x, w0) {})

wtloss.init <- function(obj, w0) {
  p <- coef(obj)
  d0 <- - log((w0 - p["b0"])/p["b1"])/log(2) * p["th"]
  c(p[c("b0", "b1")], d0 = as.vector(d0))
}

out <- NULL
w0s <- c(110, 100, 90)
for(w0 in w0s) {
  fm <- nls(Weight ~ expn2(b0, b1, d0, Days, w0),
           wtloss, start = wtloss.init(wtloss.gr, w0))
  out <- rbind(out, c(coef(fm)["d0"], confint(fm, "d0")))
}
```

```

    }
  dimnames(out) <- list(paste(w0s, "kg:"), c("d0", "low", "high"))
  out

  ldose <- rep(0:5, 2)
  numdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
  sex <- factor(rep(c("M", "F"), c(6, 6)))
  SF <- cbind(numdead, numalive = 20 - numdead)
  budworm.lg0 <- glm(SF ~ sex + ldose - 1, family = binomial)
  confint(budworm.lg0)
  confint(budworm.lg0, "ldose")

```

---

 contr.sdif

*Successive Differences Contrast Coding*


---

### Description

A coding for factors based on successive differences.

### Usage

```
contr.sdif(n, contrasts = TRUE, sparse = FALSE)
```

### Arguments

<code>n</code>	The number of levels required.
<code>contrasts</code>	logical: Should there be $n - 1$ columns orthogonal to the mean (the default) or $n$ columns spanning the space?
<code>sparse</code>	logical. If true and the result would be sparse (only true for <code>contrasts = FALSE</code> ), return a sparse matrix.

### Details

The contrast coefficients are chosen so that the coded coefficients in a one-way layout are the differences between the means of the second and first levels, the third and second levels, and so on. This makes most sense for ordered factors, but does not assume that the levels are equally spaced.

### Value

If `contrasts` is TRUE, a matrix with  $n$  rows and  $n - 1$  columns, and the  $n$  by  $n$  identity matrix if `contrasts` is FALSE.

### References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth Edition, Springer.

### See Also

[contr.treatment](#), [contr.sum](#), [contr.helmert](#).

### Examples

```

contr.sdif(6)
zapsmall(ginv(contr.sdif(6)))

```

---

`coop`*Co-operative Trial in Analytical Chemistry*

---

**Description**

Seven specimens were sent to 6 laboratories in 3 separate batches and each analysed for Analyte. Each analysis was duplicated.

**Usage**`coop`**Format**

This data frame contains the following columns:

Lab Laboratory, L1, L2, ..., L6.

Spc Specimen, S1, S2, ..., S7.

Bat Batch, B1, B2, B3 (nested within Spc/Lab),

Conc Concentration of Analyte in *g/kg*.

**Source**

Analytical Methods Committee (1987) Recommendations for the conduct and interpretation of co-operative trials, *The Analyst* **112**, 679–686.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[chem](#), [abbey](#).

---

`corresp`*Simple Correspondence Analysis*

---

**Description**

Find the principal canonical correlation and corresponding row- and column-scores from a correspondence analysis of a two-way contingency table.



**Usage**

```
corresp(x, ...)

## S3 method for class 'matrix':
corresp(x, nf = 1, ...)

## S3 method for class 'factor':
corresp(x, y, ...)

## S3 method for class 'data.frame':
corresp(x, ...)

## S3 method for class 'xtabs':
corresp(x, ...)

## S3 method for class 'formula':
corresp(formula, data, ...)
```

**Arguments**

<code>x</code> , <code>formula</code>	The function is generic, accepting various forms of the principal argument for specifying a two-way frequency table. Currently accepted forms are matrices, data frames (coerced to frequency tables), objects of class " <code>xtabs</code> " and formulae of the form $\sim F1 + F2$ , where <code>F1</code> and <code>F2</code> are factors.
<code>nf</code>	The number of factors to be computed. Note that although 1 is the most usual, one school of thought takes the first two singular vectors for a sort of biplot.
<code>y</code>	a second factor for a cross-classification.
<code>data</code>	a data frame against which to preferentially resolve variables in the formula.
<code>...</code>	If the principal argument is a formula, a data frame may be specified as well from which variables in the formula are preferentially satisfied.

**Details**

See Venables & Ripley (2002). The `plot` method produces a graphical representation of the table if `nf=1`, with the *areas* of circles representing the numbers of points. If `nf` is two or more the `biplot` method is called, which plots the second and third columns of the matrices  $A = D r^{(-1/2)} U L$  and  $B = D c^{(-1/2)} V L$  where the singular value decomposition is  $U L V$ . Thus the x-axis is the canonical correlation times the row and column scores. Although this is called a biplot, it does *not* have any useful inner product relationship between the row and column scores. Think of this as an equally-scaled plot with two unrelated sets of labels. The origin is marked on the plot with a cross. (For other versions of this plot see the book.)

**Value**

An list object of class "`correspondence`" for which `print`, `plot` and `biplot` methods are supplied. The main components are the canonical correlation(s) and the row and column scores.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.  
 Gower, J. C. and Hand, D. J. (1996) *Biplots*. Chapman & Hall.

**See Also**

[svd](#), [princomp](#).

**Examples**

```
(ct <- corresp(~ Age + Eth, data = quine))
## Not run: plot(ct)

corresp(caith)
biplot(corresp(caith, nf = 2))
```

---

 cov.rob

*Resistant Estimation of Multivariate Location and Scatter*


---

**Description**

Compute a multivariate location and scale estimate with a high breakdown point – this can be thought of as estimating the mean and covariance of the `good` part of the data. `cov.mve` and `cov.mcd` are compatibility wrappers.

**Usage**

```
cov.rob(x, cor = FALSE, quantile.used = floor((n + p + 1)/2),
        method = c("mve", "mcd", "classical"),
        nsamp = "best", seed)

cov.mve(...)
cov.mcd(...)
```

**Arguments**

<code>x</code>	a matrix or data frame.
<code>cor</code>	should the returned result include a correlation matrix?
<code>quantile.used</code>	the minimum number of the data points regarded as good points.
<code>method</code>	the method to be used – minimum volume ellipsoid, minimum covariance determinant or classical product-moment. Using <code>cov.mve</code> or <code>cov.mcd</code> forces <code>mve</code> or <code>mcd</code> respectively.
<code>nsamp</code>	the number of samples or "best" or "exact" or "sample". If "sample" the number chosen is $\min(5 \cdot p, 3000)$ , taken from Rousseeuw and Hubert (1997). If "best" exhaustive enumeration is done up to 5000 samples: if "exact" exhaustive enumeration will be attempted however many samples are needed.
<code>seed</code>	the seed to be used for random sampling: see <a href="#">RNGkind</a> . The current value of <code>.Random.seed</code> will be preserved if it is set.
<code>...</code>	arguments to <code>cov.rob</code> other than <code>method</code> .

## Details

For method "mve", an approximate search is made of a subset of size `quantile.used` with an enclosing ellipsoid of smallest volume; in method "mcd" it is the volume of the Gaussian confidence ellipsoid, equivalently the determinant of the classical covariance matrix, that is minimized. The mean of the subset provides a first estimate of the location, and the rescaled covariance matrix a first estimate of scatter. The Mahalanobis distances of all the points from the location estimate for this covariance matrix are calculated, and those points within the 97.5% point under Gaussian assumptions are declared to be `good`. The final estimates are the mean and rescaled covariance of the `good` points.

The rescaling is by the appropriate percentile under Gaussian data; in addition the first covariance matrix has an *ad hoc* finite-sample correction given by Marazzi.

For method "mve" the search is made over ellipsoids determined by the covariance matrix of `p` of the data points. For method "mcd" an additional improvement step suggested by Rousseeuw and van Driessen (1999) is used, in which once a subset of size `quantile.used` is selected, an ellipsoid based on its covariance is tested (as this will have no larger a determinant, and may be smaller).

## Value

A list with components

<code>center</code>	the final estimate of location.
<code>cov</code>	the final estimate of scatter.
<code>cor</code>	(only is <code>cor = TRUE</code> ) the estimate of the correlation matrix.
<code>sing</code>	message giving number of singular samples out of total
<code>crit</code>	the value of the criterion on log scale. For MCD this is the determinant, and for MVE it is proportional to the volume.
<code>best</code>	the subset used. For MVE the best sample, for MCD the best set of size <code>quantile.used</code> .
<code>n.obs</code>	total number of observations.

## References

- P. J. Rousseeuw and A. M. Leroy (1987) *Robust Regression and Outlier Detection*. Wiley.
- A. Marazzi (1993) *Algorithms, Routines and S Functions for Robust Statistics*. Wadsworth and Brooks/Cole.
- P. J. Rousseeuw and B. C. van Zomeren (1990) Unmasking multivariate outliers and leverage points, *Journal of the American Statistical Association*, **85**, 633–639.
- P. J. Rousseeuw and K. van Driessen (1999) A fast algorithm for the minimum covariance determinant estimator. *Technometrics* **41**, 212–223.
- P. Rousseeuw and M. Hubert (1997) Recent developments in PROGRESS. In *L1-Statistical Procedures and Related Topics* ed Y. Dodge, IMS Lecture Notes volume **31**, pp. 201–214.

## See Also

[lqs](#)

**Examples**

```
set.seed(123)
cov.rob(stackloss)
cov.rob(stack.x, method = "mcd", nsamp = "exact")
```

cov.trob

*Covariance Estimation for Multivariate t Distribution***Description**

Estimates a covariance or correlation matrix assuming the data came from a multivariate t distribution: this provides some degree of robustness to outlier without giving a high breakdown point.

**Usage**

```
cov.trob(x, wt = rep(1, n), cor = FALSE, center = TRUE, nu = 5,
         maxit = 25, tol = 0.01)
```

**Arguments**

<code>x</code>	data matrix. Missing values (NAs) are not allowed.
<code>wt</code>	A vector of weights for each case: these are treated as if the case <code>i</code> actually occurred <code>wt[i]</code> times.
<code>cor</code>	Flag to choose between returning the correlation ( <code>cor = TRUE</code> ) or covariance ( <code>cor = FALSE</code> ) matrix.
<code>center</code>	a logical value or a numeric vector providing the location about which the covariance is to be taken. If <code>center = FALSE</code> , no centering is done; if <code>center = TRUE</code> the MLE of the location vector is used.
<code>nu</code>	'degrees of freedom' for the multivariate t distribution. Must exceed 2 (so that the covariance matrix is finite).
<code>maxit</code>	Maximum number of iterations in fitting.
<code>tol</code>	Convergence tolerance for fitting.

**Value**

A list with the following components

<code>cov</code>	the fitted covariance matrix.
<code>center</code>	the estimated or specified location vector.
<code>wt</code>	the specified weights: only returned if the <code>wt</code> argument was given.
<code>n.obs</code>	the number of cases used in the fitting.
<code>cor</code>	the fitted correlation matrix: only returned if <code>cor = TRUE</code> .
<code>call</code>	The matched call.
<code>iter</code>	The number of iterations used.

**References**

J. T. Kent, D. E. Tyler and Y. Vardi (1994) A curious likelihood identity for the multivariate t-distribution. *Communications in Statistics—Simulation and Computation* **23**, 441–453.

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

**See Also**

[cov](#), [cov.wt](#), [cov.mve](#)

**Examples**

```
cov.trob(stackloss)
```

---

cpus

*Performance of Computer CPUs*


---

**Description**

A relative performance measure and characteristics of 209 CPUs.

**Usage**

```
cpus
```

**Format**

The components are:

`name` manufacturer and model.

`syct` cycle time in nanoseconds.

`mmin` minimum main memory in kilobytes.

`mmax` maximum main memory in kilobytes.

`cach` cache size in kilobytes.

`chmin` minimum number of channels.

`chmax` maximum number of channels.

`perf` published performance on a benchmark mix relative to an IBM 370/158-3.

`estperf` estimated performance (by Ein-Dor & Feldmesser).

**Source**

P. Ein-Dor and J. Feldmesser (1987) Attributes of the performance of central processing units: a relative performance prediction model. *Comm. ACM.* **30**, 308–317.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

`crabs`*Morphological Measurements on Leptograpsus Crabs*

---

**Description**

The `crabs` data frame has 200 rows and 8 columns, describing 5 morphological measurements on 50 crabs each of two colour forms and both sexes, of the species *Leptograpsus variegatus* collected at Fremantle, W. Australia.

**Usage**`crabs`**Format**

This data frame contains the following columns:

`sp` species - "B" or "O" for blue or orange.

`sex` as it says.

`index` index 1 : 50 within each of the four groups.

`FL` frontal lobe size (mm).

`RW` rear width (mm).

`CL` carapace length (mm).

`CW` carapace width (mm).

`BD` body depth (mm).

**Source**

Campbell, N.A. and Mahon, R.J. (1974) A multivariate study of variation in two species of rock crab of genus *Leptograpsus*. *Australian Journal of Zoology* **22**, 417–425.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

`Cushings`*Diagnostic Tests on Patients with Cushing's Syndrome*

---

**Description**

Cushing's syndrome is a hypertensive disorder associated with over-secretion of cortisol by the adrenal gland. The observations are urinary excretion rates of two steroid metabolites.

**Usage**`Cushings`

**Format**

The Cushings data frame has 27 rows and 3 columns:

Tetrahydrocortisone urinary excretion rate (mg/24hr) of Tetrahydrocortisone.

Pregnanetriol urinary excretion rate (mg/24hr) of Pregnanetriol.

Type underlying type of syndrome, coded a (adenoma) , b (bilateral hyperplasia), c (carcinoma) or u for unknown.

**Source**

J. Aitchison and I. R. Dunsmore (1975) *Statistical Prediction Analysis*. Cambridge University Press, Tables 11.1–3.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

 DDT

*DDT in Kale*


---

**Description**

A numeric vector of 15 measurements by different laboratories of the pesticide DDT in kale, in ppm (parts per million) using the multiple pesticide residue measurement.

**Usage**

DDT

**Source**

C. E. Finsterwalder (1976) Collaborative study of an extension of the Mills *et al* method for the determination of pesticide residues in food. *J. Off. Anal. Chem.* **59**, 169–171

R. G. Staudte and S. J. Sheather (1990) *Robust Estimation and Testing*. Wiley

---

 deaths

*Monthly Deaths from Lung Diseases in the UK*


---

**Description**

A time series giving the monthly deaths from bronchitis, emphysema and asthma in the UK, 1974–1979, both sexes (deaths),

**Usage**

deaths

**Source**

P. J. Diggle (1990) *Time Series: A Biostatistical Introduction*. Oxford, table A.3

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

This the same as dataset [ldeaths](#) in R's **datasets** package.

---

 denumerate

*Transform an Allowable Formula for 'loglm' into one for 'terms'*


---

**Description**

`loglm` allows dimension numbers to be used in place of names in the formula. `denumerate` modifies such a formula into one that `terms` can process.

**Usage**

```
denumerate(x)
```

**Arguments**

`x` A formula conforming to the conventions of `loglm`, that is, it may allow dimension numbers to stand in for names when specifying a log-linear model.

**Details**

The model fitting function `loglm` fits log-linear models to frequency data using iterative proportional scaling. To specify the model the user must nominate the margins in the data that remain fixed under the log-linear model. It is convenient to allow the user to use dimension numbers, 1, 2, 3, ... for the first, second, third, ..., margins in a similar way to variable names. As the model formula has to be parsed by `terms`, which treats 1 in a special way and requires parseable variable names, these formulae have to be modified by giving genuine names for these margin, or dimension numbers. `denumerate` replaces these numbers with names of a special form, namely `n` is replaced by `.vn`. This allows `terms` to parse the formula in the usual way.

**Value**

A linear model formula like that presented, except that where dimension numbers, say `n`, have been used to specify fixed margins these are replaced by names of the form `.vn` which may be processed by `terms`.

**See Also**

[renumerate](#)

**Examples**

```
denumerate(~(1+2+3)^3 + a/b)
## Not run: ~ (.v1 + .v2 + .v3)^3 + a/b
```



---

dose.p

*Predict Doses for Binomial Assay model*


---

**Description**

Calibrate binomial assays, generalizing the calculation of LD50.

**Usage**

```
dose.p(obj, cf = 1:2, p = 0.5)
```

**Arguments**

obj	A fitted model object of class inheriting from "glm".
cf	The terms in the coefficient vector giving the intercept and coefficient of (log-)dose
p	Probabilities at which to predict the dose needed.

**Value**

An object of class "glm.dose" giving the prediction (attribute "p" and standard error (attribute "SE") at each response probability.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Springer.

**Examples**

```
ldose <- rep(0:5, 2)
numdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
sex <- factor(rep(c("M", "F"), c(6, 6)))
SF <- cbind(numdead, numalive = 20 - numdead)
budworm.lg0 <- glm(SF ~ sex + ldose - 1, family = binomial)

dose.p(budworm.lg0, cf = c(1,3), p = 1:3/4)
dose.p(update(budworm.lg0, family = binomial(link=probit)),
        cf = c(1,3), p = 1:3/4)
```

---

drivers

*Deaths of Car Drivers in Great Britain 1969-84*


---

**Description**

A regular time series giving the monthly totals of car drivers in Great Britain killed or seriously injured Jan 1969 to Dec 1984. Compulsory wearing of seat belts was introduced on 31 Jan 1983

**Usage**

```
drivers
```

**Source**

Harvey, A.C. (1989) *Forecasting, Structural Time Series Models and the Kalman Filter*. Cambridge University Press, pp. 519–523.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

---

dropterm

*Try All One-Term Deletions from a Model*


---

**Description**

Try fitting all models that differ from the current model by dropping a single term, maintaining marginality.

This function is generic; there exist methods for classes `lm` and `glm` and the default method will work for many other classes.

**Usage**

```
dropterm (object, ...)

## Default S3 method:
dropterm(object, scope, scale = 0, test = c("none", "Chisq"),
         k = 2, sorted = FALSE, trace = FALSE, ...)

## S3 method for class 'lm':
dropterm(object, scope, scale = 0, test = c("none", "Chisq", "F"),
         k = 2, sorted = FALSE, ...)

## S3 method for class 'glm':
dropterm(object, scope, scale = 0, test = c("none", "Chisq", "F"),
         k = 2, sorted = FALSE, trace = FALSE, ...)
```

**Arguments**

<code>object</code>	A object fitted by some model-fitting function.
<code>scope</code>	a formula giving terms which might be dropped. By default, the model formula. Only terms that can be dropped and maintain marginality are actually tried.
<code>scale</code>	used in the definition of the AIC statistic for selecting the models, currently only for <code>lm</code> , <code>aoV</code> and <code>glm</code> models. Specifying <code>scale</code> asserts that the residual standard error or dispersion is known.
<code>test</code>	should the results include a test statistic relative to the original model? The F test is only appropriate for <code>lm</code> and <code>aoV</code> models, and perhaps for some over-dispersed <code>glm</code> models. The Chisq test can be an exact test ( <code>lm</code> models with known scale) or a likelihood-ratio test depending on the method.
<code>k</code>	the multiple of the number of degrees of freedom used for the penalty. Only <code>k = 2</code> gives the genuine AIC: <code>k = log(n)</code> is sometimes referred to as BIC or SBC.

sorted	should the results be sorted on the value of AIC?
trace	if TRUE additional information may be given on the fits as they are tried.
...	arguments passed to or from other methods.

### Details

The definition of AIC is only up to an additive constant: when appropriate (lm models with specified scale) the constant is taken to be that used in Mallows' Cp statistic and the results are labelled accordingly.

### Value

A table of class "anova" containing at least columns for the change in degrees of freedom and AIC (or Cp) for the models. Some methods will give further information, for example sums of squares, deviances, log-likelihoods and test statistics.

### References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### See Also

[addterm](#), [stepAIC](#)

### Examples

```
quine.hi <- aov(log(Days + 2.5) ~ .^4, quine)
quine.nxt <- update(quine.hi, . ~ . - Eth:Sex:Age:Lrn)
dropterm(quine.nxt, test= "F")
quine.stp <- stepAIC(quine.nxt,
  scope = list(upper = ~Eth*Sex*Age*Lrn, lower = ~1),
  trace = FALSE)
dropterm(quine.stp, test = "F")
quine.3 <- update(quine.stp, . ~ . - Eth:Age:Lrn)
dropterm(quine.3, test = "F")
quine.4 <- update(quine.3, . ~ . - Eth:Age)
dropterm(quine.4, test = "F")
quine.5 <- update(quine.4, . ~ . - Age:Lrn)
dropterm(quine.5, test = "F")

house.glm0 <- glm(Freq ~ Infl*Type*Cont + Sat, family=poisson,
  data = housing)
house.glm1 <- update(house.glm0, . ~ . + Sat*(Infl+Type+Cont))
dropterm(house.glm1, test = "Chisq")
```

### Description

Knight and Skagen collected during a field study on the foraging behaviour of wintering Bald Eagles in Washington State, USA data concerning 160 attempts by one (pirating) Bald Eagle to steal a chum salmon from another (feeding) Bald Eagle.

**Usage**

eagles

**Format**

The eagles data frame has 8 rows and 5 columns.

y Number of successful attempts.

n Total number of attempts.

P Size of pirating eagle (L = large, S = small).

A Age of pirating eagle (I = immature, A = adult).

V Size of victim eagle (L = large, S = small).

**Source**

Knight, R. L. and Skagen, S. K. (1988) Agonistic asymmetries and the foraging ecology of Bald Eagles. *Ecology* **69**, 1188–1194.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

**Examples**

```
eagles.glm <- glm(cbind(y, n - y) ~ P*A + V, data = eagles,  
                 family = binomial)  
dropterm(eagles.glm)  
prof <- profile(eagles.glm)  
plot(prof)  
pairs(prof)
```

---

epil

*Seizure Counts for Epileptics*

---

**Description**

Thall and Vail (1990) give a data set on two-week seizure counts for 59 epileptics. The number of seizures was recorded for a baseline period of 8 weeks, and then patients were randomly assigned to a treatment group or a control group. Counts were then recorded for four successive two-week periods. The subject's age is the only covariate.

**Usage**

epil

**Format**

This data frame has 236 rows and the following 9 columns:

`y` the count for the 2-week period.  
`trt` treatment, "placebo" or "progabide".  
`base` the counts in the baseline 8-week period.  
`age` subject's age, in years.  
`V4` 0/1 indicator variable of period 4.  
`subject` subject number, 1 to 59.  
`period` period, 1 to 4.  
`lbase` log-counts for the baseline period, centred to have zero mean.  
`lage` log-ages, centred to have zero mean.

**Source**

Thall, P. F. and Vail, S. C. (1990) Some covariance models for longitudinal count data with over-dispersion. *Biometrics* **46**, 657–671.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth Edition. Springer.

**Examples**

```
summary(glm(y ~ lbase*trt + lage + V4, family = poisson,
            data = epil), cor = FALSE)
epil2 <- epil[epil$period == 1, ]
epil2["period"] <- rep(0, 59); epil2["y"] <- epil2["base"]
epil["time"] <- 1; epil2["time"] <- 4
epil2 <- rbind(epil, epil2)
epil2$pred <- unclass(epil2$trt) * (epil2$period > 0)
epil2$subject <- factor(epil2$subject)
epil3 <- aggregate(epil2, list(epil2$subject, epil2$period > 0),
                  function(x) if(is.numeric(x)) sum(x) else x[1])
epil3$pred <- factor(epil3$pred,
                  labels = c("base", "placebo", "drug"))

contrasts(epil3$pred) <- structure(contr.sdif(3),
                                dimnames = list(NULL, c("placebo-base", "drug-placebo")))
summary(glm(y ~ pred + factor(subject) + offset(log(time)),
            family = poisson, data = epil3), cor = FALSE)

summary(glmmPQL(y ~ lbase*trt + lage + V4,
                random = ~ 1 | subject,
                family = poisson, data = epil))
summary(glmmPQL(y ~ pred, random = ~1 | subject,
                family = poisson, data = epil3))
```

---

`eqsplot`*Plots with Geometrically Equal Scales*

---

**Description**

Version of a scatterplot with scales chosen to be equal on both axes, that is 1cm represents the same units on each

**Usage**

```
eqsplot(x, y, ratio = 1, tol = 0.04, uin, ...)
```

**Arguments**

<code>x</code>	vector of x values, or a 2-column matrix, or a list with components <code>x</code> and <code>y</code>
<code>y</code>	vector of y values
<code>ratio</code>	desired ratio of units on the axes. Units on the y axis are drawn at <code>ratio</code> times the size of units on the x axis. Ignored if <code>uin</code> is specified and of length 2.
<code>tol</code>	proportion of white space at the margins of plot
<code>uin</code>	desired values for the units-per-inch parameter. If of length 1, the desired units per inch on the x axis.
<code>...</code>	further arguments for <code>plot</code> and graphical parameters. Note that <code>par(xaxs="i", yaxs="i")</code> is enforced, and <code>xlim</code> and <code>ylim</code> will be adjusted accordingly.

**Details**

Limits for the x and y axes are chosen so that they include the data. One of the sets of limits is then stretched from the midpoint to make the units in the ratio given by `ratio`. Finally both are stretched by  $1 + \text{tol}$  to move points away from the axes, and the points plotted.

**Value**

invisibly, the values of `uin` used for the plot.

**Side Effects**

performs the plot.

**Note**

Arguments `ratio` and `uin` were suggested by Bill Dunlap.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[plot](#), [par](#)

---

farms

*Ecological Factors in Farm Management*

---

### Description

The `farms` data frame has 20 rows and 4 columns. The rows are farms on the Dutch island of Terschelling and the columns are factors describing the management of grassland.

### Usage

```
farms
```

### Format

This data frame contains the following columns:

`Mois` Five levels of soil moisture – level 3 does not occur at these 20 farms.

`Manag` Grassland management type (SF = standard, BF = biological, HF = hobby farming, NM = nature conservation).

`Use` Grassland use (U1 = hay production, U2 = intermediate, U3 = grazing).

`Manure` Manure usage – classes C0 to C4.

### Source

J.C. Gower and D.J. Hand (1996) *Biplots*. Chapman & Hall, Table 4.6.

Quoted as from:

R.H.G. Jongman, C.J.F. ter Braak and O.F.R. van Tongeren (1987) *Data Analysis in Community and Landscape Ecology*. PUDOC, Wageningen.

### References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### Examples

```
farms.mca <- mca(farms, abbrev = TRUE) # Use levels as names
eqscplot(farms.mca$cs, type = "n")
text(farms.mca$rs, cex = 0.7)
text(farms.mca$cs, labels = dimnames(farms.mca$cs)[[1]], cex = 0.7)
```

---

`fgl`*Measurements of Forensic Glass Fragments*

---

**Description**

The `fgl` data frame has 214 rows and 10 columns. It was collected by B. German on fragments of glass collected in forensic work.

**Usage**`fgl`**Format**

This data frame contains the following columns:

RI refractive index; more precisely the refractive index is 1.518xxxx.

The next 8 measurements are percentages by weight of oxides.

Na sodium.

Mg manganese.

Al aluminium.

Si silicon.

K potassium.

Ca calcium.

Ba barium.

Fe iron.

`type` The fragments were originally classed into seven types, one of which was absent in this dataset. The categories which occur are window float glass (`WinF`: 70), window non-float glass (`WinNF`: 76), vehicle window glass (`Veh`: 17), containers (`Con`: 13), tableware (`Tabl`: 9) and vehicle headlamps (`Head`: 29).

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

`fitdistr`*Maximum-likelihood Fitting of Univariate Distributions*

---

**Description**

Maximum-likelihood fitting of univariate distributions, allowing parameters to be held fixed if desired.

**Usage**`fitdistr(x, densfun, start, ...)`



**Arguments**

<code>x</code>	A numeric vector of length at least one containing only <a href="#">finite</a> values.
<code>densfun</code>	Either a character string or a function returning a density evaluated at its first argument. Distributions "beta", "cauchy", "chi-squared", "exponential", "f", "gamma", "geometric", "log-normal", "lognormal", "logistic", "negative binomial", "normal", "Poisson", "t" and "weibull" are recognised, case being ignored.
<code>start</code>	A named list giving the parameters to be optimized with initial values. This can be omitted for some of the named distributions and must be for others (see <a href="#">Details</a> ).
<code>...</code>	Additional parameters, either for <code>densfun</code> or for <code>optim</code> . In particular, it can be used to specify bounds via <code>lower</code> or <code>upper</code> or both. If arguments of <code>densfun</code> (or the density function corresponding to a character-string specification) are included they will be held fixed.

**Details**

For the Normal, log-Normal, exponential and Poisson distributions the closed-form MLEs (and exact standard errors) are used, and `start` should not be supplied.

For all other distributions, direct optimization of the log-likelihood is performed using `optim`. The estimated standard errors are taken from the observed information matrix, calculated by a numerical approximation. For one-dimensional problems the Nelder-Mead method is used and for multi-dimensional problems the BFGS method, unless arguments named `lower` or `upper` are supplied (when `L=BFGS=B` is used) or `method` is supplied explicitly.

For the "t" named distribution the density is taken to be the location-scale family with location `m` and scale `s`.

For the following named distributions, reasonable starting values will be computed if `start` is omitted or only partially specified: "cauchy", "gamma", "logistic", "negative binomial" (parametrized by `mu` and `size`), "t" and "weibull". Note that these starting values may not be good enough if the fit is poor: in particular they are not resistant to outliers unless the fitted distribution is long-tailed.

There are `print`, `coef`, `vcov` and `logLik` methods for class "fitdistr".

**Value**

An object of class "fitdistr", a list with four components,

<code>estimate</code>	the parameter estimates,
<code>sd</code>	the estimated standard errors,
<code>vcov</code>	the estimated variance-covariance matrix, and
<code>loglik</code>	the log-likelihood.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```
set.seed(123)
x <- rgamma(100, shape = 5, rate = 0.1)
fitdistr(x, "gamma")
## now do this directly with more control.
fitdistr(x, dgamma, list(shape = 1, rate = 0.1), lower = 0.001)

set.seed(123)
x2 <- rt(250, df = 9)
fitdistr(x2, "t", df = 9)
## allow df to vary: not a very good idea!
fitdistr(x2, "t")
## now do fixed-df fit directly with more control.
mydt <- function(x, m, s, df) dt((x-m)/s, df)/s
fitdistr(x2, mydt, list(m = 0, s = 1), df = 9, lower = c(-Inf, 0))

set.seed(123)
x3 <- rweibull(100, shape = 4, scale = 100)
fitdistr(x3, "weibull")

set.seed(123)
x4 <- rnegbin(500, mu = 5, theta = 4)
fitdistr(x4, "Negative Binomial")
```

---

forbes

*Forbes' Data on Boiling Points in the Alps*

---

**Description**

A data frame with 17 observations on boiling point of water and barometric pressure in inches of mercury.

**Usage**

```
forbes
```

**Format**

bp boiling point (degrees Farenheit).  
pres barometric pressure in inches of mercury.

**Source**

A. C. Atkinson (1985) *Plots, Transformations and Regression*. Oxford.  
S. Weisberg (1980) *Applied Linear Regression*. Wiley.

fractions

*Rational Approximation***Description**

Find rational approximations to the components of a real numeric object using a standard continued fraction method.

**Usage**

```
fractions(x, cycles = 10, max.denominator = 2000, ...)
```

**Arguments**

`x` Any object of mode numeric. Missing values are now allowed.

`cycles` The maximum number of steps to be used in the continued fraction approximation process.

`max.denominator` An early termination criterion. If any partial denominator exceeds `max.denominator` the continued fraction stops at that point.

`...` arguments passed to or from other methods.

**Details**

Each component is first expanded in a continued fraction of the form

$$x = \text{floor}(x) + 1/(p_1 + 1/(p_2 + \dots))$$

where  $p_1, p_2, \dots$  are positive integers, terminating either at `cycles` terms or when a  $p_j > \text{max.denominator}$ . The continued fraction is then re-arranged to retrieve the numerator and denominator as integers.

The numerators and denominators are then combined into a character vector that becomes the "fracs" attribute and used in printed representations.

Arithmetic operations on "fractions" objects have full floating point accuracy, but the character representation printed out may not.

**Value**

An object of class "fractions". A structure with `.Data` component the same as the input numeric `x`, but with the rational approximations held as a character vector attribute, "fracs". Arithmetic operations on "fractions" objects are possible.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth Edition. Springer.

**See Also**

[rational](#)

**Examples**

```
X <- matrix(runif(25), 5, 5)
zapsmall(solve(X, X/5)) # print near-zeroes as zero
fractions(solve(X, X/5))
fractions(solve(X, X/5)) + 1
```

---

GAGurine

*Level of GAG in Urine of Children*

---

**Description**

Data were collected on the concentration of a chemical GAG in the urine of 314 children aged from zero to seventeen years. The aim of the study was to produce a chart to help a paediatrician to assess if a child's GAG concentration is 'normal'.

**Usage**

GAGurine

**Format**

This data frame contains the following columns:

Age age of child in years.

GAG concentration of GAG (the units have been lost).

**Source**

Mrs Susan Prosser, Paediatrics Department, University of Oxford, via Department of Statistics Consulting Service.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

galaxies

*Velocities for 82 Galaxies*

---

**Description**

A numeric vector of velocities in km/sec of 82 galaxies from 6 well-separated conic sections of an unfilled survey of the Corona Borealis region. Multimodality in such surveys is evidence for voids and superclusters in the far universe.

**Usage**

galaxies

**Note**

There is an 83rd measurement of 5607 km/sec in the Postman *et al.* paper which is omitted in Roeder (1990) and from the dataset here.

There is also a typo: this dataset has 78th observation 26690 which should be 26960.

**Source**

Roeder, K. (1990) Density estimation with confidence sets exemplified by superclusters and voids in galaxies. *Journal of the American Statistical Association* **85**, 617–624.

Postman, M., Huchra, J. P. and Geller, M. J. (1986) Probes of large-scale structures in the Corona Borealis region. *Astrophysical Journal* **92**, 1238–1247.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```
gal <- galaxies/1000
c(width.SJ(gal, method = "dpi"), width.SJ(gal))
plot(x = c(0, 40), y = c(0, 0.3), type = "n", bty = "l",
      xlab = "velocity of galaxy (1000km/s)", ylab = "density")
rug(gal)
lines(density(gal, width = 3.25, n = 200), lty = 1)
lines(density(gal, width = 2.56, n = 200), lty = 3)
```

---

gamma.dispersion     *Calculate the MLE of the Gamma Dispersion Parameter in a GLM Fit*

---

**Description**

A front end to `gamma.shape` for convenience. Finds the reciprocal of the estimate of the shape parameter only.

**Usage**

```
gamma.dispersion(object, ...)
```

**Arguments**

<code>object</code>	Fitted model object giving the gamma fit.
<code>...</code>	Additional arguments passed on to <code>gamma.shape</code> .

**Value**

The MLE of the dispersion parameter of the gamma distribution.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[gamma.shape.glm](#), including the example on its help page.

---

gamma.shape	<i>Estimate the Shape Parameter of the Gamma Distribution in a GLM Fit</i>
-------------	--

---

**Description**

Find the maximum likelihood estimate of the shape parameter of the gamma distribution after fitting a Gamma generalized linear model.

**Usage**

```
## S3 method for class 'glm':
gamma.shape(object, it.lim = 10,
            eps.max = .Machine$double.eps^0.25, verbose = FALSE, ...)
```

**Arguments**

object	Fitted model object from a Gamma family or quasi family with variance = "mu^2".
it.lim	Upper limit on the number of iterations.
eps.max	Maximum discrepancy between approximations for the iteration process to continue.
verbose	If TRUE, causes successive iterations to be printed out. The initial estimate is taken from the deviance.
...	further arguments passed to or from other methods.

**Details**

A glm fit for a Gamma family correctly calculates the maximum likelihood estimate of the mean parameters but provides only a crude estimate of the dispersion parameter. This function takes the results of the glm fit and solves the maximum likelihood equation for the reciprocal of the dispersion parameter, which is usually called the shape (or exponent) parameter.

**Value**

List of two components

alpha	the maximum likelihood estimate
SE	the approximate standard error, the square-root of the reciprocal of the observed information.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[gamma.dispersion](#)

**Examples**

```

clotting <- data.frame(
  u = c(5,10,15,20,30,40,60,80,100),
  lot1 = c(118,58,42,35,27,25,21,19,18),
  lot2 = c(69,35,26,21,18,16,13,12,12))
clot1 <- glm(lot1 ~ log(u), data = clotting, family = Gamma)
gamma.shape(clot1)

gm <- glm(Days + 0.1 ~ Age*Eth*Sex*Lrn,
  quasi(link=log, variance="mu^2"), quine,
  start = c(3, rep(0,31)))
gamma.shape(gm, verbose = TRUE)
summary(gm, dispersion = gamma.dispersion(gm)) # better summary

```

---

gehan

*Remission Times of Leukaemia Patients*


---

**Description**

A data frame from a trial of 42 leukaemia patients. Some were treated with the drug *6-mercaptopurine* and the rest are controls. The trial was designed as matched pairs, both withdrawn from the trial when either came out of remission.

**Usage**

```
gehan
```

**Format**

This data frame contains the following columns:

`pair` label for pair.

`time` remission time in weeks.

`cens` censoring, 0/1.

`treat` treatment, control or 6-MP.

**Source**

Cox, D. R. and Oakes, D. (1984) *Analysis of Survival Data*. Chapman & Hall, p. 7. Taken from

Gehan, E.A. (1965) A generalized Wilcoxon test for comparing arbitrarily single-censored samples. *Biometrika* **52**, 203–233.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```
library(survival)
gehan.surv <- survfit(Surv(time, cens) ~ treat, data = gehan,
  conf.type = "log-log")
summary(gehan.surv)
survreg(Surv(time, cens) ~ factor(pair) + treat, gehan, dist = "exponential")
summary(survreg(Surv(time, cens) ~ treat, gehan, dist = "exponential"))
summary(survreg(Surv(time, cens) ~ treat, gehan))
gehan.cox <- coxph(Surv(time, cens) ~ treat, gehan)
summary(gehan.cox)
```

---

genotype

*Rat Genotype Data*

---

**Description**

Data from a foster feeding experiment with rat mothers and litters of four different genotypes: A, B, I and J. Rat litters were separated from their natural mothers at birth and given to foster mothers to rear.

**Usage**

genotype

**Format**

The data frame has the following components:

`Litter` genotype of the litter.

`Mother` genotype of the foster mother.

`Wt` Litter average weight gain of the litter, in grams at age 28 days. (The source states that the within-litter variability is negligible.)

**Source**

Scheffe, H. (1959) *The Analysis of Variance* Wiley p. 140.

Bailey, D. W. (1953) *The Inheritance of Maternal Influences on the Growth of the Rat*. Unpublished Ph.D. thesis, University of California. Table B of the Appendix.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.



---

 geyser

*Old Faithful Geyser Data*


---

### Description

A version of the eruptions data from the ‘Old Faithful’ geyser in Yellowstone National Park, Wyoming. This version comes from Azzalini and Bowman (1990) and is of continuous measurement from August 1 to August 15, 1985.

Some nocturnal duration measurements were coded as 2, 3 or 4 minutes, having originally been described as ‘short’, ‘medium’ or ‘long’.

### Usage

geyser

### Format

A data frame with 299 observations on 2 variables.

duration	numeric	Eruption time in mins
waiting	numeric	Waiting time to next eruption

### References

Azzalini, A. and Bowman, A. W. (1990) A look at some data on the Old Faithful geyser. *Applied Statistics* **39**, 357–365.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### See Also

[faithful](#)

---

 gilgais

*Line Transect of Soil in Gilgai Territory*


---

### Description

This dataset was collected on a line transect survey in gilgai territory in New South Wales, Australia. Gilgais are natural gentle depressions in otherwise flat land, and sometimes seem to be regularly distributed. The data collection was stimulated by the question: are these patterns reflected in soil properties? At each of 365 sampling locations on a linear grid of 4 meters spacing, samples were taken at depths 0-10 cm, 30-40 cm and 80-90 cm below the surface. pH, electrical conductivity and chloride content were measured on a 1:5 soil:water extract from each sample.

### Usage

gilgais

**Format**

This data frame contains the following columns:

- pH00 pH at depth 0–10 cm.
- pH30 pH at depth 30–40 cm.
- pH80 pH at depth 80–90 cm.
- e00 electrical conductivity in mS/cm (0–10 cm).
- e30 electrical conductivity in mS/cm (30–40 cm).
- e80 electrical conductivity in mS/cm (80–90 cm).
- c00 chloride content in ppm (0–10 cm).
- c30 chloride content in ppm (30–40 cm).
- c80 chloride content in ppm (80–90 cm).

**Source**

- Webster, R. (1977) Spectral analysis of gilgai soil. *Australian Journal of Soil Research* **15**, 191–204.
- Laslett, G. M. (1989) Kriging and splines: An empirical comparison of their predictive performance in some applications (with discussion). *Journal of the American Statistical Association* **89**, 319–409

**References**

- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

ginv

*Generalized Inverse of a Matrix*


---

**Description**

Calculates the Moore-Penrose generalized inverse of a matrix X.

**Usage**

```
ginv(X, tol = sqrt(.Machine$double.eps))
```

**Arguments**

- X Matrix for which the Moore-Penrose inverse is required.
- tol A relative tolerance to detect zero singular values.

**Value**

A MP generalized inverse matrix for X.

**References**

- Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer. p.100.

**See Also**

[solve](#), [svd](#), [eigen](#)

**Examples**

```
## Not run:
# The function is currently defined as
function(X, tol = sqrt(.Machine$double.eps))
{
  ## Generalized Inverse of a Matrix
  dnx <- dimnames(X)
  if(is.null(dnx)) dnx <- vector("list", 2)
  s <- svd(X)
  nz <- s$d > tol * s$d[1]
  structure(
    if(any(nz)) s$v[, nz] %*% (t(s$u[, nz])/s$d[nz]) else X,
    dimnames = dnx[2:1])
}

## End(Not run)
```

---

 glm.convert

*Change a Negative Binomial fit to a GLM fit*


---

**Description**

This function modifies an output object from `glm.nb()` to one that looks like the output from `glm()` with a negative binomial family. This allows it to be updated keeping the theta parameter fixed.

**Usage**

```
glm.convert(object)
```

**Arguments**

`object` An object of class "negbin", typically the output from `glm.nb()`.

**Details**

Convenience function needed to effect some low level changes to the structure of the fitted model object.

**Value**

An object of class "glm" with negative binomial family. The theta parameter is then fixed at its present estimate.

**See Also**

[glm.nb](#), [negative.binomial](#), [glm](#)

**Examples**

```
quine.nb1 <- glm.nb(Days ~ Sex/(Age + Eth*Lrn), data = quine)
quine.nbA <- glm.convert(quine.nb1)
quine.nbB <- update(quine.nb1, . ~ . + Sex:Age:Lrn)
anova(quine.nbA, quine.nbB)
```

glm.nb

*Fit a Negative Binomial Generalized Linear Model***Description**

A modification of the system function `glm()` to include estimation of the additional parameter, `theta`, for a Negative Binomial generalized linear model.

**Usage**

```
glm.nb(formula, data, weights, subset, na.action,
       start = NULL, etastart, mustart,
       control = glm.control(...), method = "glm.fit",
       model = TRUE, x = FALSE, y = TRUE, contrasts = NULL, ...,
       init.theta, link = log)
```

**Arguments**

`formula`, `data`, `weights`, `subset`, `na.action`, `start`, `etastart`, `mustart`, `control`, `method`, `model`, `x`, `y`, `contrasts`, `...` arguments for the `glm()` function. Note that these exclude family and offset (but `offset()` can be used).

`init.theta` Optional initial value for the `theta` parameter. If omitted a moment estimator after an initial fit using a Poisson GLM is used.

`link` The link function. Currently must be one of `log`, `sqrt` or `identity`.

**Details**

An alternating iteration process is used. For given `theta` the GLM is fitted using the same process as used by `glm()`. For fixed means the `theta` parameter is estimated using score and information iterations. The two are alternated until convergence of both. (The number of alternations and the number of iterations when estimating `theta` are controlled by the `maxit` parameter of `glm.control()`.)

Setting `trace > 0` traces the alternating iteration process. Setting `trace > 1` traces the `glm` fit, and setting `trace > 2` traces the estimation of `theta`.

**Value**

A fitted model object of class `negbin` inheriting from `glm` and `lm`. The object is like the output of `glm` but contains three additional components, namely `theta` for the ML estimate of `theta`, `SE.theta` for its approximate standard error (using observed rather than expected information), and `twologlik` for twice the log-likelihood function.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[glm](#), [negative.binomial](#), [anova.negbin](#), [summary.negbin](#), [theta.md](#)

There is a [simulate](#) method.

**Examples**

```
quine.nb1 <- glm.nb(Days ~ Sex/(Age + Eth*Lrn), data = quine)
quine.nb2 <- update(quine.nb1, . ~ . + Sex:Age:Lrn)
quine.nb3 <- update(quine.nb2, Days ~ .^4)
anova(quine.nb1, quine.nb2, quine.nb3)
```

---

 glmmPQL

*Fit Generalized Linear Mixed Models via PQL*


---

**Description**

Fit a GLMM model with multivariate normal random effects, using Penalized Quasi-Likelihood.

**Usage**

```
glmmPQL(fixed, random, family, data, correlation, weights,
        control, niter = 10, verbose = TRUE, ...)
```

**Arguments**

<code>fixed</code>	a two-sided linear formula giving fixed-effects part of the model.
<code>random</code>	a formula or list of formulae describing the random effects.
<code>family</code>	a GLM family.
<code>data</code>	an optional data frame used as the first place to find variables in the formulae, weights and if present in <code>...</code> , subset.
<code>correlation</code>	an optional correlation structure.
<code>weights</code>	optional case weights as in <code>glm</code> .
<code>control</code>	an optional argument to be passed to <code>lme</code> .
<code>niter</code>	maximum number of iterations.
<code>verbose</code>	logical: print out record of iterations?
<code>...</code>	Further arguments for <code>lme</code> .

**Details**

`glmmPQL` works by repeated calls to `lme`, so package `nlme` will be loaded at first use if necessary.

**Value**

A object of class `"lme"`: see [lmeObject](#).

**References**

- Schall, R. (1991) Estimation in generalized linear models with random effects. *Biometrika* **78**, 719–727.
- Breslow, N. E. and Clayton, D. G. (1993) Approximate inference in generalized linear mixed models. *Journal of the American Statistical Association* **88**, 9–25.
- Wolfinger, R. and O’Connell, M. (1993) Generalized linear mixed models: a pseudo-likelihood approach. *Journal of Statistical Computation and Simulation* **48**, 233–243.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[lme](#)

**Examples**

```
library(nlme) # will be loaded automatically if omitted
summary(glmmPQL(y ~ trt + I(week > 2), random = ~ 1 | ID,
               family = binomial, data = bacteria))
```

---

hills

*Record Times in Scottish Hill Races*

---

**Description**

The record times in 1984 for 35 Scottish hill races.

**Usage**

```
hills
```

**Format**

The components are:

```
dist distance in miles (on the map).
climb total height gained during the route, in feet.
time record time in minutes.
```

**Source**

A.C. Atkinson (1986) Comment: Aspects of diagnostic regression analysis. *Statistical Science* **1**, 397–402.

[A.C. Atkinson (1988) Transformations unmasked. *Technometrics* **30**, 311–318 “corrects” the time for Knock Hill from 78.65 to 18.65. It is unclear if this based on the original records.]

**References**

- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

`hist.scott`*Plot a Histogram with Automatic Bin Width Selection*

---

**Description**

Plot a histogram with automatic bin width selection, using the Scott or Freedman–Diaconis formulae.

**Usage**

```
hist.scott(x, prob = TRUE, xlab = deparse(substitute(x)), ...)  
hist.FD(x, prob = TRUE, xlab = deparse(substitute(x)), ...)
```

**Arguments**

<code>x</code>	A data vector
<code>prob</code>	Should the plot have unit area, so be a density estimate?
<code>xlab, ...</code>	Further arguments to <code>hist</code> .

**Value**

For the `nclass.*` functions, the suggested number of classes.

**Side Effects**

Plot a histogram.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Springer.

**See Also**

[hist](#)

---

`housing`*Frequency Table from a Copenhagen Housing Conditions Survey*

---

**Description**

The `housing` data frame has 72 rows and 5 variables.

**Usage**

```
housing
```

**Format**

Sat Satisfaction of householders with their present housing circumstances, (High, Medium or Low, ordered factor).

Infl Perceived degree of influence householders have on the management of the property (High, Medium, Low).

Type Type of rental accommodation, (Tower, Atrium, Apartment, Terrace).

Cont Contact residents are afforded with other residents, (Low, High).

Freq Frequencies: the numbers of residents in each class.

**Source**

Madsen, M. (1976) Statistical analysis of multiple contingency tables. Two examples. *Scand. J. Statist.* **3**, 97–106.

Cox, D. R. and Snell, E. J. (1984) *Applied Statistics, Principles and Examples*. Chapman & Hall.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```
options(contrasts = c("contr.treatment", "contr.poly"))

# Surrogate Poisson models
house.glm0 <- glm(Freq ~ Infl*Type*Cont + Sat, family = poisson,
                 data = housing)
summary(house.glm0, cor = FALSE)

addterm(house.glm0, ~. + Sat:(Infl+Type+Cont), test = "Chisq")

house.glm1 <- update(house.glm0, . ~ . + Sat*(Infl+Type+Cont))
summary(house.glm1, cor = FALSE)

1 - pchisq(deviance(house.glm1), house.glm1$df.residual)

dropterm(house.glm1, test = "Chisq")

addterm(house.glm1, ~. + Sat:(Infl+Type+Cont)^2, test = "Chisq")

hnames <- lapply(housing[, -5], levels) # omit Freq
newData <- expand.grid(hnames)
newData$Sat <- ordered(newData$Sat)
house.pm <- predict(house.glm1, newData,
                   type = "response") # poisson means
house.pm <- matrix(house.pm, ncol = 3, byrow = TRUE,
                  dimnames = list(NULL, hnames[[1]]))
house.pr <- house.pm/drop(house.pm %*% rep(1, 3))
cbind(expand.grid(hnames[-1]), round(house.pr, 2))

# Iterative proportional scaling
loglm(Freq ~ Infl*Type*Cont + Sat*(Infl+Type+Cont), data = housing)

# multinomial model
```



```

library(nnet)
(house.mult<- multinom(Sat ~ Infl + Type + Cont, weights = Freq,
                      data = housing))
house.mult2 <- multinom(Sat ~ Infl*Type*Cont, weights = Freq,
                      data = housing)
anova(house.mult, house.mult2)

house.pm <- predict(house.mult, expand.grid(hnames[-1]), type = "probs")
cbind(expand.grid(hnames[-1]), round(house.pm, 2))

# proportional odds model
house.cpr <- apply(house.pr, 1, cumsum)
logit <- function(x) log(x/(1-x))
house.ld <- logit(house.cpr[2, ]) - logit(house.cpr[1, ])
(ratio <- sort(drop(house.ld)))
mean(ratio)

(house.plr <- polr(Sat ~ Infl + Type + Cont,
                  data = housing, weights = Freq))

house.pr1 <- predict(house.plr, expand.grid(hnames[-1]), type = "probs")
cbind(expand.grid(hnames[-1]), round(house.pr1, 2))

Fr <- matrix(housing$Freq, ncol = 3, byrow = TRUE)
2*sum(Fr*log(house.pr/house.pr1))

house.plr2 <- stepAIC(house.plr, ~.^2)
house.plr2$anova

```

---

huber

*Huber M-estimator of Location with MAD Scale*


---

### Description

Finds the Huber M-estimator of location with MAD scale.

### Usage

```
huber(y, k = 1.5, tol = 1e-06)
```

### Arguments

y	vector of data values
k	Winsorizes at k standard deviations
tol	convergence tolerance

### Value

list of location and scale parameters

mu	location estimate
s	MAD scale estimate

**References**

- Huber, P. J. (1981) *Robust Statistics*. Wiley.  
 Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[hubers, mad](#)

**Examples**

```
huber (chem)
```

---

hubers

*Huber Proposal 2 Robust Estimator of Location and/or Scale*

---

**Description**

Finds the Huber M-estimator for location with scale specified, scale with location specified, or both if neither is specified.

**Usage**

```
hubers(y, k = 1.5, mu, s, initmu = median(y), tol = 1e-06)
```

**Arguments**

y	vector y of data values
k	Winsorizes at k standard deviations
mu	specified location
s	specified scale
initmu	initial value of mu
tol	convergence tolerance

**Value**

list of location and scale estimates

mu	location estimate
s	scale estimate

**References**

- Huber, P. J. (1981) *Robust Statistics*. Wiley.  
 Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[huber](#)

**Examples**

```
hubers(chem)
hubers(chem, mu=3.68)
```

---

 immer

*Yields from a Barley Field Trial*


---

**Description**

The `immer` data frame has 30 rows and 4 columns. Five varieties of barley were grown in six locations in each of 1931 and 1932.

**Usage**

```
immer
```

**Format**

This data frame contains the following columns:

`Loc` The location.

`Var` The variety of barley ("manchuria", "svansota", "velvet", "trebi" and "peatland").

`Y1` Yield in 1931.

`Y2` Yield in 1932.

**Source**

Immer, F.R., Hayes, H.D. and LeRoy Powers (1934) Statistical determination of barley varietal adaptation. *Journal of the American Society for Agronomy* **26**, 403–419.

Fisher, R.A. (1947) *The Design of Experiments*. 4th edition. Edinburgh: Oliver and Boyd.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

**Examples**

```
immer.aov <- aov(cbind(Y1,Y2) ~ Loc + Var, data = immer)
summary(immer.aov)

immer.aov <- aov((Y1+Y2)/2 ~ Var + Loc, data = immer)
summary(immer.aov)
model.tables(immer.aov, type = "means", se = TRUE, cterms = "Var")
```

---

Insurance

*Numbers of Car Insurance claims*

---

### Description

The data given in data frame `Insurance` consist of the numbers of policyholders of an insurance company who were exposed to risk, and the numbers of car insurance claims made by those policyholders in the third quarter of 1973.

### Usage

```
Insurance
```

### Format

This data frame contains the following columns:

`District` factor: district of residence of policyholder (1 to 4): 4 is major cities.

`Group` an ordered factor: group of car with levels <1 litre, 1–1.5 litre, 1.5–2 litre, >2 litre.

`Age` an ordered factor: the age of the insured in 4 groups labelled <25, 25–29, 30–35, >35.

`Holders` numbers of policyholders.

`Claims` numbers of claims

### Source

L. A. Baxter, S. M. Coutts and G. A. F. Ross (1980) Applications of linear models in motor insurance. *Proceedings of the 21st International Congress of Actuaries, Zurich* pp. 11–29.

M. Aitkin, D. Anderson, B. Francis and J. Hinde (1989) *Statistical Modelling in GLIM*. Oxford University Press.

### References

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

### Examples

```
## main-effects fit as Poisson GLM with offset
glm(Claims ~ District + Group + Age + offset(log(Holders)),
     data = Insurance, family = poisson)

# same via loglm
loglm(Claims ~ District + Group + Age + offset(log(Holders)),
      data = Insurance)
```

isoMDS

*Kruskal's Non-metric Multidimensional Scaling***Description**

One form of non-metric multidimensional scaling

**Usage**

```
isoMDS(d, y = cmdscale(d, k), k = 2, maxit = 50, trace = TRUE,
       tol = 1e-3, p = 2)
```

```
Shepard(d, x, p = 2)
```

**Arguments**

d	distance structure of the form returned by <code>dist</code> , or a full, symmetric matrix. Data are assumed to be dissimilarities or relative distances, but must be positive except for self-distance. Both missing and infinite values are allowed.
y	An initial configuration. If none is supplied, <code>cmdscale</code> is used to provide the classical solution, unless there are missing or infinite dissimilarities.
k	The desired dimension for the solution, passed to <code>cmdscale</code> .
maxit	The maximum number of iterations.
trace	Logical for tracing optimization. Default <code>TRUE</code> .
tol	convergence tolerance.
p	Power for Minkowski distance in the configuration space.
x	A final configuration.

**Details**

This chooses a  $k$ -dimensional (default  $k = 2$ ) configuration to minimize the stress, the square root of the ratio of the sum of squared differences between the input distances and those of the configuration to the sum of configuration distances squared. However, the input distances are allowed a monotonic transformation.

An iterative algorithm is used, which will usually converge in around 10 iterations. As this is necessarily an  $O(n^2)$  calculation, it is slow for large datasets. Further, since for the default  $p = 2$  the configuration is only determined up to rotations and reflections (by convention the centroid is at the origin), the result can vary considerably from machine to machine.

**Value**

Two components:

points	A $k$ -column vector of the fitted configuration.
stress	The final stress achieved (in percent).

**Side Effects**

If `trace` is true, the initial stress and the current stress are printed out every 5 iterations.

## References

- T. F. Cox and M. A. A. Cox (1994, 2001) *Multidimensional Scaling*. Chapman & Hall.  
 Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge University Press.  
 Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

## See Also

[cmdscale](#), [sammon](#)

## Examples

```
swiss.x <- as.matrix(swiss[, -1])
swiss.dist <- dist(swiss.x)
swiss.mds <- isoMDS(swiss.dist)
plot(swiss.mds$points, type = "n")
text(swiss.mds$points, labels = as.character(1:nrow(swiss.x)))
swiss.sh <- Shepard(swiss.dist, swiss.mds$points)
plot(swiss.sh, pch = ".")
lines(swiss.sh$x, swiss.sh$yf, type = "S")
```

---

kde2d

*Two-Dimensional Kernel Density Estimation*


---

## Description

Two-dimensional kernel density estimation with an axis-aligned bivariate normal kernel, evaluated on a square grid.

## Usage

```
kde2d(x, y, h, n = 25, lims = c(range(x), range(y)))
```

## Arguments

x	x coordinate of data
y	y coordinate of data
h	vector of bandwidths for x and y directions. Defaults to normal reference bandwidth (see <a href="#">bandwidth.nrd</a> ). A scalar value will be taken to apply to both directions.
n	Number of grid points in each direction. Can be scalar or a length-2 integer vector.
lims	The limits of the rectangle covered by the grid as <code>c(xl, xu, yl, yu)</code> .

## Value

A list of three components.

x, y	The x and y coordinates of the grid points, vectors of length n.
z	An <code>n[1]</code> by <code>n[2]</code> matrix of the estimated density: rows correspond to the value of x, columns to the value of y.

## References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

## Examples

```
attach(geyser)
plot(duration, waiting, xlim = c(0.5,6), ylim = c(40,100))
f1 <- kde2d(duration, waiting, n = 50, lims = c(0.5, 6, 40, 100))
image(f1, zlim = c(0, 0.05))
f2 <- kde2d(duration, waiting, n = 50, lims = c(0.5, 6, 40, 100),
          h = c(width.SJ(duration), width.SJ(waiting)) )
image(f2, zlim = c(0, 0.05))
persp(f2, phi = 30, theta = 20, d = 5)

plot(duration[-272], duration[-1], xlim = c(0.5, 6),
      ylim = c(1, 6), xlab = "previous duration", ylab = "duration")
f1 <- kde2d(duration[-272], duration[-1],
          h = rep(1.5, 2), n = 50, lims = c(0.5, 6, 0.5, 6))
contour(f1, xlab = "previous duration",
        ylab = "duration", levels = c(0.05, 0.1, 0.2, 0.4) )
f1 <- kde2d(duration[-272], duration[-1],
          h = rep(0.6, 2), n = 50, lims = c(0.5, 6, 0.5, 6))
contour(f1, xlab = "previous duration",
        ylab = "duration", levels = c(0.05, 0.1, 0.2, 0.4) )
f1 <- kde2d(duration[-272], duration[-1],
          h = rep(0.4, 2), n = 50, lims = c(0.5, 6, 0.5, 6))
contour(f1, xlab = "previous duration",
        ylab = "duration", levels = c(0.05, 0.1, 0.2, 0.4) )
detach("geyser")
```

---

 lda

*Linear Discriminant Analysis*


---

## Description

Linear discriminant analysis.

## Usage

```
lda(x, ...)

## S3 method for class 'formula':
lda(formula, data, ..., subset, na.action)

## Default S3 method:
lda(x, grouping, prior = proportions, tol = 1.0e-4,
    method, CV = FALSE, nu, ...)

## S3 method for class 'data.frame':
lda(x, ...)

## S3 method for class 'matrix':
lda(x, grouping, ..., subset, na.action)
```

**Arguments**

<code>formula</code>	A formula of the form <code>groups ~ x1 + x2 + ...</code> . That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
<code>data</code>	Data frame from which variables specified in <code>formula</code> are preferentially to be taken.
<code>x</code>	(required if no formula is given as the principal argument.) a matrix or data frame or Matrix containing the explanatory variables.
<code>grouping</code>	(required if no formula principal argument is given.) a factor specifying the class for each observation.
<code>prior</code>	the prior probabilities of class membership. If unspecified, the class proportions for the training set are used. If present, the probabilities should be specified in the order of the factor levels.
<code>tol</code>	A tolerance to decide if a matrix is singular; it will reject variables and linear combinations of unit-variance variables whose variance is less than <code>tol^2</code> .
<code>subset</code>	An index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)
<code>na.action</code>	A function to specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is <code>na.omit</code> , which leads to rejection of cases with missing values on any required variable. (NOTE: If given, this argument must be named.)
<code>method</code>	"moment" for standard estimators of the mean and variance, "mle" for MLEs, "mve" to use <code>cov.mve</code> , or "t" for robust estimates based on a <i>t</i> distribution.
<code>CV</code>	If true, returns results (classes and posterior probabilities) for leave-one-out cross-validation. Note that if the prior is estimated, the proportions in the whole dataset are used.
<code>nu</code>	degrees of freedom for <code>method = "t"</code> .
<code>...</code>	arguments passed to or from other methods.

**Details**

The function tries hard to detect if the within-class covariance matrix is singular. If any variable has within-group variance less than `tol^2` it will stop and report the variable as constant. This could result from poor scaling of the problem, but is more likely to result from constant variables.

Specifying the `prior` will affect the classification unless over-ridden in `predict.lda`. Unlike in most statistical packages, it will also affect the rotation of the linear discriminants within their space, as a weighted between-groups covariance matrix is used. Thus the first few linear discriminants emphasize the differences between groups with the weights given by the prior, which may differ from their prevalence in the dataset.

If one or more groups is missing in the supplied data, they are dropped with a warning, but the classifications produced are with respect to the original set of levels.

**Value**

If `CV = TRUE` the return value is a list with components `class`, the MAP classification (a factor), and `posterior`, posterior probabilities for the classes.

Otherwise it is an object of class "lda" containing the following components:

`prior`            the prior probabilities used.



means	the group means.
scaling	a matrix which transforms observations to discriminant functions, normalized so that within groups covariance matrix is spherical.
svd	the singular values, which give the ratio of the between- and within-group standard deviations on the linear discriminant variables. Their squares are the canonical F-statistics.
N	The number of observations used.
call	The (matched) function call.

### Note

This function may be called giving either a formula and optional data frame, or a matrix and grouping factor as the first two arguments. All other arguments are optional, but `subset=` and `na.action=`, if required, must be fully named.

If a formula is given as the principal argument the object may be modified using `update()` in the usual way.

### References

- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.  
 Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge University Press.

### See Also

[predict.lda](#), [qda](#), [predict.qda](#)

### Examples

```
Iris <- data.frame(rbind(iris3[,1], iris3[,2], iris3[,3]),
                  Sp = rep(c("s","c","v"), rep(50,3)))
train <- sample(1:150, 75)
table(Iris$Sp[train])
## your answer may differ
## c s v
## 22 23 30
z <- lda(Sp ~ ., Iris, prior = c(1,1,1)/3, subset = train)
predict(z, Iris[-train, ])$class
## [1] s s s s s s s s s s s s s s s s s s s s s s s s s s s s s s s s c c c
## [31] c c c c c c c v c c c c v c c c c c c c c c c c c c v v v v v
## [61] v v v v v v v v v v v v v v v
(z1 <- update(z, . ~ . - Petal.W.))
```

---

 ldahist

*Histograms or Density Plots of Multiple Groups*


---

### Description

Plot histograms or density plots of data on a single Fisher linear discriminant.

**Usage**

```
ldahist(data, g, nbins = 25, h, x0 = - h/1000, breaks,
        xlim = range(breaks), ymax = 0, width,
        type = c("histogram", "density", "both"),
        sep = (type != "density"),
        col = 5, xlab = deparse(substitute(data)), bty = "n", ...)
```

**Arguments**

data	vector of data. Missing values (NAs) are allowed and omitted.
g	factor or vector giving groups, of the same length as data.
nbins	Suggested number of bins to cover the whole range of the data.
h	The bin width (takes precedence over nbins).
x0	Shift for the bins - the breaks are at $x0 + h * (... , -1, 0, 1, ...)$
breaks	The set of breakpoints to be used. (Usually omitted, takes precedence over h and nbins).
xlim	The limits for the x-axis.
ymax	The upper limit for the y-axis.
width	Bandwidth for density estimates. If missing, the Sheather-Jones selector is used for each group separately.
type	Type of plot.
sep	Whether there is a separate plot for each group, or one combined plot.
col	The colour number for the bar fill.
xlab	label for the plot x-axis. By default, this will be the name of data.
bty	The box type for the plot - defaults to none.
...	additional arguments to polygon.

**Side Effects**

Histogram and/or density plots are plotted on the current device.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[plot.lda](#).

---

`leuk`*Survival Times and White Blood Counts for Leukaemia Patients*

---

**Description**

A data frame of data from 33 leukaemia patients.

**Usage**`leuk`**Format**

A data frame with columns:

`wbc` white blood count.

`ag` a test result, "present" or "absent".

`time` survival time in weeks.

**Details**

Survival times are given for 33 patients who died from acute myelogenous leukaemia. Also measured was the patient's white blood cell count at the time of diagnosis. The patients were also factored into 2 groups according to the presence or absence of a morphologic characteristic of white blood cells. Patients termed AG positive were identified by the presence of Auer rods and/or significant granulation of the leukaemic cells in the bone marrow at the time of diagnosis.

**Source**

Cox, D. R. and Oakes, D. (1984) *Analysis of Survival Data*. Chapman & Hall, p. 9.

Taken from

Feigl, P. & Zelen, M. (1965) Estimation of exponential survival probabilities with concomitant information. *Biometrics* **21**, 826–838.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```
library(survival)
plot(survfit(Surv(time) ~ ag, data = leuk), lty = 2:3, col = 2:3)

# now Cox models
leuk.cox <- coxph(Surv(time) ~ ag + log(wbc), leuk)
summary(leuk.cox)
```

---

`lm.gls`*Fit Linear Models by Generalized Least Squares*

---

**Description**

Fit linear models by Generalized Least Squares

**Usage**

```
lm.gls(formula, data, W, subset, na.action, inverse = FALSE,
        method = "qr", model = FALSE, x = FALSE, y = FALSE,
        contrasts = NULL, ...)
```

**Arguments**

<code>formula</code>	a formula expression as for regression models, of the form <code>response ~ predictors</code> . See the documentation of <code>formula</code> for other details.
<code>data</code>	an optional data frame in which to interpret the variables occurring in <code>formula</code> .
<code>W</code>	a weight matrix.
<code>subset</code>	expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.
<code>na.action</code>	a function to filter missing data.
<code>inverse</code>	logical: if true <code>W</code> specifies the inverse of the weight matrix: this is appropriate if a variance matrix is used.
<code>method</code>	method to be used by <code>lm.fit</code> .
<code>model</code>	should the model frame be returned?
<code>x</code>	should the design matrix be returned?
<code>y</code>	should the response be returned?
<code>contrasts</code>	a list of contrasts to be used for some or all of
<code>...</code>	additional arguments to <code>lm.fit</code> .

**Details**

The problem is transformed to uncorrelated form and passed to `lm.fit`.

**Value**

An object of class `"lm.gls"`, which is similar to an `"lm"` object. There is no `"weights"` component, and only a few `"lm"` methods will work correctly. As from version 7.1-22 the residuals and fitted values refer to the untransformed problem.

**See Also**

`gls`, `lm`, `lm.ridge`

---

lm.ridge	<i>Ridge Regression</i>
----------	-------------------------

---

**Description**

Fit a linear model by ridge regression.

**Usage**

```
lm.ridge(formula, data, subset, na.action, lambda = 0, model = FALSE,
          x = FALSE, y = FALSE, contrasts = NULL, ...)
```

**Arguments**

formula	a formula expression as for regression models, of the form <code>response ~ predictors</code> . See the documentation of <code>formula</code> for other details. <code>offset</code> terms are allowed.
data	an optional data frame in which to interpret the variables occurring in <code>formula</code> .
subset	expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.
na.action	a function to filter missing data.
lambda	A scalar or vector of ridge constants.
model	should the model frame be returned? Not implemented.
x	should the design matrix be returned? Not implemented.
y	should the response be returned? Not implemented.
contrasts	a list of contrasts to be used for some or all of factor terms in the formula. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
...	additional arguments to <code>lm.fit</code> .

**Details**

If an intercept is present in the model, its coefficient is not penalized. (If you want to penalize an intercept, put in your own constant term and remove the intercept.)

**Value**

A list with components

coef	matrix of coefficients, one row for each value of <code>lambda</code> . Note that these are not on the original scale and are for use by the <code>coef</code> method.
scales	scalings used on the X matrix.
Inter	was intercept included?
lambda	vector of <code>lambda</code> values
ym	mean of <code>y</code>
xm	column means of <code>x</code> matrix
GCV	vector of GCV values
kHKB	HKB estimate of the ridge constant.
kLW	L-W estimate of the ridge constant.

**References**

Brown, P. J. (1994) *Measurement, Regression and Calibration* Oxford.

**See Also**

[lm](#)

**Examples**

```
longley # not the same as the S-PLUS dataset
names(longley)[1] <- "y"
lm.ridge(y ~ ., longley)
plot(lm.ridge(y ~ ., longley,
             lambda = seq(0,0.1,0.001)))
select(lm.ridge(y ~ ., longley,
               lambda = seq(0,0.1,0.0001)))
```

---

loglm

*Fit Log-Linear Models by Iterative Proportional Scaling*


---

**Description**

This function provides a front-end to the standard function, `loglin`, to allow log-linear models to be specified and fitted in a manner similar to that of other fitting functions, such as `glm`.

**Usage**

```
loglm(formula, data, subset, na.action, ...)
```

**Arguments**

<code>formula</code>	A linear model formula specifying the log-linear model. If the left-hand side is empty, the <code>data</code> argument is required and must be a (complete) array of frequencies. In this case the variables on the right-hand side may be the names of the <code>dimnames</code> attribute of the frequency array, or may be the positive integers: 1, 2, 3, ... used as alternative names for the 1st, 2nd, 3rd, ... dimension (classifying factor). If the left-hand side is not empty it specifies a vector of frequencies. In this case the <code>data</code> argument, if present, must be a data frame from which the left-hand side vector and the classifying factors on the right-hand side are (preferentially) obtained. The usual abbreviation of a <code>.</code> to stand for 'all other variables in the data frame' is allowed. Any non-factors on the right-hand side of the formula are coerced to factor.
<code>data</code>	Numeric array or data frame. In the first case it specifies the array of frequencies; in the second it provides the data frame from which the variables occurring in the formula are preferentially obtained in the usual way. This argument may be the result of a call to <a href="#">xtabs</a> .
<code>subset</code>	Specifies a subset of the rows in the data frame to be used. The default is to take all rows.
<code>na.action</code>	Specifies a method for handling missing observations. The default is to fail if missing values are present.
<code>...</code>	May supply other arguments to the function <a href="#">loglm1</a> .

## Details

If the left-hand side of the formula is empty the `data` argument supplies the frequency array and the right-hand side of the formula is used to construct the list of fixed faces as required by `loglin`. Structural zeros may be specified by giving a `start` argument with those entries set to zero, as described in the help information for `loglin`.

If the left-hand side is not empty, all variables on the right-hand side are regarded as classifying factors and an array of frequencies is constructed. If some cells in the complete array are not specified they are treated as structural zeros. The right-hand side of the formula is again used to construct the list of faces on which the observed and fitted totals must agree, as required by `loglin`. Hence terms such as `a:b`, `a*b` and `a/b` are all equivalent.

## Value

An object of class "loglm" conveying the results of the fitted log-linear model. Methods exist for the generic functions `print`, `summary`, `deviance`, `fitted`, `coef`, `resid`, `anova` and `update`, which perform the expected tasks. Only log-likelihood ratio tests are allowed using `anova`.

The deviance is simply an alternative name for the log-likelihood ratio statistic for testing the current model within a saturated model, in accordance with standard usage in generalized linear models.

## Warning

If structural zeros are present, the calculation of degrees of freedom may not be correct. `loglin` itself takes no action to allow for structural zeros. `loglm` deducts one degree of freedom for each structural zero, but cannot make allowance for gains in error degrees of freedom due to loss of dimension in the model space. (This would require checking the rank of the model matrix, but since iterative proportional scaling methods are developed largely to avoid constructing the model matrix explicitly, the computation is at least difficult.)

When structural zeros (or zero fitted values) are present the estimated coefficients will not be available due to infinite estimates. The deviances will normally continue to be correct, though.

## References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

## See Also

`loglm1`, `loglin`

## Examples

```
# The data frames Cars93, minn38 and quine are available
# in the MASS package.

# Case 1: frequencies specified as an array.
sapply(minn38, function(x) length(levels(x)))
## hs phs fol sex f
## 3 4 7 2 0
minn38a <- array(0, c(3,4,7,2), lapply(minn38[, -5], levels))
minn38a[data.matrix(minn38[, -5])] <- minn38$fol
fm <- loglm(~1 + 2 + 3 + 4, minn38a) # numerals as names.
deviance(fm)
##[1] 3711.9
```

```

fm1 <- update(fm, .~.^2)
fm2 <- update(fm, .~.^3, print = TRUE)
## 5 iterations: deviation 0.0750732
anova(fm, fm1, fm2)
## Not run: LR tests for hierarchical log-linear models

Model 1:
~ 1 + 2 + 3 + 4
Model 2:
. ~ 1 + 2 + 3 + 4 + 1:2 + 1:3 + 1:4 + 2:3 + 2:4 + 3:4
Model 3:
. ~ 1 + 2 + 3 + 4 + 1:2 + 1:3 + 1:4 + 2:3 + 2:4 + 3:4 +
  1:2:3 + 1:2:4 + 1:3:4 + 2:3:4

          Deviance  df Delta(Dev) Delta(df) P(> Delta(Dev)
Model 1  3711.915  155
Model 2   220.043  108   3491.873      47      0.00000
Model 3    47.745   36    172.298      72      0.00000
Saturated   0.000    0     47.745      36      0.09114

## End(Not run)
# Case 1. An array generated with xtabs.

loglm(~ Type + Origin, xtabs(~ Type + Origin, Cars93))
## Not run: Call:
loglm(formula = ~Type + Origin, data = xtabs(~Type + Origin,
  Cars93))

Statistics:
              X^2 df  P(> X^2)
Likelihood Ratio 18.362  5 0.0025255
Pearson 14.080  5 0.0151101

## End(Not run)
# Case 2. Frequencies given as a vector in a data frame
names(quine)
## [1] "Eth" "Sex" "Age" "Lrn" "Days"
fm <- loglm(Days ~ .^2, quine)
gm <- glm(Days ~ .^2, poisson, quine) # check glm.
c(deviance(fm), deviance(gm))      # deviances agree
## [1] 1368.7 1368.7
c(fm$df, gm$df)                    # resid df do not!
c(fm$df, gm$df.residual)           # resid df do not!
## [1] 127 128
# The loglm residual degrees of freedom is wrong because of
# a non-detectable redundancy in the model matrix.

```



**Description**

Find and optionally plot the marginal (profile) likelihood for alpha for a transformation model of the form  $\log(y + \text{alpha}) \sim x_1 + x_2 + \dots$

**Usage**

```
logtrans(object, ...)

## Default S3 method:
logtrans(object, ..., alpha = seq(0.5, 6, by = 0.25) - min(y),
         plotit = TRUE, interp =, xlab = "alpha",
         ylab = "log Likelihood")

## S3 method for class 'formula':
logtrans(object, data, ...)

## S3 method for class 'lm':
logtrans(object, ...)
```

**Arguments**

object	Fitted linear model object, or formula defining the untransformed model that is $y \sim x_1 + x_2 + \dots$ . The function is generic.
...	If object is a formula, this argument may specify a data frame as for <code>lm</code> .
alpha	Set of values for the transformation parameter, alpha.
plotit	Should plotting be done?
interp	Should the marginal log-likelihood be interpolated with a spline approximation? (Default is <code>TRUE</code> if plotting is to be done and the number of real points is less than 100.)
xlab	as for plot.
ylab	as for plot.
data	optional data argument for <code>lm</code> fit.

**Value**

List with components `x` (for alpha) and `y` (for the marginal log-likelihood values).

**Side Effects**

A plot of the marginal log-likelihood is produced, if requested, together with an approximate mle and 95% confidence interval.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[boxcox](#)

**Examples**

```
logtrans(Days ~ Age*Sex*Eth*Lrn, data = quine,
         alpha = seq(0.75, 6.5, len=20))
```

---

lqs	<i>Resistant Regression</i>
-----	-----------------------------

---

**Description**

Fit a regression to the *good* points in the dataset, thereby achieving a regression estimator with a high breakdown point. `lmsreg` and `ltsreg` are compatibility wrappers.

**Usage**

```
lqs(x, ...)

## S3 method for class 'formula':
lqs(formula, data, ...,
     method = c("lts", "lqs", "lms", "S", "model.frame"),
     subset, na.action, model = TRUE,
     x.ret = FALSE, y.ret = FALSE, contrasts = NULL)

## Default S3 method:
lqs(x, y, intercept = TRUE, method = c("lts", "lqs", "lms", "S"),
     quantile, control = lqs.control(...), k0 = 1.548, seed, ...)

lmsreg(...)
ltsreg(...)
```

**Arguments**

<code>formula</code>	a formula of the form $y \sim x_1 + x_2 + \dots$
<code>data</code>	data frame from which variables specified in <code>formula</code> are preferentially to be taken.
<code>subset</code>	an index vector specifying the cases to be used in fitting. (NOTE: If given, this argument must be named exactly.)
<code>na.action</code>	function to specify the action to be taken if NAs are found. The default action is for the procedure to fail. Alternatives include <code>na.omit</code> and <code>na.exclude</code> , which lead to omission of cases with missing values on any required variable. (NOTE: If given, this argument must be named exactly.)
<code>model</code> , <code>x.ret</code> , <code>y.ret</code>	logical. If TRUE the model frame, the model matrix and the response are returned, respectively.
<code>contrasts</code>	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
<code>x</code>	a matrix or data frame containing the explanatory variables.
<code>y</code>	the response: a vector of length the number of rows of <code>x</code> .
<code>intercept</code>	should the model include an intercept?

method	the method to be used. <code>model.frame</code> returns the model frame: for the others see the <code>Details</code> section. Using <code>lmsreg</code> or <code>ltsreg</code> forces "lms" and "lts" respectively.
quantile	the quantile to be used: see <code>Details</code> . This is over-ridden if <code>method = "lms"</code> .
control	additional control items: see <code>Details</code> .
k0	the cutoff / tuning constant used for $\chi()$ and $\psi()$ functions when <code>method = "S"</code> , currently corresponding to Tukey's 'biweight'.
seed	the seed to be used for random sampling: see <code>.Random.seed</code> . The current value of <code>.Random.seed</code> will be preserved if it is set.
...	arguments to be passed to <code>lqs.default</code> or <code>lqs.control</code> , see <code>control</code> above and <code>Details</code> .

### Details

Suppose there are  $n$  data points and  $p$  regressors, including any intercept.

The first three methods minimize some function of the sorted squared residuals. For methods "lqs" and "lms" is the quantile squared residual, and for "lts" it is the sum of the quantile smallest squared residuals. "lqs" and "lms" differ in the defaults for `quantile`, which are  $\text{floor}((n+p+1)/2)$  and  $\text{floor}((n+1)/2)$  respectively. For "lts" the default is  $\text{floor}(n/2) + \text{floor}((p+1)/2)$ .

The "S" estimation method solves for the scale  $s$  such that the average of a function  $\chi$  of the residuals divided by  $s$  is equal to a given constant.

The `control` argument is a list with components

`psamp`: the size of each sample. Defaults to  $p$ .

`nsamp`: the number of samples or "best" (the default) or "exact" or "sample". If "sample" the number chosen is  $\min(5*p, 3000)$ , taken from Rousseeuw and Hubert (1997). If "best" exhaustive enumeration is done up to 5000 samples; if "exact" exhaustive enumeration will be attempted however many samples are needed.

`adjust`: should the intercept be optimized for each sample? Defaults to TRUE.

### Value

An object of class "lqs". This is a list with components

crit	the value of the criterion for the best solution found, in the case of <code>method == "S"</code> before IWLS refinement.
sing	character. A message about the number of samples which resulted in singular fits.
coefficients	of the fitted linear model
bestone	the indices of those points fitted by the best sample found (prior to adjustment of the intercept, if requested).
fitted.values	the fitted values.
residuals	the residuals.
scale	estimate(s) of the scale of the error. The first is based on the fit criterion. The second (not present for <code>method == "S"</code> ) is based on the variance of those residuals whose absolute value is less than 2.5 times the initial estimate.

**Note**

There seems no reason other than historical to use the `lms` and `lqs` options. LMS estimation is of low efficiency (converging at rate  $n^{-1/3}$ ) whereas LTS has the same asymptotic efficiency as an M estimator with trimming at the quartiles (Marazzi, 1993, p.201). LQS and LTS have the same maximal breakdown value of  $(\text{floor}((n-p)/2) + 1)/n$  attained if  $\text{floor}((n+p)/2) \leq \text{quantile} \leq \text{floor}((n+p+1)/2)$ . The only drawback mentioned of LTS is greater computation, as a sort was thought to be required (Marazzi, 1993, p.201) but this is not true as a partial sort can be used (and is used in this implementation).

Adjusting the intercept for each trial fit does need the residuals to be sorted, and may be significant extra computation if  $n$  is large and  $p$  small.

Opinions differ over the choice of `psamp`. Rousseeuw and Hubert (1997) only consider  $p$ ; Marazzi (1993) recommends  $p+1$  and suggests that more samples are better than adjustment for a given computational limit.

The computations are exact for a model with just an intercept and adjustment, and for LQS for a model with an intercept plus one regressor and exhaustive search with adjustment. For all other cases the minimization is only known to be approximate.

**References**

- P. J. Rousseeuw and A. M. Leroy (1987) *Robust Regression and Outlier Detection*. Wiley.
- A. Marazzi (1993) *Algorithms, Routines and S Functions for Robust Statistics*. Wadsworth and Brooks/Cole.
- P. Rousseeuw and M. Hubert (1997) Recent developments in PROGRESS. In *L1-Statistical Procedures and Related Topics*, ed Y. Dodge, IMS Lecture Notes volume **31**, pp. 201–214.

**See Also**

[predict.lqs](#)

**Examples**

```
set.seed(123) # make reproducible
lqs(stack.loss ~ ., data = stackloss)
lqs(stack.loss ~ ., data = stackloss, method = "S", nsamp = "exact")
```

---

mammals

*Brain and Body Weights for 62 Species of Land Mammals*

---

**Description**

A data frame with average brain and body weights for 62 species of land mammals.

**Usage**

```
mammals
```

**Format**

body body weight in kg.

brain brain weight in g.

name Common name of species. (Rock hyrax-a = *Heterohyrax brucii*, Rock hyrax-b = *Procavia habessinica*..)

**Source**

Weisberg, S. (1985) *Applied Linear Regression*. 2nd edition. Wiley, pp. 144–5.

Selected from: Allison, T. and Cicchetti, D. V. (1976) Sleep in mammals: ecological and constitutional correlates. *Science* **194**, 732–734.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

---

 mca

---

*Multiple Correspondence Analysis*


---

**Description**

Computes a multiple correspondence analysis of a set of factors.

**Usage**

```
mca(df, nf = 2, abbrev = FALSE)
```

**Arguments**

df A data frame containing only factors

nf The number of dimensions for the MCA. Rarely 3 might be useful.

abbrev Should the vertex names be abbreviated? By default these are of the form ‘factor.level’ but if `abbrev = TRUE` they are just ‘level’ which will suffice if the factors have distinct levels.

**Value**

An object of class "mca", with components

rs The coordinates of the rows, in `nf` dimensions.

cs The coordinates of the column vertices, one for each level of each factor.

fs Weights for each row, used to interpolate additional factors in `predict.mca`.

p The number of factors

d The singular values for the `nf` dimensions.

call The matched call.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[predict.mca](#), [plot.mca](#), [corresp](#)

**Examples**

```
farms.mca <- mca(farms, abbrev=TRUE)
farms.mca
plot(farms.mca)
```

---

mcycle

*Data from a Simulated Motorcycle Accident*

---

**Description**

A data frame giving a series of measurements of head acceleration in a simulated motorcycle accident, used to test crash helmets.

**Usage**

```
mcycle
```

**Format**

times in milliseconds after impact.

accel in g.

**Source**

Silverman, B. W. (1985) Some aspects of the spline smoothing approach to non-parametric curve fitting. *Journal of the Royal Statistical Society series B* **47**, 1–52.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

---

 Melanoma

*Survival from Malignant Melanoma*


---

**Description**

The Melanoma data frame has data on 205 patients in Denmark with malignant melanoma.

**Usage**

Melanoma

**Format**

This data frame contains the following columns:

`time` survival time in days, possibly censored.

`status` 1 died from melanoma, 2 alive, 3 dead from other causes.

`sex` 1 = male, 0 = female.

`age` age in years.

`year` of operation.

`thickness` tumour thickness in mm.

`ulcer` 1 = presence, 0 = absence.

**Source**

P. K. Andersen, O. Borgan, R. D. Gill and N. Keiding (1993) *Statistical Models based on Counting Processes*. Springer.

---

 menarche

*Age of Menarche in Warsaw*


---

**Description**

Proportions of female children at various ages during adolescence who have reached menarche.

**Usage**

menarche

**Format**

This data frame contains the following columns:

`Age` Average age of the group. (The groups are reasonably age homogeneous.)

`Total` Total number of children in the group.

`Menarche` Number who have reached menarche.

**Source**

Milicer, H. and Szczotka, F. (1966) Age at Menarche in Warsaw girls in 1965. *Human Biology* **38**, 199–203.

The data are also given in

Aranda-Ordaz, F.J. (1981) On two families of transformations to additivity for binary response data. *Biometrika* **68**, 357–363.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```
mprob <- glm(cbind(Menarche, Total - Menarche) ~ Age,  
             binomial(link = probit), data = menarche)
```

---

michelson

*Michelson's Speed of Light Data*

---

**Description**

Measurements of the speed of light in air, made between 5th June and 2nd July, 1879. The data consists of five experiments, each consisting of 20 consecutive runs. The response is the speed of light in km/s, less 299000. The currently accepted value, on this scale of measurement, is 734.5.

**Usage**

```
michelson
```

**Format**

The data frame contains the following components:

Expt The experiment number, from 1 to 5.

Run The run number within each experiment.

Speed Speed-of-light measurement.

**Source**

A.J. Weekes (1986) *A Genstat Primer*. Edward Arnold.

S. M. Stigler (1977) Do robust estimators work with real data? *Annals of Statistics* **5**, 1055–1098.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.



---

 minn38

*Minnesota High School Graduates of 1938*


---

**Description**

The Minnesota high school graduates of 1938 were classified according to four factors, described below. The `minn38` data frame has 168 rows and 5 columns.

**Usage**

```
minn38
```

**Format**

This data frame contains the following columns:

`hs` high school rank: "L", "M" and "U" for lower, middle and upper third.

`phs` post high school status: Enrolled in college, ("C"), enrolled in non-collegiate school, ("N"), employed full-time, ("E") and other, ("O").

`fol` father's occupational level, (seven levels, "F1", "F2", ..., "F7").

`sex` sex: factor with levels "F" or "M".

`f` frequency.

**Source**

From R. L. Plackett, (1974) *The Analysis of Categorical Data*. London: Griffin

who quotes the data from

Hoyt, C. J., Krishnaiah, P. R. and Torrance, E. P. (1959) Analysis of complex contingency tables, *J. Exp. Ed.* **27**, 187–194.

---

 motors

*Accelerated Life Testing of Motorettes*


---

**Description**

The `motors` data frame has 40 rows and 3 columns. It describes an accelerated life test at each of four temperatures of 10 motorettes, and has rather discrete times.

**Usage**

```
motors
```

**Format**

This data frame contains the following columns:

`temp` the temperature (degrees C) of the test.

`time` the time in hours to failure or censoring at 8064 hours (= 336 days).

`cens` an indicator variable for death.

**Source**

Kalbfleisch, J. D. and Prentice, R. L. (1980) *The Statistical Analysis of Failure Time Data*. New York: Wiley.

taken from

Nelson, W. D. and Hahn, G. J. (1972) Linear regression of a regression relationship from censored data. Part 1 – simple methods and their application. *Technometrics*, **14**, 247–276.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```
library(survival)
plot(survfit(Surv(time, cens) ~ factor(temp), motors), conf.int = FALSE)
# fit Weibull model
motor.wei <- survreg(Surv(time, cens) ~ temp, motors)
summary(motor.wei)
# and predict at 130C
unlist(predict(motor.wei, data.frame(temp=130), se.fit = TRUE))

motor.cox <- coxph(Surv(time, cens) ~ temp, motors)
summary(motor.cox)
# predict at temperature 200
plot(survfit(motor.cox, newdata = data.frame(temp=200),
  conf.type = "log-log"))
summary(survfit(motor.cox, newdata = data.frame(temp=130)) )
```

---

muscle

*Effect of Calcium Chloride on Muscle Contraction in Rat Hearts*

---

**Description**

The purpose of this experiment was to assess the influence of calcium in solution on the contraction of heart muscle in rats. The left auricle of 21 rat hearts was isolated and on several occasions a constant-length strip of tissue was electrically stimulated and dipped into various concentrations of calcium chloride solution, after which the shortening of the strip was accurately measured as the response.

**Usage**

muscle

**Format**

This data frame contains the following columns:

Strip which heart muscle strip was used?

Conc concentration of calcium chloride solution, in multiples of 2.2 mM.

Length the change in length (shortening) of the strip, (allegedly) in mm.

**Source**

Linder, A., Chakravarti, I. M. and Vuagnat, P. (1964) Fitting asymptotic regression curves with different asymptotes. In *Contributions to Statistics. Presented to Professor P. C. Mahalanobis on the occasion of his 70th birthday*, ed. C. R. Rao, pp. 221–228. Oxford: Pergamon Press.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth Edition. Springer.

**Examples**

```
A <- model.matrix(~ Strip - 1, data=muscle)
rats.nls1 <- nls(log(Length) ~ cbind(A, rho^Conc),
  data = muscle, start = c(rho=0.1), algorithm="plinear")
B <- coef(rats.nls1)
B

st <- list(alpha = B[2:22], beta = B[23], rho = B[1])
(rats.nls2 <- nls(log(Length) ~ alpha[Strip] + beta*rho^Conc,
  data = muscle, start = st))

attach(muscle)
Muscle <- expand.grid(Conc = sort(unique(Conc)), Strip = levels(Strip))
Muscle$Yhat <- predict(rats.nls2, Muscle)
Muscle <- cbind(Muscle, logLength = rep(as.numeric(NA), 126))
ind <- match(paste(Strip, Conc),
  paste(Muscle$Strip, Muscle$Conc))
Muscle$logLength[ind] <- log(Length)
detach()

require(lattice)
xyplot(Yhat ~ Conc | Strip, Muscle, as.table = TRUE,
  ylim = range(c(Muscle$Yhat, Muscle$logLength), na.rm = TRUE),
  subscripts = TRUE, xlab = "Calcium Chloride concentration (mM)",
  ylab = "log(Length in mm)", panel =
  function(x, y, subscripts, ...) {
    lines(spline(x, y))
    panel.xyplot(x, Muscle$logLength[subscripts], ...)
  })
```

---

mvrnorm

*Simulate from a Multivariate Normal Distribution*


---

**Description**

Produces one or more samples from the specified multivariate normal distribution.

**Usage**

```
mvrnorm(n = 1, mu, Sigma, tol = 1e-6, empirical = FALSE)
```

**Arguments**

n	the number of samples required.
mu	a vector giving the means of the variables.
Sigma	a positive-definite symmetric matrix specifying the covariance matrix of the variables.
tol	tolerance (relative to largest variance) for numerical lack of positive-definiteness in Sigma.
empirical	logical. If true, mu and Sigma specify the empirical not population mean and covariance matrix.

**Details**

The matrix decomposition is done via `eigen`; although a Choleski decomposition might be faster, the eigendecomposition is stabler.

**Value**

If `n = 1` a vector of the same length as `mu`, otherwise an `n` by `length(mu)` matrix with one sample in each row.

**Side Effects**

Causes creation of the dataset `.Random.seed` if it does not already exist, otherwise its value is updated.

**References**

B. D. Ripley (1987) *Stochastic Simulation*. Wiley. Page 98.

**See Also**

[rnorm](#)

**Examples**

```
Sigma <- matrix(c(10,3,3,2),2,2)
Sigma
var(mvrnorm(n=1000, rep(0, 2), Sigma))
var(mvrnorm(n=1000, rep(0, 2), Sigma, empirical = TRUE))
```

---

negative.binomial *Family function for Negative Binomial GLMs*

---

**Description**

Specifies the information required to fit a Negative Binomial generalized linear model, with known `theta` parameter, using `glm()`.

**Usage**

```
negative.binomial(theta = stop("'theta' must be specified"), link = "log")
```

**Arguments**

theta	The known value of the additional parameter, <code>theta</code> .
link	The link function, as a character string, name or one-element character vector specifying one of <code>log</code> , <code>sqrt</code> or <code>identity</code> , or an object of class " <a href="#">link-glm</a> ".

**Value**

An object of class "`family`", a list of functions and expressions needed by `glm()` to fit a Negative Binomial generalized linear model.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

**See Also**

[glm.nb](#), [anova.negbin](#), [summary.negbin](#)

**Examples**

```
# Fitting a Negative Binomial model to the quine data
# with theta = 2 assumed known.
#
glm(Days ~ .^4, family = negative.binomial(2), data = quine)
```

---

newcomb

*Newcomb's Measurements of the Passage Time of Light*

---

**Description**

A numeric vector giving the 'Third Series' of measurements of the passage time of light recorded by Newcomb in 1882. The given values divided by 1000 plus 24 give the time in millionths of a second for light to traverse a known distance. The 'true' value is now considered to be 33.02.

**Usage**

```
newcomb
```

**Source**

S. M. Stigler (1973) Simon Newcomb, Percy Daniell, and the history of robust estimation 1885–1920. *Journal of the American Statistical Association* **68**, 872–879.

R. G. Staudte and S. J. Sheather (1990) *Robust Estimation and Testing*. Wiley.

nlschools

*Eighth-Grade Pupils in the Netherlands***Description**

Snijders and Bosker (1999) use as a running example a study of 2287 eighth-grade pupils (aged about 11) in 132 classes in 131 schools in the Netherlands. Only the variables used in our examples are supplied.

**Usage**

```
nlschools
```

**Format**

This data frame contains 2287 rows and the following columns:

lang language test score.

IQ verbal IQ.

class class ID.

GS class size: number of eighth-grade pupils recorded in the class (there may be others: see COMB, and some may have been omitted with missing values).

SES social-economic status of pupil's family.

COMB were the pupils taught in a multi-grade class (0/1)? Classes which contained pupils from grades 7 and 8 are coded 1, but only eighth-graders were tested.

**Source**

Snijders, T. A. B. and Bosker, R. J. (1999) *Multilevel Analysis. An Introduction to Basic and Advanced Multilevel Modelling*. London: Sage.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```
library(nlme)
n11 <- nlschools
attach(n11)
classMeans <- tapply(IQ, class, mean)
n11$IQave <- classMeans[as.character(class)]
n11$IQ <- n11$IQ - n11$IQave
detach()
cen <- c("IQ", "IQave", "SES")
n11[cen] <- scale(n11[cen], center = TRUE, scale = FALSE)

nl.lme <- lme(lang ~ IQ*COMB + IQave + SES,
             random = ~ IQ | class, data = n11)
summary(nl.lme)
```

npk

*Classical N, P, K Factorial Experiment***Description**

A classical N, P, K (nitrogen, phosphate, potassium) factorial experiment on the growth of peas conducted on 6 blocks. Each half of a fractional factorial design confounding the NPK interaction was used on 3 of the plots.

**Usage**

npk

**Format**

The npk data frame has 24 rows and 5 columns:

`block` which block (label 1 to 6).

`N` indicator (0/1) for the application of nitrogen.

`P` indicator (0/1) for the application of phosphate.

`K` indicator (0/1) for the application of potassium.

`yield` Yield of peas, in pounds/plot (the plots were (1/70) acre).

**Source**

Imperial College, London, M.Sc. exercise sheet.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```
options(contrasts = c("contr.sum", "contr.poly"))
npk.aov <- aov(yield ~ block + N*P*K, npk)
npk.aov
summary(npk.aov)
alias(npk.aov)
coef(npk.aov)
options(contrasts = c("contr.treatment", "contr.poly"))
npk.aov1 <- aov(yield ~ block + N + K, data = npk)
summary.lm(npk.aov1)
se.contrast(npk.aov1, list(N=="0", N=="1"), data = npk)
model.tables(npk.aov1, type = "means", se = TRUE)
```

---

npr1

*US Naval Petroleum Reserve No. 1 data*


---

**Description**

Data on the locations, porosity and permeability (a measure of oil flow) on 104 oil wells in the US Naval Petroleum Reserve No. 1 in California.

**Usage**

npr1

**Format**

This data frame contains the following columns:

*x*, *y* *x* and *y* coordinates, in miles from an arbitrary origin.

*perm* permeability in milli-Darcies.

*por* porosity (%).

**Source**

Maher, J.C., Carter, R.D. and Lantz, R.J. (1975) Petroleum geology of Naval Petroleum Reserve No. 1, Elk Hills, Kern County, California. *USGS Professional Paper 912*.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

Null

*Null Spaces of Matrices*


---

**Description**

Given a matrix, *M*, find a matrix *N* giving a basis for the null space. That is  $\mathbf{t}(N) * \mathbf{M}$  is the zero and *N* has the maximum number of linearly independent columns.

**Usage**Null(*M*)**Arguments**

*M* Input matrix. A vector is coerced to a 1-column matrix.

**Value**

The matrix *N* with the basis for the null space, or an empty vector if the matrix *M* is square and of maximal rank.



## References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

## See Also

[qr](#), [qr.Q](#).

## Examples

```
# The function is currently defined as
function(M)
{
  tmp <- qr(M)
  set <- if(tmp$rank == 0) 1:ncol(M) else - (1:tmp$rank)
  qr.Q(tmp, complete = TRUE)[, set, drop = FALSE]
}
```

---

oats

*Data from an Oats Field Trial*

---

## Description

The yield of oats from a split-plot field trial using three varieties and four levels of manurial treatment. The experiment was laid out in 6 blocks of 3 main plots, each split into 4 sub-plots. The varieties were applied to the main plots and the manurial treatments to the sub-plots.

## Usage

```
oats
```

## Format

This data frame contains the following columns:

B Blocks, levels I, II, III, IV, V and VI.

V Varieties, 3 levels.

N Nitrogen (manurial) treatment, levels 0.0cwt, 0.2cwt, 0.4cwt and 0.6cwt, showing the application in cwt/acre.

Y Yields in 1/4lbs per sub-plot, each of area 1/80 acre.

## Source

Yates, F. (1935) Complex experiments, *Journal of the Royal Statistical Society Suppl.* **2**, 181–247.

Also given in Yates, F. (1970) *Experimental design: Selected papers of Frank Yates, C.B.E, F.R.S.* London: Griffin.

## References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```

oats$Nf <- ordered(oats$N, levels = sort(levels(oats$N)))
oats.aov <- aov(Y ~ Nf*V + Error(B/V), data = oats, qr = TRUE)
summary(oats.aov)
summary(oats.aov, split = list(Nf=list(L=1, Dev=2:3)))
par(mfrow = c(1,2), pty = "s")
plot(fitted(oats.aov[[4]]), studres(oats.aov[[4]]))
abline(h = 0, lty = 2)
oats.pr <- proj(oats.aov)
qqnorm(oats.pr[[4]][,"Residuals"], ylab = "Stratum 4 residuals")
qqline(oats.pr[[4]][,"Residuals"])

par(mfrow = c(1,1), pty = "m")
oats.aov2 <- aov(Y ~ N + V + Error(B/V), data = oats, qr = TRUE)
model.tables(oats.aov2, type = "means", se = TRUE)

```

OME

*Tests of Auditory Perception in Children with OME***Description**

Experiments were performed on children on their ability to differentiate a signal in broad-band noise. The noise was played from a pair of speakers and a signal was added to just one channel; the subject had to turn his/her head to the channel with the added signal. The signal was either coherent (the amplitude of the noise was increased for a period) or incoherent (independent noise was added for the same period to form the same increase in power).

The threshold used in the original analysis was the stimulus loudness needs to get 75% correct responses. Some of the children had suffered from otitis media with effusion (OME).

**Usage**

OME

**Format**

The OME data frame has 1129 rows and 7 columns:

**ID** Subject ID (1 to 99, with some IDs missing). A few subjects were measured at different ages.

**OME** "low" or "high" or "N/A" (at ages other than 30 and 60 months).

**Age** Age of the subject (months).

**Loud** Loudness of stimulus, in decibels.

**Noise** Whether the signal in the stimulus was "coherent" or "incoherent".

**Correct** Number of correct responses from `Trials` trials.

**Trials** Number of trials performed.

## Background

The experiment was to study otitis media with effusion (OME), a very common childhood condition where the middle ear space, which is normally air-filled, becomes congested by a fluid. There is a concomitant fluctuating, conductive hearing loss which can result in various language, cognitive and social deficits. The term ‘binaural hearing’ is used to describe the listening conditions in which the brain is processing information from both ears at the same time. The brain computes differences in the intensity and/or timing of signals arriving at each ear which contributes to sound localisation and also to our ability to hear in background noise.

Some years ago, it was found that children of 7–8 years with a history of significant OME had significantly worse binaural hearing than children without such a history, despite having equivalent sensitivity. The question remained as to whether it was the timing, the duration, or the degree of severity of the otitis media episodes during critical periods, which affected later binaural hearing. In an attempt to begin to answer this question, 95 children were monitored for the presence of effusion every month since birth. On the basis of OME experience in their first two years, the test population was split into one group of high OME prevalence and one of low prevalence.

## Source

Sarah Hogan, Dept of Physiology, University of Oxford, via Dept of Statistics Consulting Service

## Examples

```
# Fit logistic curve from p = 0.5 to p = 1.0
fp1 <- deriv(~ 0.5 + 0.5/(1 + exp(-(x-L75)/scal)),
            c("L75", "scal"),
            function(x,L75,scal) NULL)
nls(Correct/Trials ~ fp1(Loud, L75, scal), data = OME,
    start = c(L75=45, scal=3))
nls(Correct/Trials ~ fp1(Loud, L75, scal),
    data = OME[OME$Noise == "coherent",],
    start=c(L75=45, scal=3))
nls(Correct/Trials ~ fp1(Loud, L75, scal),
    data = OME[OME$Noise == "incoherent",],
    start = c(L75=45, scal=3))

# individual fits for each experiment

aa <- factor(OME$Age)
ab <- 10*OME$ID + unclass(aa)
ac <- unclass(factor(ab))
OME$UID <- as.vector(ac)
OME$UIDn <- OME$UID + 0.1*(OME$Noise == "incoherent")
rm(aa, ab, ac)
OMEi <- OME

library(nlme)
fp2 <- deriv(~ 0.5 + 0.5/(1 + exp(-(x-L75)/2)),
            "L75", function(x,L75) NULL)
dec <- getOption("OutDec")
options(show.error.messages = FALSE, OutDec=".")
OMEi.nls <- nlsList(Correct/Trials ~ fp2(Loud, L75) | UIDn,
                  data = OMEi, start = list(L75=45), control = list(maxiter=100))
options(show.error.messages = TRUE, OutDec=dec)
tmp <- sapply(OMEi.nls, function(X)
             {if(is.null(X)) NA else as.vector(coef(X))})
```

```

OMEif <- data.frame(UID = round(as.numeric((names(tmp)))),
  Noise = rep(c("coherent", "incoherent"), 110),
  L75 = as.vector(tmp), stringsAsFactors = TRUE)
OMEif$Age <- OME$Age[match(OMEif$UID, OME$UID)]
OMEif$OME <- OME$OME[match(OMEif$UID, OME$UID)]
OMEif <- OMEif[OMEif$L75 > 30,]
summary(lm(L75 ~ Noise/Age, data = OMEif, na.action = na.omit))
summary(lm(L75 ~ Noise/(Age + OME), data = OMEif,
  subset = (Age >= 30 & Age <= 60),
  na.action = na.omit), cor = FALSE)

# Or fit by weighted least squares
fpl75 <- deriv(~ sqrt(n)*(r/n - 0.5 - 0.5/(1 + exp(-(x-L75)/scal))),
  c("L75", "scal"),
  function(r,n,x,L75,scal) NULL)
nls(0 ~ fpl75(Correct, Trials, Loud, L75, scal),
  data = OME[OME$Noise == "coherent",],
  start = c(L75=45, scal=3))
nls(0 ~ fpl75(Correct, Trials, Loud, L75, scal),
  data = OME[OME$Noise == "incoherent",],
  start = c(L75=45, scal=3))

# Test to see if the curves shift with age
fpl75age <- deriv(~sqrt(n)*(r/n - 0.5 - 0.5/(1 +
  exp(-(x-L75-slope*age)/scal))),
  c("L75", "slope", "scal"),
  function(r,n,x,age,L75,slope,scal) NULL)
OME.nls1 <-
nls(0 ~ fpl75age(Correct, Trials, Loud, Age, L75, slope, scal),
  data = OME[OME$Noise == "coherent",],
  start = c(L75=45, slope=0, scal=2))
sqrt(diag(vcov(OME.nls1)))

OME.nls2 <-
nls(0 ~ fpl75age(Correct, Trials, Loud, Age, L75, slope, scal),
  data = OME[OME$Noise == "incoherent",],
  start = c(L75=45, slope=0, scal=2))
sqrt(diag(vcov(OME.nls2)))

# Now allow random effects by using NLME
OMEf <- OME[rep(1:nrow(OME), OME$Trials),]
OMEf$Resp <- with(OME, rep(rep(c(1,0), length(Trials)),
  t(cbind(Correct, Trials-Correct))))
OMEf <- OMEf[, -match(c("Correct", "Trials"), names(OMEf))]

## Not run: ## this fails in R on some platforms
fp2 <- deriv(~ 0.5 + 0.5/(1 + exp(-(x-L75)/exp(lsc))),
  c("L75", "lsc"),
  function(x, L75, lsc) NULL)
G1.nlme <- nlme(Resp ~ fp2(Loud, L75, lsc),
  fixed = list(L75 ~ Age, lsc ~ 1),
  random = L75 + lsc ~ 1 | UID,
  data = OMEf[OMEf$Noise == "coherent",], method = "ML",
  start = list(fixed=c(L75=c(48.7, -0.03), lsc=0.24)), verbose = TRUE)
summary(G1.nlme)

G2.nlme <- nlme(Resp ~ fp2(Loud, L75, lsc),

```

```

fixed = list(L75 ~ Age, lsc ~ 1),
random = L75 + lsc ~ 1 | UID,
data = OMEf[OMEf$Noise == "incoherent",], method="ML",
start = list(fixed=c(L75=c(41.5, -0.1), lsc=0)), verbose = TRUE)
summary(G2.nlme)

## End(Not run)

```

---

painters

*The Painter's Data of de Piles*

---

### Description

The subjective assessment, on a 0 to 20 integer scale, of 54 classical painters. The painters were assessed on four characteristics: composition, drawing, colour and expression. The data is due to the Eighteenth century art critic, de Piles.

### Usage

```
painters
```

### Format

The row names of the data frame are the painters. The components are:

Composition Composition score.

Drawing Drawing score.

Colour Colour score.

Expression Expression score.

School The school to which a painter belongs, as indicated by a factor level code as follows:  
 "A": Renaissance; "B": Mannerist; "C": Seicento; "D": Venetian; "E": Lombard; "F":  
 Sixteenth Century; "G": Seventeenth Century; "H": French.

### Source

A. J. Weekes (1986) *A Genstat Primer*. Edward Arnold.

M. Davenport and G. Studdert-Kennedy (1972) The statistical analysis of aesthetic judgement: an exploration. *Applied Statistics* **21**, 324–333.

I. T. Jolliffe (1986) *Principal Component Analysis*. Springer.

### References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

pairs.lda

*Produce Pairwise Scatterplots from an 'lda' Fit*

---

## Description

Pairwise scatterplot of the data on the linear discriminants.

## Usage

```
## S3 method for class 'lda':
pairs(x, labels = colnames(x), panel = panel.lda,
      dimen, abbrev = FALSE, ..., cex=0.7, type = c("std", "trellis"))
```

## Arguments

x	Object of class "lda".
labels	vector of character strings for labelling the variables.
panel	panel function to plot the data in each panel.
dimen	The number of linear discriminants to be used for the plot; if this exceeds the number determined by x the smaller value is used.
abbrev	whether the group labels are abbreviated on the plots. If abbrev > 0 this gives minlength in the call to abbreviate.
...	additional arguments for pairs.default.
cex	graphics parameter cex for labels on plots.
type	type of plot. The default is in the style of pairs.default; the style "trellis" uses the Trellis function splom.

## Details

This function is a method for the generic function pairs() for class "lda". It can be invoked by calling pairs(x) for an object x of the appropriate class, or directly by calling pairs.lda(x) regardless of the class of the object.

## References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

## See Also

[pairs](#)

---

parcoord

*Parallel Coordinates Plot*

---

### Description

Parallel coordinates plot

### Usage

```
parcoord(x, col = 1, lty = 1, var.label = FALSE, ...)
```

### Arguments

x	a matrix or data frame who columns represent variables. Missing values are allowed.
col	A vector of colours, recycled as necessary for each observation.
lty	A vector of line types, recycled as necessary for each observation.
var.label	If TRUE, each variable's axis is labelled with maximum and minimum values.
...	Further graphics parameters which are passed to <code>matplot</code> .

### Side Effects

a parallel coordinates plots is drawn.

### Author(s)

B. D. Ripley. Enhancements based on ideas and code by Fabian Scheipl.

### References

Wegman, E. J. (1990) Hyperdimensional data analysis using parallel coordinates. *Journal of the American Statistical Association* **85**, 664–675.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### Examples

```
parcoord(state.x77[, c(7, 4, 6, 2, 5, 3)])  
  
ir <- rbind(iris3[,1], iris3[,2], iris3[,3])  
parcoord(log(ir)[, c(3, 4, 2, 1)], col = 1 + (0:149)%/%50)
```

---

petrol

*N. L. Prater's Petrol Refinery Data*

---

### Description

The yield of a petroleum refining process with four covariates. The crude oil appears to come from only 10 distinct samples.

These data were originally used by Prater (1956) to build an estimation equation for the yield of the refining process of crude oil to gasoline.

### Usage

```
petrol
```

### Format

The variables are as follows

No crude oil sample identification label. (Factor.)

SG specific gravity, degrees API. (Constant within sample.)

VP vapour pressure in pounds per square inch. (Constant within sample.)

V10 volatility of crude; ASTM 10% point. (Constant within sample.)

EP desired volatility of gasoline. (The end point. Varies within sample.)

Y yield as a percentage of crude.

### Source

N. H. Prater (1956) Estimate gasoline yields from crudes. *Petroleum Refiner* **35**, 236–238.

This dataset is also given in D. J. Hand, F. Daly, K. McConway, D. Lunn and E. Ostrowski (eds) (1994) *A Handbook of Small Data Sets*. Chapman & Hall.

### References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### Examples

```
library(nlme)
Petrol <- petrol
Petrol[, 2:5] <- scale(as.matrix(Petrol[, 2:5]), scale = FALSE)
pet3.lme <- lme(Y ~ SG + VP + V10 + EP,
              random = ~ 1 | No, data = Petrol)
pet3.lme <- update(pet3.lme, method = "ML")
pet4.lme <- update(pet3.lme, fixed = Y ~ V10 + EP)
anova(pet4.lme, pet3.lme)
```



---

Pima.tr

*Diabetes in Pima Indian Women*

---

### Description

A population of women who were at least 21 years old, of Pima Indian heritage and living near Phoenix, Arizona, was tested for diabetes according to World Health Organization criteria. The data were collected by the US National Institute of Diabetes and Digestive and Kidney Diseases. We used the 532 complete records after dropping the (mainly missing) data on serum insulin.

### Usage

Pima.tr  
Pima.tr2  
Pima.te

### Format

These data frames contains the following columns:

npreg number of pregnancies.  
glu plasma glucose concentration in an oral glucose tolerance test.  
bp diastolic blood pressure (mm Hg).  
skin triceps skin fold thickness (mm).  
bmi body mass index (weight in kg/(height in m)<sup>2</sup>).  
ped diabetes pedigree function.  
age age in years.  
type Yes or No, for diabetic according to WHO criteria.

### Details

The training set Pima.tr contains a randomly selected set of 200 subjects, and Pima.te contains the remaining 332 subjects. Pima.tr2 contains Pima.tr plus 100 subjects with missing values in the explanatory variables.

### Source

Smith, J. W., Everhart, J. E., Dickson, W. C., Knowler, W. C. and Johannes, R. S. (1988) Using the ADAP learning algorithm to forecast the onset of *diabetes mellitus*. In *Proceedings of the Symposium on Computer Applications in Medical Care (Washington, 1988)*, ed. R. A. Greenes, pp. 261–265. Los Alamitos, CA: IEEE Computer Society Press.

Ripley, B.D. (1996) *Pattern Recognition and Neural Networks*. Cambridge: Cambridge University Press.

---

`plot.lda`*Plot Method for Class 'lda'*

---

### Description

Plots a set of data on one, two or more linear discriminants.

### Usage

```
## S3 method for class 'lda':
plot(x, panel = panel.lda, ..., cex = 0.7, dimen,
      abbrev = FALSE, xlab = "LD1", ylab = "LD2")
```

### Arguments

<code>x</code>	An object of class "lda".
<code>panel</code>	the panel function used to plot the data.
<code>...</code>	additional arguments to <code>pairs</code> , <code>ldahist</code> or <code>eqscplot</code> .
<code>cex</code>	graphics parameter <code>cex</code> for labels on plots.
<code>dimen</code>	The number of linear discriminants to be used for the plot; if this exceeds the number determined by <code>x</code> the smaller value is used.
<code>abbrev</code>	whether the group labels are abbreviated on the plots. If <code>abbrev &gt; 0</code> this gives <code>minlength</code> in the call to abbreviate.
<code>xlab</code>	label for the x axis
<code>ylab</code>	label for the y axis

### Details

This function is a method for the generic function `plot()` for class "lda". It can be invoked by calling `plot(x)` for an object `x` of the appropriate class, or directly by calling `plot.lda(x)` regardless of the class of the object.

The behaviour is determined by the value of `dimen`. For `dimen > 2`, a `pairs` plot is used. For `dimen = 2`, an equiscaled scatter plot is drawn. For `dimen = 1`, a set of histograms or density plots are drawn. Use argument `type` to match "histogram" or "density" or "both".

### References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### See Also

[pairs.lda](#), [ldahist](#), [lda](#), [predict.lda](#)

---

plot.mca

*Plot Method for Objects of Class 'mca'*


---

### Description

Plot a multiple correspondence analysis.

### Usage

```
## S3 method for class 'mca':
plot(x, rows = TRUE, col, cex = par("cex"), ...)
```

### Arguments

x	An object of class "mca".
rows	Should the coordinates for the rows be plotted, or just the vertices for the levels?
col, cex	The colours and cex to be used for the row points and level vertices respectively.
...	Additional parameters to plot.

### References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### See Also

[mca](#), [predict.mca](#)

### Examples

```
plot(mca(farms, abbrev = TRUE))
```

---

plot.profile

*Plottig Functions for 'profile' Objects*


---

### Description

[plot](#) and [pairs](#) methods for objects of class "profile".

### Usage

```
## S3 method for class 'profile':
plot(x, ...)
## S3 method for class 'profile':
pairs(x, colours = 2:3, ...)
```

### Arguments

x	an object inheriting from class "profile".
colours	Colours to be used for the mean curves conditional on x and y respectively.
...	arguments passed to or from other methods.

**Details**

This is the main `plot` method for objects created by `profile.glm`. It can also be called on objects created by `profile.nls`, but they have a specific method, `plot.profile.nls`.

The `pairs` method shows, for each pair of parameters  $x$  and  $y$ , two curves intersecting at the maximum likelihood estimate, which give the loci of the points at which the tangents to the contours of the bivariate profile likelihood become vertical and horizontal, respectively. In the case of an exactly bivariate normal profile likelihood, these two curves would be straight lines giving the conditional means of  $y|x$  and  $x|y$ , and the contours would be exactly elliptical.

**Author(s)**

Originally, D. M. Bates and W. N. Venables. (For S in 1996.)

**See Also**

`profile.glm`, `profile.nls`.

**Examples**

```
## see ?profile.glm for an example using glm fits.

## a version of example(profile.nls) from R >= 2.8.0
fm1 <- nls(demand ~ SSasymptOrig(Time, A, lrc), data = BOD)
pr1 <- profile(fm1, alpha = 0.1)
MASS:::plot.profile(pr1)
pairs(pr1) # a little odd since the parameters are highly correlated

## an example from ?nls
x <- -(1:100)/10
y <- 100 + 10 * exp(x / 2) + rnorm(x)/10
nlmod <- nls(y ~ Const + A * exp(B * x), start=list(Const=100, A=10, B=1))
pairs(profile(nlmod))
```

---

polr

*Ordered Logistic or Probit Regression*

---

**Description**

Fits a logistic or probit regression model to an ordered factor response. The default logistic case is *proportional odds logistic regression*, after which the function is named.

**Usage**

```
polr(formula, data, weights, start, ..., subset, na.action,
      contrasts = NULL, Hess = FALSE, model = TRUE,
      method = c("logistic", "probit", "cloglog", "cauchit"))
```

**Arguments**

<code>formula</code>	a formula expression as for regression models, of the form <code>response ~ predictors</code> . The response should be a factor (preferably an ordered factor), which will be interpreted as an ordinal response, with levels ordered as in the factor. The model must have an intercept: attempts to remove one will lead to a warning and be ignored. An offset may be used. See the documentation of <code>formula</code> for other details.
<code>data</code>	an optional data frame in which to interpret the variables occurring in <code>formula</code> .
<code>weights</code>	optional case weights in fitting. Default to 1.
<code>start</code>	initial values for the parameters. This is in the format <code>c(coefficients, zeta)</code> : see the Values section.
<code>...</code>	additional arguments to be passed to <code>optim</code> , most often a <code>control</code> argument.
<code>subset</code>	expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.
<code>na.action</code>	a function to filter missing data.
<code>contrasts</code>	a list of contrasts to be used for some or all of the factors appearing as variables in the model formula.
<code>Hess</code>	logical for whether the Hessian (the observed information matrix) should be returned. Use this if you intend to call <code>summary</code> or <code>vcov</code> on the fit.
<code>model</code>	logical for whether the model matrix should be returned.
<code>method</code>	logistic or probit or complementary log-log or <code>cauchit</code> (corresponding to a Cauchy latent variable).

**Details**

This model is what Agresti (2002) calls a *cumulative link* model. The basic interpretation is as a *coarsened* version of a latent variable  $Y_i$  which has a logistic or normal or extreme-value or Cauchy distribution with scale parameter one and a linear model for the mean. The ordered factor which is observed is which bin  $Y_i$  falls into with breakpoints

$$\zeta_0 = -\infty < \zeta_1 < \dots < \zeta_K = \infty$$

This leads to the model

$$\text{logit}P(Y \leq k|x) = \zeta_k - \eta$$

with *logit* replaced by *probit* for a normal latent variable, and  $\eta$  being the linear predictor, a linear function of the explanatory variables (with no intercept). Note that it is quite common for other software to use the opposite sign for  $\eta$  (and hence the coefficients `beta`).

In the logistic case, the left-hand side of the last display is the log odds of category  $k$  or less, and since these are log odds which differ only by a constant for different  $k$ , the odds are proportional. Hence the term *proportional odds logistic regression*.

In the complementary log-log case, we have a *proportional hazards* model for grouped survival times.

There are methods for the standard model-fitting functions, including `predict`, `summary`, `vcov`, `anova`, `model.frame` and an `extractAIC` method for use with `stepAIC`. There are also `profile` and `confint` methods.

**Value**

A object of class "polr". This has components

coefficients	the coefficients of the linear predictor, which has no intercept.
zeta	the intercepts for the class boundaries.
deviance	the residual deviance.
fitted.values	a matrix, with a column for each level of the response.
lev	the names of the response levels.
terms	the terms structure describing the model.
df.residual	the number of residual degrees of freedoms, calculated using the weights.
edf	the (effective) number of degrees of freedom used by the model
n, nobs	the (effective) number of observations, calculated using the weights. (nobs is for use by <a href="#">stepAIC</a> ).
call	the matched call.
method	the matched method used.
convergence	the convergence code returned by <code>optim</code> .
niter	the number of function and gradient evaluations used by <code>optim</code> .
lp	the linear predictor (including any offset).
Hessian	(if <code>Hess</code> is true).
model	(if <code>model</code> is true).

**References**

Agresti, A. (2002) *Categorical Data*. Second edition. Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[optim](#), [glm](#), [multinom](#).

**Examples**

```
options(contrasts = c("contr.treatment", "contr.poly"))
house.plr <- polr(Sat ~ Infl + Type + Cont, weights = Freq, data = housing)
house.plr
summary(house.plr, digits = 3)
## slightly worse fit from
summary(update(house.plr, method = "probit", Hess = TRUE), digits = 3)
## although it is not really appropriate, can fit
summary(update(house.plr, method = "cloglog", Hess = TRUE), digits = 3)

predict(house.plr, housing, type = "p")
addterm(house.plr, ~.^2, test = "Chisq")
house.plr2 <- stepAIC(house.plr, ~.^2)
house.plr2$anova
anova(house.plr, house.plr2)

house.plr <- update(house.plr, Hess=TRUE)
pr <- profile(house.plr)
```

```
confint(pr)
plot(pr)
pairs(pr)
```

---

```
predict.glmmPQL Predict Method for glmmPQL Fits
```

---

## Description

Obtains predictions from a fitted generalized linear model with random effects.

## Usage

```
## S3 method for class 'glmmPQL':
predict(object, newdata = NULL, type = c("link", "response"),
        level, na.action = na.pass, ...)
```

## Arguments

<code>object</code>	a fitted object of class inheriting from "glmmPQL".
<code>newdata</code>	optionally, a data frame in which to look for variables with which to predict.
<code>type</code>	the type of prediction required. The default is on the scale of the linear predictors; the alternative "response" is on the scale of the response variable. Thus for a default binomial model the default predictions are of log-odds (probabilities on logit scale) and <code>type = "response"</code> gives the predicted probabilities.
<code>level</code>	an optional integer vector giving the level(s) of grouping to be used in obtaining the predictions. Level values increase from outermost to innermost grouping, with level zero corresponding to the population predictions. Defaults to the highest or innermost level of grouping.
<code>na.action</code>	function determining what should be done with missing values in <code>newdata</code> . The default is to predict NA.
<code>...</code>	further arguments passed to or from other methods.

## Value

If `level` is a single integer, a vector otherwise a data frame.

## See Also

[glmmPQL](#), [predict.lme](#).

## Examples

```
fit <- glmmPQL(y ~ trt + I(week > 2), random = ~1 | ID,
              family = binomial, data = bacteria)
predict(fit, bacteria, level = 0, type="response")
predict(fit, bacteria, level = 1, type="response")
```

predict.lda

*Classify Multivariate Observations by Linear Discrimination***Description**

Classify multivariate observations in conjunction with `lda`, and also project data onto the linear discriminants.

**Usage**

```
## S3 method for class 'lda':
predict(object, newdata, prior = object$prior, dimen,
        method = c("plug-in", "predictive", "debiased"), ...)
```

**Arguments**

<code>object</code>	object of class "lda"
<code>newdata</code>	data frame of cases to be classified or, if <code>object</code> has a formula, a data frame with columns of the same names as the variables used. A vector will be interpreted as a row vector. If <code>newdata</code> is missing, an attempt will be made to retrieve the data used to fit the <code>lda</code> object.
<code>prior</code>	The prior probabilities of the classes, by default the proportions in the training set or what was set in the call to <code>lda</code> .
<code>dimen</code>	the dimension of the space to be used. If this is less than $\min(p, ng-1)$ , only the first <code>dimen</code> discriminant components are used (except for <code>method="predictive"</code> ), and only those dimensions are returned in <code>x</code> .
<code>method</code>	This determines how the parameter estimation is handled. With "plug-in" (the default) the usual unbiased parameter estimates are used and assumed to be correct. With "debiased" an unbiased estimator of the log posterior probabilities is used, and with "predictive" the parameter estimates are integrated out using a vague prior.
<code>...</code>	arguments based from or to other methods

**Details**

This function is a method for the generic function `predict()` for class "lda". It can be invoked by calling `predict(x)` for an object `x` of the appropriate class, or directly by calling `predict.lda(x)` regardless of the class of the object.

Missing values in `newdata` are handled by returning `NA` if the linear discriminants cannot be evaluated. If `newdata` is omitted and the `na.action` of the fit omitted cases, these will be omitted on the prediction.

This version centres the linear discriminants so that the weighted mean (weighted by `prior`) of the group centroids is at the origin.

**Value**

a list with components

<code>class</code>	The MAP classification (a factor)
<code>posterior</code>	posterior probabilities for the classes
<code>x</code>	the scores of test cases on up to <code>dimen</code> discriminant variables



**References**

- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.
- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge University Press.

**See Also**

[lda](#), [qda](#), [predict.qda](#)

**Examples**

```
tr <- sample(1:50, 25)
train <- rbind(iris3[tr,,1], iris3[tr,,2], iris3[tr,,3])
test <- rbind(iris3[-tr,,1], iris3[-tr,,2], iris3[-tr,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
z <- lda(train, cl)
predict(z, test)$class
```

---

predict.lqs

*Predict from an lqs Fit*

---

**Description**

Predict from an resistant regression fitted by lqs.

**Usage**

```
## S3 method for class 'lqs':
predict(object, newdata, na.action = na.pass, ...)
```

**Arguments**

object	object inheriting from class "lqs"
newdata	matrix or data frame of cases to be predicted or, if object has a formula, a data frame with columns of the same names as the variables used. A vector will be interpreted as a row vector. If newdata is missing, an attempt will be made to retrieve the data used to fit the lqs object.
na.action	function determining what should be done with missing values in newdata. The default is to predict NA.
...	arguments to be passed from or to other methods.

**Details**

This function is a method for the generic function `predict()` for class `lqs`. It can be invoked by calling `predict(x)` for an object `x` of the appropriate class, or directly by calling `predict.lqs(x)` regardless of the class of the object.

Missing values in `newdata` are handled by returning `NA` if the linear fit cannot be evaluated. If `newdata` is omitted and the `na.action` of the fit omitted cases, these will be omitted on the prediction.

**Value**

A vector of predictions.

**Author(s)**

B.D. Ripley

**See Also**

[lqs](#)

**Examples**

```
set.seed(123)
fm <- lqs(stack.loss ~ ., data = stackloss, method = "S", nsamp = "exact")
predict(fm, stackloss)
```

---

predict.mca

*Predict Method for Class 'mca'*

---

**Description**

Used to compute coordinates for additional rows or additional factors in a multiple correspondence analysis.

**Usage**

```
## S3 method for class 'mca':
predict(object, newdata, type = c("row", "factor"), ...)
```

**Arguments**

object	An object of class "mca", usually the result of a call to <code>mca</code> .
newdata	A data frame containing <i>either</i> additional rows of the factors used to fit <code>object</code> <i>or</i> additional factors for the cases used in the original fit.
type	Are predictions required for further rows or for new factors?
...	Additional arguments from <code>predict</code> : unused.

**Value**

If `type = "row"`, the coordinates for the additional rows.

If `type = "factor"`, the coordinates of the column vertices for the levels of the new factors.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[mca](#), [plot.mca](#)

predict.qda

*Classify from Quadratic Discriminant Analysis***Description**

Classify multivariate observations in conjunction with `qda`

**Usage**

```
## S3 method for class 'qda':
predict(object, newdata, prior = object$prior,
        method = c("plug-in", "predictive", "debiased", "looCV"), ...)
```

**Arguments**

<code>object</code>	object of class "qda"
<code>newdata</code>	data frame of cases to be classified or, if <code>object</code> has a formula, a data frame with columns of the same names as the variables used. A vector will be interpreted as a row vector. If <code>newdata</code> is missing, an attempt will be made to retrieve the data used to fit the <code>qda</code> object.
<code>prior</code>	The prior probabilities of the classes, by default the proportions in the training set or what was set in the call to <code>qda</code> .
<code>method</code>	This determines how the parameter estimation is handled. With "plug-in" (the default) the usual unbiased parameter estimates are used and assumed to be correct. With "debiased" an unbiased estimator of the log posterior probabilities is used, and with "predictive" the parameter estimates are integrated out using a vague prior. With "looCV" the leave-one-out cross-validation fits to the original dataset are computed and returned.
<code>...</code>	arguments based from or to other methods

**Details**

This function is a method for the generic function `predict()` for class "qda". It can be invoked by calling `predict(x)` for an object `x` of the appropriate class, or directly by calling `predict.qda(x)` regardless of the class of the object.

Missing values in `newdata` are handled by returning `NA` if the quadratic discriminants cannot be evaluated. If `newdata` is omitted and the `na.action` of the fit omitted cases, these will be omitted on the prediction.

**Value**

a list with components

<code>class</code>	The MAP classification (a factor)
<code>posterior</code>	posterior probabilities for the classes

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.  
 Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge University Press.

**See Also**

[qda](#), [lda](#), [predict.lda](#)

**Examples**

```
tr <- sample(1:50, 25)
train <- rbind(iris3[tr,,1], iris3[tr,,2], iris3[tr,,3])
test <- rbind(iris3[-tr,,1], iris3[-tr,,2], iris3[-tr,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
zq <- qda(train, cl)
predict(zq, test)$class
```

---

 profile.glm

---

*Method for Profiling glm Objects*


---

**Description**

Investigates the profile log-likelihood function for a fitted model of class "glm".

**Usage**

```
## S3 method for class 'glm':
profile(fitted, which = 1:p, alpha = 0.01, maxsteps = 10,
       del = zmax/5, trace = FALSE, ...)
```

**Arguments**

fitted	the original fitted model object.
which	the original model parameters which should be profiled. This can be a numeric or character vector. By default, all parameters are profiled.
alpha	highest significance level allowed for the profile t-statistics.
maxsteps	maximum number of points to be used for profiling each parameter.
del	suggested change on the scale of the profile t-statistics. Default value chosen to allow profiling at about 10 parameter values.
trace	logical: should the progress of profiling be reported?
...	further arguments passed to or from other methods.

**Details**

The profile t-statistic is defined as the square root of change in sum-of-squares divided by residual standard error with an appropriate sign.

**Value**

A list of classes "profile.glm" and "profile" with an element for each parameter being profiled. The elements are data-frames with two variables

par.vals	a matrix of parameter values for each fitted model.
tau	the profile t-statistics.

**Author(s)**

Originally, D. M. Bates and W. N. Venables. (For S in 1996.)

**See Also**

[glm](#), [profile](#), [plot.profile](#)

**Examples**

```
options(contrasts = c("contr.treatment", "contr.poly"))
ldose <- rep(0:5, 2)
numdead <- c(1, 4, 9, 13, 18, 20, 0, 2, 6, 10, 12, 16)
sex <- factor(rep(c("M", "F"), c(6, 6)))
SF <- cbind(numdead, numalive = 20 - numdead)
budworm.lg <- glm(SF ~ sex*ldose, family = binomial)
pr1 <- profile(budworm.lg)
plot(pr1)
pairs(pr1)
```

---

qda

*Quadratic Discriminant Analysis*


---

**Description**

Quadratic discriminant analysis.

**Usage**

```
qda(x, ...)

## S3 method for class 'formula':
qda(formula, data, ..., subset, na.action)

## Default S3 method:
qda(x, grouping, prior = proportions,
     method, CV = FALSE, nu, ...)

## S3 method for class 'data.frame':
qda(x, ...)

## S3 method for class 'matrix':
qda(x, grouping, ..., subset, na.action)
```

**Arguments**

formula	A formula of the form $\text{groups} \sim x_1 + x_2 + \dots$ . That is, the response is the grouping factor and the right hand side specifies the (non-factor) discriminators.
data	Data frame from which variables specified in <code>formula</code> are preferentially to be taken.

x	(required if no formula is given as the principal argument.) a matrix or data frame or Matrix containing the explanatory variables.
grouping	(required if no formula principal argument is given.) a factor specifying the class for each observation.
prior	the prior probabilities of class membership. If unspecified, the class proportions for the training set are used. If specified, the probabilities should be specified in the order of the factor levels.
subset	An index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)
na.action	A function to specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is na.omit, which leads to rejection of cases with missing values on any required variable. (NOTE: If given, this argument must be named.)
method	"moment" for standard estimators of the mean and variance, "mle" for MLEs, "mve" to use cov.mve, or "t" for robust estimates based on a t distribution.
CV	If true, returns results (classes and posterior probabilities) for leave-out-out cross-validation. Note that if the prior is estimated, the proportions in the whole dataset are used.
nu	degrees of freedom for method = "t".
...	arguments passed to or from other methods.

### Details

Uses a QR decomposition which will give an error message if the within-group variance is singular for any group.

### Value

an object of class "qda" containing the following components:

prior	the prior probabilities used.
means	the group means.
scaling	for each group <i>i</i> , scaling[, , <i>i</i> ] is an array which transforms observations so that within-groups covariance matrix is spherical.
ldet	a vector of half log determinants of the dispersion matrix.
lev	the levels of the grouping factor.
terms	(if formula is a formula) an object of mode expression and class term summarizing the formula.
call	the (matched) function call.

unless CV=TRUE, when the return value is a list with components:

class	The MAP classification (a factor)
posterior	posterior probabilities for the classes

### References

- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.
- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge University Press.

**See Also**

`predict.qda`, `lda`

**Examples**

```
tr <- sample(1:50, 25)
train <- rbind(iris3[tr,,1], iris3[tr,,2], iris3[tr,,3])
test <- rbind(iris3[-tr,,1], iris3[-tr,,2], iris3[-tr,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
z <- qda(train, cl)
predict(z,test)$class
```

---

quine

*Absenteeism from School in Rural New South Wales*

---

**Description**

The `quine` data frame has 146 rows and 5 columns. Children from Walgett, New South Wales, Australia, were classified by Culture, Age, Sex and Learner status and the number of days absent from school in a particular school year was recorded.

**Usage**

`quine`

**Format**

This data frame contains the following columns:

`Eth` ethnic background: Aboriginal or Not, ("A" or "N").

`Sex` sex: factor with levels ("F" or "M").

`Age` age group: Primary ("F0"), or forms "F1", "F2" or "F3".

`Lrn` learner status: factor with levels Average or Slow learner, ("AL" or "SL").

`Days` days absent from school in the year.

**Source**

S. Quine, quoted in Aitkin, M. (1978) The analysis of unbalanced cross classifications (with discussion). *Journal of the Royal Statistical Society series A* **141**, 195–223.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

Rabbit

*Blood Pressure in Rabbits***Description**

Five rabbits were studied on two occasions, after treatment with saline (control) and after treatment with the  $5-HT_3$  antagonist MDL 72222. After each treatment ascending doses of phenylbiguanide were injected intravenously at 10 minute intervals and the responses of mean blood pressure measured. The goal was to test whether the cardiogenic chemoreflex elicited by phenylbiguanide depends on the activation of  $5-HT_3$  receptors.

**Usage**

Rabbit

**Format**

This data frame contains 60 rows and the following variables:

BPchange change in blood pressure relative to the start of the experiment.

Dose dose of Phenylbiguanide in micrograms.

Run label of run ("C1" to "C5", then "M1" to "M5").

Treatment placebo or the  $5-HT_3$  antagonist MDL 72222.

Animal label of animal used ("R1" to "R5").

**Source**

J. Ludbrook (1994) Repeated measurements and multiple comparisons in cardiovascular research. *Cardiovascular Research* **28**, 303–311.

[The numerical data are not in the paper but were supplied by Professor Ludbrook]

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

rational

*Rational Approximation***Description**

Find rational approximations to the components of a real numeric object using a standard continued fraction method.

**Usage**

```
rational(x, cycles = 10, max.denominator = 2000, ...)
```



**Arguments**

<code>x</code>	Any object of mode numeric. Missing values are now allowed.
<code>cycles</code>	The maximum number of steps to be used in the continued fraction approximation process.
<code>max.denominator</code>	An early termination criterion. If any partial denominator exceeds <code>max.denominator</code> the continued fraction stops at that point.
<code>...</code>	arguments passed to or from other methods.

**Details**

Each component is first expanded in a continued fraction of the form

$$x = \text{floor}(x) + 1/(p_1 + 1/(p_2 + \dots))$$

where  $p_1, p_2, \dots$  are positive integers, terminating either at `cycles` terms or when a  $p_j > \text{max.denominator}$ . The continued fraction is then re-arranged to retrieve the numerator and denominator as integers and the ratio returned as the value.

**Value**

A numeric object with the same attributes as `x` but with entries rational approximations to the values. This effectively rounds relative to the size of the object and replaces very small entries by zero.

**See Also**

[fractions](#)

**Examples**

```
X <- matrix(runif(25), 5, 5)
zapsmall(solve(X, X/5)) # print near-zeroes as zero
rational(solve(X, X/5))
```

---

renumerate

*Convert a Formula Transformed by 'denumerate'*

---

**Description**

`denumerate` converts a formula written using the conventions of `loglm` into one that `terms` is able to process. `renumerate` converts it back again to a form like the original.

**Usage**

```
renumerate(x)
```

**Arguments**

<code>x</code>	A formula, normally as modified by <code>denumerate</code> .
----------------	--

**Details**

This is an inverse function to [denumerate](#). It is only needed since [terms](#) returns an expanded form of the original formula where the non-marginal terms are exposed. This expanded form is mapped back into a form corresponding to the one that the user originally supplied.

**Value**

A formula where all variables with names of the form `.vn`, where `n` is an integer, converted to numbers, `n`, as allowed by the formula conventions of [loglm](#).

**See Also**

[denumerate](#)

**Examples**

```
denumerate(~(1+2+3)^3 + a/b)
## ~ (.v1 + .v2 + .v3)^3 + a/b
renumerate(.Last.value)
## ~ (1 + 2 + 3)^3 + a/b
```

---

 rlm

*Robust Fitting of Linear Models*


---

**Description**

Fit a linear model by robust regression using an M estimator.

**Usage**

```
rlm(x, ...)

## S3 method for class 'formula':
rlm(formula, data, weights, ..., subset, na.action,
     method = c("M", "MM", "model.frame"),
     wt.method = c("inv.var", "case"),
     model = TRUE, x.ret = TRUE, y.ret = FALSE, contrasts = NULL)

## Default S3 method:
rlm(x, y, weights, ..., w = rep(1, nrow(x)),
     init = "ls", psi = psi.huber,
     scale.est = c("MAD", "Huber", "proposal 2"), k2 = 1.345,
     method = c("M", "MM"), wt.method = c("inv.var", "case"),
     maxit = 20, acc = 1e-4, test.vec = "resid", lqs.control = NULL)

psi.huber(u, k = 1.345, deriv = 0)
psi.hampel(u, a = 2, b = 4, c = 8, deriv = 0)
psi.bisquare(u, c = 4.685, deriv = 0)
```

**Arguments**

<code>formula</code>	a formula of the form $y \sim x_1 + x_2 + \dots$
<code>data</code>	data frame from which variables specified in <code>formula</code> are preferentially to be taken.
<code>weights</code>	a vector of prior weights for each case.
<code>subset</code>	An index vector specifying the cases to be used in fitting.
<code>na.action</code>	A function to specify the action to be taken if NAs are found. The ‘factory-fresh’ default action in R is <code>na.omit</code> , and can be changed by <code>options(na.action=)</code> .
<code>x</code>	a matrix or data frame containing the explanatory variables.
<code>y</code>	the response: a vector of length the number of rows of <code>x</code> .
<code>method</code>	currently either M-estimation or MM-estimation or (for the <code>formula</code> method only) find the model frame. MM-estimation is M-estimation with Tukey’s bi-weight initialized by a specific S-estimator. See the ‘Details’ section.
<code>wt.method</code>	are the weights case weights (giving the relative importance of case, so a weight of 2 means there are two of these) or the inverse of the variances, so a weight of two means this error is half as variable?
<code>model</code>	should the model frame be returned in the object?
<code>x.ret</code>	should the model matrix be returned in the object?
<code>y.ret</code>	should the response be returned in the object?
<code>contrasts</code>	optional contrast specifications: see <a href="#">lm</a> .
<code>w</code>	(optional) initial down-weighting for each case.
<code>init</code>	(optional) initial values for the coefficients OR a method to find initial values OR the result of a fit with a <code>coef</code> component. Known methods are "ls" (the default) for an initial least-squares fit using weights <code>w*weights</code> , and "lts" for an unweighted least-trimmed squares fit with 200 samples.
<code>psi</code>	the <code>psi</code> function is specified by this argument. It must give (possibly by name) a function <code>g(x, ..., deriv)</code> that for <code>deriv=0</code> returns <code>psi(x)/x</code> and for <code>deriv=1</code> returns <code>psi'(x)</code> . Tuning constants will be passed in via <code>...</code>
<code>scale.est</code>	method of scale estimation: re-scaled MAD of the residuals (default) or Huber’s proposal 2 (which can be selected by either "Huber" or "proposal 2").
<code>k2</code>	tuning constant used for Huber proposal 2 scale estimation.
<code>maxit</code>	the limit on the number of IWLS iterations.
<code>acc</code>	the accuracy for the stopping criterion.
<code>test.vec</code>	the stopping criterion is based on changes in this vector.
<code>...</code>	additional arguments to be passed to <code>rlm.default</code> or to the <code>psi</code> function.
<code>lqs.control</code>	An optional list of control values for <a href="#">lqs</a> .
<code>u</code>	numeric vector of evaluation points.
<code>k, a, b, c</code>	tuning constants.
<code>deriv</code>	0 or 1: compute values of the <code>psi</code> function or of its first derivative.

## Details

Fitting is done by iterated re-weighted least squares (IWLS).

Psi functions are supplied for the Huber, Hampel and Tukey bisquare proposals as `psi.huber`, `psi.hampel` and `psi.bisquare`. Huber's corresponds to a convex optimization problem and gives a unique solution (up to collinearity). The other two will have multiple local minima, and a good starting point is desirable.

Selecting `method = "MM"` selects a specific set of options which ensures that the estimator has a high breakdown point. The initial set of coefficients and the final scale are selected by an S-estimator with  $k_0 = 1.548$ ; this gives (for  $n \gg p$ ) breakdown point 0.5. The final estimator is an M-estimator with Tukey's biweight and fixed scale that will inherit this breakdown point provided  $c > k_0$ ; this is true for the default value of  $c$  that corresponds to 95% relative efficiency at the normal. Case weights are not supported for `method = "MM"`.

## Value

An object of class `"rlm"` inheriting from `"lm"`. Note that the `df.residual` component is deliberately set to NA to avoid inappropriate estimation of the residual scale from the residual mean square by `"lm"` methods.

The additional components not in an `lm` object are

<code>s</code>	the robust scale estimate used
<code>w</code>	the weights used in the IWLS process
<code>psi</code>	the psi function with parameters substituted
<code>conv</code>	the convergence criteria at each iteration
<code>converged</code>	did the IWLS converge?
<code>wresid</code>	a working residual, weighted for <code>"inv.var"</code> weights only.

## References

P. J. Huber (1981) *Robust Statistics*. Wiley.

F. R. Hampel, E. M. Ronchetti, P. J. Rousseeuw and W. A. Stahel (1986) *Robust Statistics: The Approach based on Influence Functions*. Wiley.

A. Marazzi (1993) *Algorithms, Routines and S Functions for Robust Statistics*. Wadsworth & Brooks/Cole.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

## See Also

[lm](#), [lqs](#).

## Examples

```
summary(rlm(stack.loss ~ ., stackloss))
rlm(stack.loss ~ ., stackloss, psi = psi.hampel, init = "lts")
rlm(stack.loss ~ ., stackloss, psi = psi.bisquare)
```

rms.curv

*Relative Curvature Measures for Non-Linear Regression***Description**

Calculates the root mean square parameter effects and intrinsic relative curvatures,  $c^\theta$  and  $c^\iota$ , for a fitted nonlinear regression, as defined in Bates & Watts, section 7.3, p. 253ff

**Usage**

```
rms.curv(obj)
```

**Arguments**

`obj` Fitted model object of class "nls". The model must be fitted using the default algorithm.

**Details**

The method of section 7.3.1 of Bates & Watts is implemented. The function `deriv3` should be used generate a model function with first derivative (gradient) matrix and second derivative (Hessian) array attributes. This function should then be used to fit the nonlinear regression model.

A print method, `print.rms.curv`, prints the `pc` and `ic` components only, suitably annotated.

If either `pc` or `ic` exceeds some threshold (0.3 has been suggested) the curvature is unacceptably high for the planar assumption.

**Value**

A list of class `rms.curv` with components `pc` and `ic` for parameter effects and intrinsic relative curvatures multiplied by  $\sqrt{F}$ , `ct` and `ci` for  $c^\theta$  and  $c^\iota$  (unmultiplied), and `C` the C-array as used in section 7.3.1 of Bates & Watts.

**References**

Bates, D. M, and Watts, D. G. (1988) *Nonlinear Regression Analysis and its Applications*. Wiley, New York.

**See Also**

[deriv3](#)

**Examples**

```
# The treated sample from the Puromycin data
mmcurve <- deriv3(~ Vm * conc/(K + conc), c("Vm", "K"),
  function(Vm, K, conc) NULL)
Treated <- Puromycin[Puromycin$state == "treated", ]
(Purfit1 <- nls(rate ~ mmcurve(Vm, K, conc), data = Treated,
  start = list(Vm=200, K=0.1)))
rms.curv(Purfit1)
##Parameter effects: c^theta x sqrt(F) = 0.2121
##      Intrinsic: c^iota x sqrt(F) = 0.092
```

---

`rnegbin`*Simulate Negative Binomial Variates*

---

**Description**

Function to generate random outcomes from a Negative Binomial distribution, with mean `mu` and variance  $\mu + \mu^2/\theta$ .

**Usage**

```
rnegbin(n, mu = n, theta = stop("'theta' must be specified"))
```

**Arguments**

<code>n</code>	If a scalar, the number of sample values required. If a vector, <code>length(n)</code> is the number required and <code>n</code> is used as the mean vector if <code>mu</code> is not specified.
<code>mu</code>	The vector of means. Short vectors are recycled.
<code>theta</code>	Vector of values of the <code>theta</code> parameter. Short vectors are recycled.

**Details**

The function uses the representation of the Negative Binomial distribution as a continuous mixture of Poisson distributions with Gamma distributed means. Unlike `rnbinom` the index can be arbitrary.

**Value**

Vector of random Negative Binomial variate values.

**Side Effects**

Changes `.Random.seed` in the usual way.

**Examples**

```
# Negative Binomials with means fitted(fm) and theta = 4.5
fm <- glm.nb(Days ~ ., data = quine)
dummy <- rnegbin(fitted(fm), theta = 4.5)
```

---

`road`*Road Accident Deaths in US States*

---

**Description**

A data frame with the annual deaths in road accidents for half the US states.

**Usage**

```
road
```

**Format**

Columns are:

state name.

deaths number of deaths.

drivers number of drivers (in 10,000s).

popden population density in people per square mile.

rural length of rural roads, in 1000s of miles.

temp average daily maximum temperature in January.

fuel fuel consumption in 10,000,000 US gallons per year.

**Source**

Imperial College, London M.Sc. exercise

---

rotifer

*Numbers of Rotifers by Fluid Density*

---

**Description**

The data give the numbers of rotifers falling out of suspension for different fluid densities. There are two species, `pm` *Polyartha major* and `kc`, *Keratella cochlearis* and for each species the number falling out and the total number are given.

**Usage**

rotifer

**Format**

density specific density of fluid.

`pm.y` number falling out for *P. major*.

`pm.total` total number of *P. major*.

`kc.y` number falling out for *K. cochlearis*.

`kc.tot` total number of *K. cochlearis*.

**Source**

D. Collett (1991) *Modelling Binary Data*. Chapman & Hall. p. 217

---

Rubber

*Accelerated Testing of Tyre Rubber*

---

**Description**

Data frame from accelerated testing of tyre rubber.

**Usage**

Rubber

**Format**

loss the abrasion loss in gm/hr.

hard the hardness in Shore units.

tens tensile strength in kg/sq m.

**Source**

O.L. Davies (1947) *Statistical Methods in Research and Production*. Oliver and Boyd, Table 6.1 p. 119.

O.L. Davies and P.L. Goldsmith (1972) *Statistical Methods in Research and Production*. 4th edition, Longmans, Table 8.1 p. 239.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

---

sammon

*Sammon's Non-Linear Mapping*

---

**Description**

One form of non-metric multidimensional scaling.

**Usage**

```
sammon(d, y = cmdscale(d, k), k = 2, niter = 100, trace = TRUE,  
       magic = 0.2, tol = 1e-4)
```



**Arguments**

<code>d</code>	distance structure of the form returned by <code>dist</code> , or a full, symmetric matrix. Data are assumed to be dissimilarities or relative distances, but must be positive except for self-distance. This can contain missing values.
<code>y</code>	An initial configuration. If none is supplied, <code>cmdscale</code> is used to provide the classical solution. (If there are missing values in <code>d</code> , an initial configuration must be provided.) This must not have duplicates.
<code>k</code>	The dimension of the configuration.
<code>niter</code>	The maximum number of iterations.
<code>trace</code>	Logical for tracing optimization. Default <code>TRUE</code> .
<code>magic</code>	initial value of the step size constant in diagonal Newton method.
<code>tol</code>	Tolerance for stopping, in units of stress.

**Details**

This chooses a two-dimensional configuration to minimize the stress, the sum of squared differences between the input distances and those of the configuration, weighted by the distances, the whole sum being divided by the sum of input distances to make the stress scale-free.

An iterative algorithm is used, which will usually converge in around 50 iterations. As this is necessarily an  $O(n^2)$  calculation, it is slow for large datasets. Further, since the configuration is only determined up to rotations and reflections (by convention the centroid is at the origin), the result can vary considerably from machine to machine. In this release the algorithm has been modified by adding a step-length search (`magic`) to ensure that it always goes downhill.

**Value**

Two components:

<code>points</code>	A two-column vector of the fitted configuration.
<code>stress</code>	The final stress achieved.

**Side Effects**

If `trace` is true, the initial stress and the current stress are printed out every 10 iterations.

**References**

- Sammon, J. W. (1969) A non-linear mapping for data structure analysis. *IEEE Trans. Comput.*, **C-18** 401–409.
- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge University Press.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[cmdscale](#), [isoMDS](#)

**Examples**

```
swiss.x <- as.matrix(swiss[, -1])
swiss.sam <- sammon(dist(swiss.x))
plot(swiss.sam$points, type = "n")
text(swiss.sam$points, labels = as.character(1:nrow(swiss.x)))
```

---

 ships

*Ships Damage Data*


---

**Description**

Data frame giving the number of damage incidents and aggregate months of service by ship type, year of construction, and period of operation.

**Usage**

ships

**Format**

type type: "A" to "E".

year year of construction: 1960–64, 65–69, 70–74, 75–79 (coded as "60", "65", "70", "75").

period period of operation : 1960–74, 75–79.

service aggregate months of service.

incidents number of damage incidents.

**Source**

P. McCullagh and J. A. Nelder, (1983), *Generalized Linear Models*. Chapman & Hall, section 6.3.2, page 137

---

 shoes

*Shoe wear data of Box, Hunter and Hunter*


---

**Description**

A list of two vectors, giving the wear of shoes of materials A and B for one foot each of ten boys.

**Usage**

shoes

**Source**

G. E. P. Box, W. G. Hunter and J. S. Hunter (1978) *Statistics for Experimenters*. Wiley, p. 100

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

shrimp

*Percentage of Shrimp in Shrimp Cocktail***Description**

A numeric vector with 18 determinations by different laboratories of the amount (percentage of the declared total weight) of shrimp in shrimp cocktail.

**Usage**

shrimp

**Source**

F. J. King and J. J. Ryan (1976) Collaborative study of the determination of the amount of shrimp in shrimp cocktail. *J. Off. Anal. Chem.* **59**, 644–649.

R. G. Staudte and S. J. Sheather (1990) *Robust Estimation and Testing*. Wiley.

shuttle

*Space Shuttle Autolander Problem***Description**

The `shuttle` data frame has 256 rows and 7 columns. The first six columns are categorical variables giving example conditions; the seventh is the decision. The first 253 rows are the training set, the last 3 the test conditions.

**Usage**

shuttle

**Format**

This data frame contains the following factor columns:

`stability` stable positioning or not (`stab / xstab`).

`error` size of error (MM / SS / LX / XL).

`sign` sign of error, positive or negative (`pp / nn`).

`wind` wind sign (`head / tail`).

`magn` wind strength (`Light / Medium / Strong / Out of Range`).

`vis` visibility (`yes / no`).

`use` use the autolander or not. (`auto / noauto`.)

**Source**

D. Michie (1989) Problems of computer-aided concept formation. In *Applications of Expert Systems 2*, ed. J. R. Quinlan, Turing Institute Press / Addison-Wesley, pp. 310–333.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

`Sitka`*Growth Curves for Sitka Spruce Trees in 1988*

---

**Description**

The `Sitka` data frame has 395 rows and 4 columns. It gives repeated measurements on the log-size of 79 Sitka spruce trees, 54 of which were grown in ozone-enriched chambers and 25 were controls. The size was measured five times in 1988, at roughly monthly intervals.

**Usage**`Sitka`**Format**

This data frame contains the following columns:

`size` measured size (height times diameter squared) of tree, on log scale.

`Time` time of measurement in days since 1 January 1988.

`tree` number of tree.

`treat` either "ozone" for an ozone-enriched chamber or "control".

**Source**

P. J. Diggle, K.-Y. Liang and S. L. Zeger (1994) *Analysis of Longitudinal Data*. Clarendon Press, Oxford

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[Sitka89](#).

---

`Sitka89`*Growth Curves for Sitka Spruce Trees in 1989*

---

**Description**

The `Sitka89` data frame has 632 rows and 4 columns. It gives repeated measurements on the log-size of 79 Sitka spruce trees, 54 of which were grown in ozone-enriched chambers and 25 were controls. The size was measured eight times in 1989, at roughly monthly intervals.

**Usage**`Sitka89`

**Format**

This data frame contains the following columns:

`size` measured size (height times diameter squared) of tree, on log scale.

`Time` time of measurement in days since 1 January 1988.

`tree` number of tree.

`treat` either "ozone" for an ozone-enriched chamber or "control".

**Source**

P. J. Diggle, K.-Y. Liang and S. L. Zeger (1994) *Analysis of Longitudinal Data*. Clarendon Press, Oxford

**See Also**

[Sitka](#)

---

Skye

*AFM Compositions of Aphyric Skye Lavas*

---

**Description**

The `Skye` data frame has 23 rows and 3 columns.

**Usage**

`Skye`

**Format**

This data frame contains the following columns:

A Percentage of sodium and potassium oxides.

F Percentage of iron oxide.

M Percentage of magnesium oxide.

**Source**

R. N. Thompson, J. Esson and A. C. Duncan (1972) Major element chemical variation in the Eocene lavas of the Isle of Skye. *J. Petrology*, **13**, 219–253.

**References**

J. Aitchison (1986) *The Statistical Analysis of Compositional Data*. Chapman and Hall, p.360.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```

# ternary() is from the on-line answers.
ternary <- function(X, pch = par("pch"), lcex = 1,
                   add = FALSE, ord = 1:3, ...)
{
  X <- as.matrix(X)
  if(any(X < 0)) stop("X must be non-negative")
  s <- drop(X %*% rep(1, ncol(X)))
  if(any(s<=0)) stop("each row of X must have a positive sum")
  if(max(abs(s-1)) > 1e-6) {
    warning("row(s) of X will be rescaled")
    X <- X / s
  }
  X <- X[, ord]
  s3 <- sqrt(1/3)
  if(!add)
  {
    oldpty <- par("pty")
    on.exit(par(pty=oldpty))
    par(pty="s")
    plot(c(-s3, s3), c(0.5-s3, 0.5+s3), type="n", axes=FALSE,
         xlab="", ylab="")
    polygon(c(0, -s3, s3), c(1, 0, 0), density=0)
    lab <- NULL
    if(!is.null(dn <- dimnames(X))) lab <- dn[[2]]
    if(length(lab) < 3) lab <- as.character(1:3)
    eps <- 0.05 * lcex
    text(c(0, s3+eps*0.7, -s3-eps*0.7),
         c(1+eps, -0.1*eps, -0.1*eps), lab, cex=lcex)
  }
  points((X[,2] - X[,3])*s3, X[,1], ...)
}

ternary(Skye/100, ord=c(1,3,2))

```

snails

*Snail Mortality Data***Description**

Groups of 20 snails were held for periods of 1, 2, 3 or 4 weeks in carefully controlled conditions of temperature and relative humidity. There were two species of snail, A and B, and the experiment was designed as a 4 by 3 by 4 by 2 completely randomized design. At the end of the exposure time the snails were tested to see if they had survived; the process itself is fatal for the animals. The object of the exercise was to model the probability of survival in terms of the stimulus variables, and in particular to test for differences between species.

The data are unusual in that in most cases fatalities during the experiment were fairly small.

**Usage**

snails

**Format**

The data frame contains the following components:

Species snail species A (1) or B (2).

Exposure exposure in weeks.

Rel.Hum relative humidity (4 levels).

Temp temperature, in degrees Celsius (3 levels).

Deaths number of deaths.

N number of snails exposed.

**Source**

Zoology Department, The University of Adelaide.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

---

SP500

*Returns of the Standard and Poors 500*

---

**Description**

Returns of the Standard and Poors 500 Index in the 1990's

**Usage**

SP500

**Format**

A vector of returns of the Standard and Poors 500 index for all the trading days in 1990, 1991, ..., 1999.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

stdres	<i>Extract Standardized Residuals from a Linear Model</i>
--------	---

---

**Description**

The standardized residuals. These are normalized to unit variance, fitted including the current data point.

**Usage**

```
stdres(object)
```

**Arguments**

`object` any object representing a linear model.

**Value**

The vector of appropriately transformed residuals.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[residuals](#), [studres](#)

---

steam	<i>The Saturated Steam Pressure Data</i>
-------	--

---

**Description**

Temperature and pressure in a saturated steam driven experimental device.

**Usage**

```
steam
```

**Format**

The data frame contains the following components:

`Temp` temperature, in degrees Celsius.

`Press` pressure, in Pascals.

**Source**

N.R. Draper and H. Smith (1981) *Applied Regression Analysis*. Wiley, pp. 518–9.



## References

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

---

stepAIC

*Choose a model by AIC in a Stepwise Algorithm*

---

## Description

Performs stepwise model selection by AIC.

## Usage

```
stepAIC(object, scope, scale = 0,
        direction = c("both", "backward", "forward"),
        trace = 1, keep = NULL, steps = 1000, use.start = FALSE,
        k = 2, ...)
```

## Arguments

object	an object representing a model of an appropriate class. This is used as the initial model in the stepwise search.
scope	defines the range of models examined in the stepwise search. This should be either a single formula, or a list containing components <code>upper</code> and <code>lower</code> , both formulae. See the details for how to specify the formulae and how they are used.
scale	used in the definition of the AIC statistic for selecting the models, currently only for <code>lm</code> and <code>aov</code> models (see <code>extractAIC</code> for details).
direction	the mode of stepwise search, can be one of "both", "backward", or "forward", with a default of "both". If the <code>scope</code> argument is missing the default for <code>direction</code> is "backward".
trace	if positive, information is printed during the running of <code>stepAIC</code> . Larger values may give more information on the fitting process.
keep	a filter function whose input is a fitted model object and the associated AIC statistic, and whose output is arbitrary. Typically <code>keep</code> will select a subset of the components of the object and return them. The default is not to keep anything.
steps	the maximum number of steps to be considered. The default is 1000 (essentially as many as required). It is typically used to stop the process early.
use.start	if true the updated fits are done starting at the linear predictor for the currently selected model. This may speed up the iterative calculations for <code>glm</code> (and other fits), but it can also slow them down. <b>Not used in R.</b>
k	the multiple of the number of degrees of freedom used for the penalty. Only $k = 2$ gives the genuine AIC: $k = \log(n)$ is sometimes referred to as BIC or SBC.
...	any additional arguments to <code>extractAIC</code> . (None are currently used.)

## Details

The set of models searched is determined by the `scope` argument. The right-hand-side of its lower component is always included in the model, and right-hand-side of the model is included in the upper component. If `scope` is a single formula, it specifies the upper component, and the lower model is empty. If `scope` is missing, the initial model is used as the upper model.

Models specified by `scope` can be templates to update `object` as used by `update.formula`.

There is a potential problem in using `glm` fits with a variable `scale`, as in that case the deviance is not simply related to the maximized log-likelihood. The `glm` method for `extractAIC` makes the appropriate adjustment for a gaussian family, but may need to be amended for other cases. (The binomial and poisson families have fixed `scale` by default and do not correspond to a particular maximum-likelihood problem for variable `scale`.)

Where a conventional deviance exists (e.g. for `lm`, `aov` and `glm` fits) this is quoted in the analysis of variance table: it is the *unscaled* deviance.

## Value

the stepwise-selected model is returned, with up to two additional components. There is an "anova" component corresponding to the steps taken in the search, as well as a "keep" component if the `keep=` argument was supplied in the call. The "Resid. Dev" column of the analysis of deviance table refers to a constant minus twice the maximized log likelihood: it will be a deviance only in cases where a saturated model is well-defined (thus excluding `lm`, `aov` and `survreg` fits, for example).

## Note

The model fitting must apply the models to the same dataset. This may be a problem if there are missing values and an `na.action` other than `na.fail` is used (as is the default in R). We suggest you remove the missing values first.

## References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

## See Also

[addterm](#), [dropterm](#), [step](#)

## Examples

```
quine.hi <- aov(log(Days + 2.5) ~ .^4, quine)
quine.nxt <- update(quine.hi, . ~ . - Eth:Sex:Age:Lrn)
quine.stp <- stepAIC(quine.nxt,
  scope = list(upper = ~Eth*Sex*Age*Lrn, lower = ~1),
  trace = FALSE)
quine.stp$anova

cpus1 <- cpus
attach(cpus)
for(v in names(cpus)[2:7])
  cpus1[[v]] <- cut(cpus[[v]], unique(quantile(cpus[[v]])),
    include.lowest = TRUE)
detach()
cpus0 <- cpus1[, 2:8] # excludes names, authors' predictions
```

```

cpus.samp <- sample(1:209, 100)
cpus.lm <- lm(log10(perf) ~ ., data = cpus1[cpus.samp,2:8])
cpus.lm2 <- stepAIC(cpus.lm, trace = FALSE)
cpus.lm2$anova

example(birthwt)
birthwt.glm <- glm(low ~ ., family = binomial, data = bwt)
birthwt.step <- stepAIC(birthwt.glm, trace = FALSE)
birthwt.step$anova
birthwt.step2 <- stepAIC(birthwt.glm, ~ .^2 + I(scale(age)^2)
  + I(scale(lwt)^2), trace = FALSE)
birthwt.step2$anova

quine.nb <- glm.nb(Days ~ .^4, data = quine)
quine.nb2 <- stepAIC(quine.nb)
quine.nb2$anova

```

---

stormer

*The Stormer Viscometer Data*


---

## Description

The stormer viscometer measures the viscosity of a fluid by measuring the time taken for an inner cylinder in the mechanism to perform a fixed number of revolutions in response to an actuating weight. The viscometer is calibrated by measuring the time taken with varying weights while the mechanism is suspended in fluids of accurately known viscosity. The data comes from such a calibration, and theoretical considerations suggest a nonlinear relationship between time, weight and viscosity, of the form  $\text{Time} = (B1 * \text{Viscosity}) / (\text{Weight} - B2) + E$  where  $B1$  and  $B2$  are unknown parameters to be estimated, and  $E$  is error.

## Usage

```
stormer
```

## Format

The data frame contains the following components:

Viscosity viscosity of fluid.

Wt actuating weight.

Time time taken.

## Source

E. J. Williams (1959) *Regression Analysis*. Wiley.

## References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

 studres

---

*Extract Studentized Residuals from a Linear Model*


---

**Description**

The Studentized residuals. Like standardized residuals, these are normalized to unit variance, but the Studentized version is fitted ignoring the current data point. (They are sometimes called jack-knifed residuals).

**Usage**

```
studres(object)
```

**Arguments**

`object` any object representing a linear model.

**Value**

The vector of appropriately transformed residuals.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[residuals](#), [stdres](#)

---

 summary.loglm

---

*Summary Method Function for Objects of Class 'loglm'*


---

**Description**

Returns a summary list for log-linear models fitted by iterative proportional scaling using `loglm`.

**Usage**

```
## S3 method for class 'loglm':
summary(object, fitted = FALSE, ...)
```

**Arguments**

`object` a fitted `loglm` model object.

`fitted` if TRUE return observed and expected frequencies in the result. Using `fitted = TRUE` may necessitate re-fitting the object.

`...` arguments to be passed to or from other methods.

**Details**

This function is a method for the generic function `summary()` for class "loglm". It can be invoked by calling `summary(x)` for an object `x` of the appropriate class, or directly by calling `summary.loglm(x)` regardless of the class of the object.

**Value**

a list is returned for use by `print.summary.loglm`. This has components

<code>formula</code>	the formula used to produce <code>object</code>
<code>tests</code>	the table of test statistics (likelihood ratio, Pearson) for the fit.
<code>oe</code>	if <code>fitted = TRUE</code> , an array of the observed and expected frequencies, otherwise <code>NULL</code> .

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[loglm](#), [summary](#)

---

summary.negbin

*Summary Method Function for Objects of Class 'negbin'*

---

**Description**

Identical to `summary.glm`, but with three lines of additional output: the ML estimate of theta, its standard error, and twice the log-likelihood function.

**Usage**

```
## S3 method for class 'negbin':
summary(object, dispersion = 1, correlation = FALSE, ...)
```

**Arguments**

<code>object</code>	fitted model object of class <code>negbin</code> inheriting from <code>glm</code> and <code>lm</code> . Typically the output of <code>glm.nb</code> .
<code>dispersion</code>	as for <code>summary.glm</code> , with a default of 1.
<code>correlation</code>	as for <code>summary.glm</code> .
<code>...</code>	arguments passed to or from other methods.

**Details**

`summary.glm` is used to produce the majority of the output and supply the result. This function is a method for the generic function `summary()` for class "negbin". It can be invoked by calling `summary(x)` for an object `x` of the appropriate class, or directly by calling `summary.negbin(x)` regardless of the class of the object.

**Value**

As for `summary.glm`; the additional lines of output are not included in the resultant object.

**Side Effects**

A summary table is produced as for `summary.glm`, with the additional information described above.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[summary.glm.nb](#), [negative.binomial](#), [anova.negbin](#)

**Examples**

```
summary(glm.nb(Days ~ Eth*Age*Lrn*Sex, quine, link = log))
```

---

summary.rlm

---

*Summary Method for Robust Linear Models*


---

**Description**

`summary` method for objects of class "rlm"

**Usage**

```
## S3 method for class 'rlm':
summary(object, method = c("XtX", "XtWX"), correlation = FALSE, ...)
```

**Arguments**

<code>object</code>	the fitted model. This is assumed to be the result of some fit that produces an object inheriting from the class <code>rlm</code> , in the sense that the components returned by the <code>rlm</code> function will be available.
<code>method</code>	Should the weighted (by the IWLS weights) or unweighted cross-products matrix be used?
<code>correlation</code>	logical. Should correlations be computed (and printed)?
<code>...</code>	arguments passed to or from other methods.

**Details**

This function is a method for the generic function `summary()` for class "rlm". It can be invoked by calling `summary(x)` for an object `x` of the appropriate class, or directly by calling `summary.rlm(x)` regardless of the class of the object.

**Value**

If printing takes place, only a null value is returned. Otherwise, a list is returned with the following components. Printing always takes place if this function is invoked automatically as a method for the `summary` function.

<code>correlation</code>	The computed correlation coefficient matrix for the coefficients in the model.
<code>cov.unscaled</code>	The unscaled covariance matrix; i.e, a matrix such that multiplying it by an estimate of the error variance produces an estimated covariance matrix for the coefficients.
<code>sigma</code>	The scale estimate.
<code>stddev</code>	A scale estimate used for the standard errors.
<code>df</code>	The number of degrees of freedom for the model and for residuals.
<code>coefficients</code>	A matrix with three columns, containing the coefficients, their standard errors and the corresponding t statistic.
<code>terms</code>	The terms object used in fitting this model.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[summary](#)

**Examples**

```
summary(rlm(calls ~ year, data = phones, maxit = 50))
## Not run:
Call:
rlm(formula = calls ~ year, data = phones, maxit = 50)

Residuals:
    Min       1Q   Median       3Q      Max
-18.31  -5.95  -1.68   26.46  173.77

Coefficients:
              Value      Std. Error t value
(Intercept) -102.622    26.553   -3.86
year          2.041     0.429    4.76

Residual standard error: 9.03 on 22 degrees of freedom

Correlation of Coefficients:
[1] -0.994

## End(Not run)
```

---

survey

*Student Survey Data*

---

### Description

This data frame contains the responses of 237 Statistics I students at the University of Adelaide to a number of questions.

### Usage

```
survey
```

### Format

The components of the data frame are:

Sex The sex of the student. (Factor with levels "Male" and "Female".)

Wr.Hnd span (distance from tip of thumb to tip of little finger of spread hand) of writing hand, in centimetres.

NW.Hnd span of non-writing hand.

W.Hnd writing hand of student. (Factor, with levels "Left" and "Right".)

Fold "Fold your arms! Which is on top" (Factor, with levels "R on L", "L on R", "Neither".)

Pulse pulse rate of student (beats per minute).

Clap "Clap your hands! Which hand is on top?" (Factor, with levels "Right", "Left", "Neither".)

Exer how often the student exercises. (Factor, with levels "Freq" (frequently), "Some", "None".)

Smoke how much the student smokes. (Factor, levels "Heavy", "Regul" (regularly), "Occas" (occasionally), "Never".)

Height height of the student in centimetres.

M. I whether the student expressed height in imperial (feet/inches) or metric (centimetres/metres) units. (Factor, levels "Metric", "Imperial".)

Age age of the student in years.

### References

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.



---

 synth.tr

*Synthetic Classification Problem*


---

### Description

The `synth.tr` data frame has 250 rows and 3 columns. The `synth.te` data frame has 100 rows and 3 columns. It is intended that `synth.tr` be used from training and `synth.te` for testing.

### Usage

```
synth.tr
synth.te
```

### Format

These data frames contains the following columns:

```
xs x-coordinate
ys y-coordinate
yc class, coded as 0 or 1.
```

### Source

Ripley, B.D. (1994) Neural networks and related methods for classification (with discussion). *Journal of the Royal Statistical Society series B* **56**, 409–456.

Ripley, B.D. (1996) *Pattern Recognition and Neural Networks*. Cambridge: Cambridge University Press.

---

 theta.md

*Estimate theta of the Negative Binomial*


---

### Description

Given the estimated mean vector, estimate `theta` of the Negative Binomial Distribution.

### Usage

```
theta.md(y, mu, dfr, weights, limit = 20, eps = .Machine$double.eps^0.25)
theta.ml(y, mu, n, weights, limit = 10, eps = .Machine$double.eps^0.25,
         trace = FALSE)
theta.mm(y, mu, dfr, weights, limit = 10, eps = .Machine$double.eps^0.25)
```

**Arguments**

<code>y</code>	Vector of observed values from the Negative Binomial.
<code>mu</code>	Estimated mean vector.
<code>n</code>	Number of data points (defaults to the sum of weights)
<code>dfr</code>	Residual degrees of freedom (assuming <code>theta</code> known). For a weighted fit this is the sum of the weights minus the number of fitted parameters.
<code>weights</code>	Case weights. If missing, taken as 1.
<code>limit</code>	Limit on the number of iterations.
<code>eps</code>	Tolerance to determine convergence.
<code>trace</code>	logical: should iteration progress be printed?

**Details**

`theta.md` estimates by equating the deviance to the residual degrees of freedom, an analogue of a moment estimator.

`theta.ml` uses maximum likelihood.

`theta.mm` calculates the moment estimator of `theta` by equating the Pearson chi-square  $\sum(y - \mu)^2 / (\mu + \mu^2 / \theta)$  to the residual degrees of freedom.

**Value**

The required estimate of `theta`, as a scalar. For `theta.ml`, the standard error is given as attribute "SE".

**See Also**

[glm.nb](#)

**Examples**

```
quine.nb <- glm.nb(Days ~ .^2, data = quine)
theta.md(quine$Days, fitted(quine.nb), dfr = df.residual(quine.nb))
theta.ml(quine$Days, fitted(quine.nb))
theta.mm(quine$Days, fitted(quine.nb), dfr = df.residual(quine.nb))

## weighted example
yeast <- data.frame(cbind(numbers = 0:5, fr = c(213, 128, 37, 18, 3, 1)))
fit <- glm.nb(numbers ~ 1, weights = fr, data = yeast)
summary(fit)
attach(yeast)
mu <- fitted(fit)
theta.md(numbers, mu, dfr = 399, weights = fr)
theta.ml(numbers, mu, weights = fr)
theta.mm(numbers, mu, dfr = 399, weights = fr)
detach()
```

---

`topo`*Spatial Topographic Data*

---

**Description**

The `topo` data frame has 52 rows and 3 columns, of topographic heights within a 310 feet square.

**Usage**`topo`**Format**

This data frame contains the following columns:

`x` x coordinates (units of 50 feet)

`y` y coordinates (units of 50 feet)

`z` heights (feet)

**Source**

Davis, J.C. (1973) *Statistics and Data Analysis in Geology*. Wiley.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

---

`Traffic`*Effect of Swedish Speed Limits on Accidents*

---

**Description**

An experiment was performed in Sweden in 1961–2 to assess the effect of a speed limit on the motorway accident rate. The experiment was conducted on 92 days in each year, matched so that day `j` in 1962 was comparable to day `j` in 1961. On some days the speed limit was in effect and enforced, while on other days there was no speed limit and cars tended to be driven faster. The speed limit days tended to be in contiguous blocks.

**Usage**`Traffic`**Format**

This data frame contains the following columns:

`year` 1961 or 1962.

`day` of year.

`limit` was there a speed limit?

`y` traffic accident count for that day.

**Source**

Svensson, A. (1981) On the goodness-of-fit test for the multiplicative Poisson model. *Annals of Statistics*, **9**, 697–704.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

---

truehist	<i>Plot a Histogram</i>
----------	-------------------------

---

**Description**

Creates a histogram on the current graphics device.

**Usage**

```
truehist(data, nbins = "Scott", h, x0 = -h/1000,
         breaks, prob = TRUE, xlim = range(breaks),
         ymax = max(est), col = "cyan",
         xlab = deparse(substitute(data)), bty = "n", ...)
```

**Arguments**

data	numeric vector of data for histogram. Missing values (NAs) are allowed and omitted.
nbins	The suggested number of bins. Either a positive integer, or a character string naming a rule: "Scott" or "Freedman-Diaconis" or "FD". (Case is ignored.)
h	The bin width, a strictly positive number (takes precedence over nbins).
x0	Shift for the bins - the breaks are at $x_0 + h * (\dots, -1, 0, 1, \dots)$
breaks	The set of breakpoints to be used. (Usually omitted, takes precedence over h and nbins).
prob	If true (the default) plot a true histogram. The vertical axis has a <i>relative frequency density</i> scale, so the product of the dimensions of any panel gives the relative frequency. Hence the total area under the histogram is 1 and it is directly comparable with most other estimates of the probability density function. If false plot the counts in the bins.
xlim	The limits for the x-axis.
ymax	The upper limit for the y-axis.
col	The colour for the bar fill: the default is colour 5 in the default R palette.
xlab	label for the plot x-axis. By default, this will be the name of data.
bty	The box type for the plot - defaults to none.
...	additional arguments to <a href="#">rect</a> or <a href="#">plot</a> .

**Details**

This plots a true histogram, a density estimate of total area 1. If `breaks` is specified, those break-points are used. Otherwise if `h` is specified, a regular grid of bins is used with width `h`. If neither `breaks` nor `h` is specified, `nbins` is used to select a suitable `h`.

**Side Effects**

A histogram is plotted on the current device.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[hist](#)

---

ucv

*Unbiased Cross-Validation for Bandwidth Selection*

---

**Description**

Uses unbiased cross-validation to select the bandwidth of a Gaussian kernel density estimator.

**Usage**

```
ucv(x, nb = 1000, lower, upper)
```

**Arguments**

`x` a numeric vector  
`nb` number of bins to use.  
`lower, upper` Range over which to minimize. The default is almost always satisfactory.

**Value**

a bandwidth.

**References**

Scott, D. W. (1992) *Multivariate Density Estimation: Theory, Practice, and Visualization*. Wiley.  
Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[bcv](#), [width.SJ](#), [density](#)

**Examples**

```
ucv(geyser$duration)
```

---

`UScereal`*Nutritional and Marketing Information on US Cereals*

---

**Description**

The `UScereal` data frame has 65 rows and 11 columns. The data come from the 1993 ASA Statistical Graphics Exposition, and are taken from the mandatory F&DA food label. The data have been normalized here to a portion of one American cup.

**Usage**`UScereal`**Format**

This data frame contains the following columns:

`mfr` Manufacturer, represented by its first initial: G=General Mills, K=Kelloggs, N=Nabisco, P=Post, Q=Quaker Oats, R=Ralston Purina.

`calories` number of calories in one portion.

`protein` grams of protein in one portion.

`fat` grams of fat in one portion.

`sodium` milligrams of sodium in one portion.

`fibre` grams of dietary fibre in one portion.

`carbo` grams of complex carbohydrates in one portion.

`sugars` grams of sugars in one portion.

`shelf` display shelf (1, 2, or 3, counting from the floor).

`potassium` grams of potassium.

`vitamins` vitamins and minerals (none, enriched, or 100%).

**Source**

The original data are available at <http://lib.stat.cmu.edu/datasets/1993.expo/>.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

UScrime

*The Effect of Punishment Regimes on Crime Rates***Description**

Criminologists are interested in the effect of punishment regimes on crime rates. This has been studied using aggregate data on 47 states of the USA for 1960 given in this data frame. The variables seem to have been re-scaled to convenient numbers.

**Usage**

UScrime

**Format**

This data frame contains the following columns:

- M percentage of males aged 14–24.
- So indicator variable for a Southern state.
- Ed mean years of schooling.
- Po1 police expenditure in 1960.
- Po2 police expenditure in 1959.
- LF labour force participation rate.
- M.F number of males per 1000 females.
- Pop state population.
- NW number of non-whites per 1000 people.
- U1 unemployment rate of urban males 14–24.
- U2 unemployment rate of urban males 35–39.
- GDP gross domestic product per head.
- Ineq income inequality.
- Prob probability of imprisonment.
- Time average time served in state prisons.
- y rate of crimes in a particular category per head of population.

**Source**

Ehrlich, I. (1973) Participation in illegitimate activities: a theoretical and empirical investigation. *Journal of Political Economy*, **81**, 521–565.

Vandaele, W. (1978) Participation in illegitimate activities: Ehrlich revisited. In *Deterrence and Incapacitation*, eds A. Blumstein, J. Cohen and D. Nagin, pp. 270–335. US National Academy of Sciences.

**References**

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS*. Third Edition. Springer.

VA

*Veteran's Administration Lung Cancer Trial***Description**

Veteran's Administration lung cancer trial from Kalbfleisch & Prentice.

**Usage**

VA

**Format**

A data frame with columns:

`stime` survival or follow-up time in days.

`status` dead or censored.

`treat` treatment: standard or test.

`age` patient's age in years.

`Karn` Karnofsky score of patient's performance on a scale of 0 to 100.

`diag.time` times since diagnosis in months at entry to trial.

`cell` one of four cell types.

`prior` prior therapy?

**Source**

Kalbfleisch, J.D. and Prentice R.L. (1980) *The Statistical Analysis of Failure Time Data*. Wiley.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

waders

*Counts of Waders at 15 Sites in South Africa***Description**

The `waders` data frame has 15 rows and 19 columns. The entries are counts of waders in summer.

**Usage**

`waders`



**Format**

This data frame contains the following columns (species)

S1 Oystercatcher  
 S2 White-fronted Plover  
 S3 Kitt Lutz's Plover  
 S4 Three-banded Plover  
 S5 Grey Plover  
 S6 Ringed Plover  
 S7 Bar-tailed Godwit  
 S8 Whimbrel  
 S9 Marsh Sandpiper  
 S10 Greenshank  
 S11 Common Sandpiper  
 S12 Turnstone  
 S13 Knot  
 S14 Sanderling  
 S15 Little Stint  
 S16 Curlew Sandpiper  
 S17 Ruff  
 S18 Avocet  
 S19 Black-winged Stilt

The rows are the sites:

A = Namibia North coast  
 B = Namibia North wetland  
 C = Namibia South coast  
 D = Namibia South wetland  
 E = Cape North coast  
 F = Cape North wetland  
 G = Cape West coast  
 H = Cape West wetland  
 I = Cape South coast  
 J = Cape South wetland  
 K = Cape East coast  
 L = Cape East wetland  
 M = Transkei coast  
 N = Natal coast  
 O = Natal wetland

**Source**

J.C. Gower and D.J. Hand (1996) *Biplots* Chapman & Hall Table 9.1. Quoted as from:

R.W. Summers, L.G. Underhill, D.J. Pearson and D.A. Scott (1987) Wader migration systems in south and eastern Africa and western Asia. *Wader Study Group Bulletin* **49** Supplement, 15–34.

**Examples**

```
plot(corresp(waders, nf=2))
```

---

`whiteside`*House Insulation: Whiteside's Data*

---

### Description

Mr Derek Whiteside of the UK Building Research Station recorded the weekly gas consumption and average external temperature at his own house in south-east England for two heating seasons, one of 26 weeks before, and one of 30 weeks after cavity-wall insulation was installed. The object of the exercise was to assess the effect of the insulation on gas consumption.

### Usage

`whiteside`

### Format

The `whiteside` data frame has 56 rows and 3 columns.:

`Insul` A factor, before or after insulation.

`Temp` Purportedly the average outside temperature in degrees Celsius. (These values is far too low for any 56-week period in the 1960s in South-East England. It might be the weekly average of daily minima.)

`Gas` The weekly gas consumption in 1000s of cubic feet.

### Source

A data set collected in the 1960s by Mr Derek Whiteside of the UK Building Research Station. Reported by

Hand, D. J., Daly, F., McConway, K., Lunn, D. and Ostrowski, E. eds (1993) *A Handbook of Small Data Sets*. Chapman & Hall, p. 69.

### References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### Examples

```
require(lattice)
xyplot(Gas ~ Temp | Insul, whiteside, panel =
  function(x, y, ...) {
    panel.xyplot(x, y, ...)
    panel.lmline(x, y, ...)
  }, xlab = "Average external temperature (deg. C)",
  ylab = "Gas consumption (1000 cubic feet)", aspect = "xy",
  strip = function(...) strip.default(..., style = 1))

gasB <- lm(Gas ~ Temp, whiteside, subset = Insul=="Before")
gasA <- update(gasB, subset = Insul=="After")
summary(gasB)
summary(gasA)
gasBA <- lm(Gas ~ Insul/Temp - 1, whiteside)
summary(gasBA)
```

```
gasQ <- lm(Gas ~ Insul/(Temp + I(Temp^2)) - 1, whiteside)
coef(summary(gasQ))

gasPR <- lm(Gas ~ Insul + Temp, whiteside)
anova(gasPR, gasBA)
options(contrasts = c("contr.treatment", "contr.poly"))
gasBA1 <- lm(Gas ~ Insul*Temp, whiteside)
coef(summary(gasBA1))
```

width.SJ

*Bandwidth Selection by Pilot Estimation of Derivatives***Description**

Uses the method of Sheather & Jones (1991) to select the bandwidth of a Gaussian kernel density estimator.

**Usage**

```
width.SJ(x, nb = 1000, lower, upper, method = c("ste", "dpi"))
```

**Arguments**

x	a numeric vector
nb	number of bins to use.
upper, lower	range over which to search for solution if method = "ste".
method	Either "ste" ("solve-the-equation") or "dpi" ("direct plug-in").

**Value**

a bandwidth.

**References**

Sheather, S. J. and Jones, M. C. (1991) A reliable data-based bandwidth selection method for kernel density estimation. *Journal of the Royal Statistical Society series B* **53**, 683–690.

Scott, D. W. (1992) *Multivariate Density Estimation: Theory, Practice, and Visualization*. Wiley.

Wand, M. P. and Jones, M. C. (1995) *Kernel Smoothing*. Chapman & Hall.

**See Also**

[ucv](#), [bcv](#), [density](#)

**Examples**

```
attach(geyser)
width.SJ(duration, method = "dpi")
width.SJ(duration)
detach()

width.SJ(galaxies, method = "dpi")
width.SJ(galaxies)
```

---

write.matrix	<i>Write a Matrix or Data Frame</i>
--------------	-------------------------------------

---

**Description**

Writes a matrix or data frame to a file or the console, using column labels and a layout respecting columns.

**Usage**

```
write.matrix(x, file = "", sep = " ", blocksize)
```

**Arguments**

x	matrix or data frame.
file	name of output file. The default ("") is the console.
sep	The separator between columns.
blocksize	If supplied and positive, the output is written in blocks of <code>blocksize</code> rows. Choose as large as possible consistent with the amount of memory available.

**Details**

If `x` is a matrix, supplying `blocksize` is more memory-efficient and enables larger matrices to be written, but each block of rows might be formatted slightly differently.

If `x` is a data frame, the conversion to a matrix may negate the memory saving.

**Side Effects**

A formatted file is produced, with column headings (if `x` has them) and columns of data.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[write.table](#)

---

wtloss	<i>Weight Loss Data from an Obese Patient</i>
--------	---

---

**Description**

The data frame gives the weight, in kilograms, of an obese patient at 52 time points over an 8 month period of a weight rehabilitation programme.

**Usage**

```
wtloss
```

**Format**

This data frame contains the following columns:

Days time in days since the start of the programme.

Weight weight in kilograms of the patient.

**Source**

Dr T. Davies, Adelaide.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**Examples**

```
wtloss.fm <- nls(Weight ~ b0 + b1*2^(-Days/th),  
  data = wtloss, start = list(b0=90, b1=95, th=120),  
  trace = TRUE)
```

## Chapter 12

# The `Matrix` package

---

abIndex-class

*Class "abIndex" of Abstract Index Vectors*

---

### Description

The "abIndex" class, short for "Abstract Index Vector", is used for dealing with large index vectors more efficiently, than using integer (or `numeric`) vectors of the kind `2:1000000` or `c(0:1e5, 1000:1e6)`.

Note that the current implementation details are subject to change, and if you consider working with these classes, please contact the package maintainers (`packageDescription("Matrix")$Maintainer`).

### Objects from the Class

Objects can be created by calls of the form `new("abIndex", ...)`, but more easily and typically either by `as(x, "abIndex")` where `x` is an integer (valued) vector, or directly by `abIseq()` and combination `c(...)` of such.

### Slots

`kind`: a `character` string, one of (`"int32"`, `"double"`, `"rleDiff"`), denoting the internal structure of the `abIndex` object.

`x`: Object of class `"numLike"`; is used (i.e., not of length 0) only iff the object is *not* compressed, i.e., currently exactly when `kind != "rleDiff"`.

`rleD`: object of class `"rleDiff"`, used for compression via `rle`.

### Methods

**as.numeric** signature(x = "abIndex"):...

[ signature(x = "abIndex", i = "index", j = "ANY", drop = "ANY"):...

**coerce** signature(from = "numeric", to = "abIndex"):...

**coerce** signature(from = "abIndex", to = "numeric"):...

**coerce** signature(from = "abIndex", to = "integer"):...

**length** signature(x = "abIndex"):...

**Ops** signature(e1 = "numeric", e2 = "abIndex"): These and the following arithmetic and logic operations are **not yet implemented**; see [Ops](#) for a list of these (S4) group methods.

**Ops** signature(e1 = "abIndex", e2 = "abIndex"): ...

**Ops** signature(e1 = "abIndex", e2 = "numeric"): ...

**Summary** signature(x = "abIndex"): ...

**show** ("abIndex"): simple [show](#) method, building on `show(<rleDiff>)`.

**is.na** ("abIndex"): works analogously to regular vectors.

### Note

This is currently experimental and not yet used for our own code. Please contact us (`packageDescription("Matrix")$Maintainer`), if you plan to make use of this class.

Partly builds on ideas and code from Jens Oehlschlaegel, as implemented (around 2008, in the GPL'ed part of) package `ff`.

### See Also

[rle \(base\)](#) which is used here. [numeric](#)

### Examples

```
showClass("abIndex")
ii <- c(-3:40, 20:70)
str(ai <- as(ii, "abIndex"))# note
ai # -> show() method

stopifnot(identical(-3:20,
                    as(abIseq1(-3,20), "vector")))
```

---

abIseq

*Sequence Generation of "abIndex", Abstract Index Vectors*

---

### Description

Generation of abstract index vectors, i.e., objects of class "[abIndex](#)".

`abIseq()` is designed to work entirely like [seq](#), but producing "abIndex" vectors.

`abIseq1()` is its basic building block, where `abIseq1(n, m)` corresponds to `n:m`.

`c(x, ...)` will return an "abIndex" vector, when `x` is one.

### Usage

```
abIseq1(from = 1, to = 1)
abIseq (from = 1, to = 1, by = ((to - from)/(length.out - 1)),
        length.out = NULL, along.with = NULL)

## S3 method for class 'abIndex':
c(...)
```

**Arguments**

<code>from, to</code>	the starting and (maximal) end value of the sequence.
<code>by</code>	number: increment of the sequence.
<code>length.out</code>	desired length of the sequence. A non-negative number, which for <code>seq</code> and <code>seq.int</code> will be rounded up if fractional.
<code>along.with</code>	take the length from the length of this argument.
<code>...</code>	in general an arbitrary number of R objects; here, when the first is an "abIndex" vector, these arguments will be concatenated to a new "abIndex" object.

**Value**

An abstract index vector, i.e., object of class "abIndex".

**See Also**

the class `abIndex` documentation; `rep2abI()` for another constructor; `rle` (**base**).

**Examples**

```
stopifnot(identical(-3:20,
                    as(abIseq1(-3,20), "vector")))

if(FALSE) ## (arithmetic) not yet implemented
abIseq(1, 50, by = 3)
```

---

all-methods

---

*"Matrix" Methods for Functions all() and any()*


---

**Description**

The basic R functions `all` and `any` now have methods for `Matrix` objects and should behave as for `matrix` ones.

**Methods**

```
all signature(x = "Matrix", ..., na.rm = FALSE):...
any signature(x = "Matrix", ..., na.rm = FALSE):...
all signature(x = "ldenseMatrix", ..., na.rm = FALSE):...
all signature(x = "lspareMatrix", ..., na.rm = FALSE):...
```



**Examples**

```
M <- Matrix(1:12 +0, 3,4)
all(M >= 1) # TRUE
any(M < 0 ) # FALSE
MN <- M; MN[2,3] <- NA; MN
all(MN >= 0) # NA
any(MN < 0) # NA
any(MN < 0, na.rm = TRUE) # -> FALSE
```

---

all.equal-methods *Matrix Package Methods for Function all.equal()*

---

**Description**

Methods for function `all.equal()` (from R package **base**) are defined for all `Matrix` classes.

**Methods**

```
target = "Matrix", current = "Matrix" \
target = "ANY", current = "Matrix" \
target = "Matrix", current = "ANY" these three methods are simply using
all.equal.numeric directly and work via as.vector().
```

**Examples**

```
(A <- spMatrix(3,3, i= c(1:3,2:1), j=c(3:1,1:2), x = 1:5))
ex <- expand(lu. <- lu(A))
stopifnot( all.equal(as(A[lu.@p + 1L, lu.@q + 1L], "CsparseMatrix"),
                    lu.@L %*% lu.@U),
          with(ex, all.equal(as(P %*% A %*% Q, "CsparseMatrix"),
                              L %*% U)),
          with(ex, all.equal(as(A, "CsparseMatrix"),
                              t(P) %*% L %*% U %*% t(Q))))
```

---

atomicVector-class *Virtual Class "atomicVector" of Atomic Vectors*

---

**Description**

The class "atomicVector" is a *virtual* class containing all atomic vector classes of base R, as also implicitly defined via `is.atomic`.

**Objects from the Class**

A virtual Class: No objects may be created from it.

**Methods**

In the **Matrix** package, the "atomicVector" is used in signatures where typically "old-style" "matrix" objects can be used and can be substituted by simple vectors.

**Extends**

The atomic classes "logical", "integer", "double", "numeric", "complex", "raw" and "character" are extended directly. Note that "numeric" already contains "integer" and "double", but we want all of them to be direct subclasses of "atomicVector".

**Author(s)**

Martin Maechler

**See Also**

[is.atomic](#), [integer](#), [numeric](#), [complex](#), etc.

**Examples**

```
showClass("atomicVector")
```

---

band

*Extract bands of a matrix*

---

**Description**

Returns a new matrix formed by extracting the lower triangle (`tril`) or the upper triangle (`triu`) or a general band relative to the diagonal (`band`), and setting other elements to zero. The general forms of these functions include integer arguments to specify how many diagonal bands above or below the main diagonal are not set to zero.

**Usage**

```
band(x, k1, k2, ...)  
tril(x, k = 0, ...)  
triu(x, k = 0, ...)
```

**Arguments**

<code>x</code>	a matrix-like object
<code>k, k1, k2</code>	integers specifying the diagonal bands that will not be set to zero. These are given relative to the main diagonal, which is <code>k=0</code> . A negative value of <code>k</code> indicates a diagonal below the main diagonal and a positive value indicates a diagonal above the main diagonal.
<code>...</code>	Optional arguments used by specific methods. (None used at present.)

**Value**

An object of an appropriate matrix class. The class of the value of `tril` or `triu` inherits from [triangularMatrix](#) when appropriate. Note that the result is of class [sparseMatrix](#) only if `x` is.

**Methods**

- x = "CsparseMatrix"** method for compressed, sparse, column-oriented matrices.
- x = "TsparseMatrix"** method for sparse matrices in triplet format.
- x = "RsparseMatrix"** method for compressed, sparse, row-oriented matrices.
- x = "ddenseMatrix"** method for dense numeric matrices, including packed numeric matrices.

**See Also**

[bandSparse](#) for the *construction* of a banded sparse matrix directly from its non-zero diagonals.

**Examples**

```
## A random sparse matrix :
set.seed(7)
m <- matrix(0, 5, 5)
m[sample(length(m), size = 14)] <- rep(1:9, length=14)
(mm <- as(m, "CsparseMatrix"))

tril(mm)          # lower triangle
tril(mm, -1)     # strict lower triangle
triu(mm, 1)      # strict upper triangle
band(mm, -1, 2)  # general band
(m5 <- Matrix(rnorm(25), nc = 5))
tril(m5)         # lower triangle
tril(m5, -1)    # strict lower triangle
triu(m5, 1)     # strict upper triangle
band(m5, -1, 2) # general band
(m65 <- Matrix(rnorm(30), nc = 5)) # not square
triu(m65)       # result in not dtrMatrix unless square
(sm5 <- crossprod(m65)) # symmetric
  band(sm5, -1, 1) # symmetric band preserves symmetry property
as(band(sm5, -1, 1), "sparseMatrix") # often preferable
```

---

bandSparse

---

*Construct Sparse Banded Matrix from (Sup-/Super-) Diagonals*


---

**Description**

Construct a sparse banded matrix by specifying its non-zero sup- and super-diagonals.

**Usage**

```
bandSparse(n, m = n, k, diagonals, symmetric = FALSE)
```

**Arguments**

- n, m* the matrix dimension  $(n, m) = (nrow, ncol)$ .
- k* integer vector of “diagonal numbers”, with identical meaning as in [band](#) (\*, k).

diagonals	optional list of sub-/super- diagonals; if missing, the result will be a pattern matrix, i.e., inheriting from class <code>nMatrix</code> . diagonals can also be $n' \times d$ matrix, where $d \leftarrow \text{length}(k)$ and $n' \geq \min(n, m)$ . In that case, the sub-/super- diagonals are taken from the columns of diagonals, where only the first several rows will be used (typically) for off-diagonals.
symmetric	logical; if true the result will be symmetric (inheriting from class <code>symmetricMatrix</code> ) and only the upper or lower triangle must be specified (via <code>k</code> and <code>diagonals</code> ).

### Value

a sparse matrix (of class `CsparseMatrix`) of dimension  $n \times m$  with diagonal “bands” as specified.

### See Also

`band`, for extraction of matrix bands; `bdiag`, `diag`, `sparseMatrix`, `Matrix`.

### Examples

```
diags <- list(1:30, 10*(1:20), 100*(1:20))
s1 <- bandSparse(13, k = -c(0:2, 6), diag = c(diags, diags[2]), symm=TRUE)
s1
s2 <- bandSparse(13, k = c(0:2, 6), diag = c(diags, diags[2]), symm=TRUE)
stopifnot(identical(s1, t(s2)), is(s1, "dsCMatrix"))

## a pattern Matrix of *full* (sub-)diagonals:
bk <- c(0:4, 7, 9)
(s3 <- bandSparse(30, k = bk, symm = TRUE))

## If you want a pattern matrix, but with "sparse"-diagonals,
## you currently need to go via logical sparse:
lLis <- lapply(list(rpois(20, 2), rpois(20, 1), rpois(20, 3))[c(1:3, 2:3, 3:2)],
              as.logical)
(s4 <- bandSparse(20, k = bk, symm = TRUE, diag = lLis))
(s4. <- as(drop0(s4), "nsparseMatrix"))

n <- 1e4
bk <- c(0:5, 7, 11)
bMat <- matrix(1:8, n, 8, byrow=TRUE)
bLis <- as.data.frame(bMat)
B <- bandSparse(n, k = bk, diag = bLis)
Bs <- bandSparse(n, k = bk, diag = bLis, symmetric=TRUE)
B [1:15, 1:30]
Bs[1:15, 1:30]
## can use a list *or* a matrix for specifying the diagonals:
stopifnot(identical(B, bandSparse(n, k = bk, diag = bMat)),
          identical(Bs, bandSparse(n, k = bk, diag = bMat, symmetric=TRUE)))
```

---

`bdiag`*Construct a Block Diagonal Matrix*

---

**Description**

Build a block diagonal matrix given several building block matrices.

**Usage**

```
bdiag(...)
```

**Arguments**

... individual matrices or a [list](#) of matrices.

**Value**

A *sparse* matrix inheriting from class [CsparseMatrix](#) obtained by combining the arguments into a block diagonal matrix.

**Author(s)**

Martin Maechler, built on a version posted by Berton Gunter to R-help; earlier versions have been posted by other authors, notably Scott Chasalow to S-news. Doug Bates's faster implementation builds on [TsparseMatrix](#) objects.

**See Also**

[Diagonal](#) for constructing matrices of class [diagonalMatrix](#), or [kronecker](#) which also works for "Matrix" inheriting matrices.

[bandSparse](#) constructs a *banded* sparse matrix from its non-zero sub-/super - diagonals.

Note that other CRAN R packages have own versions of `bdiag()` which return traditional matrices.

**Examples**

```
bdiag(matrix(1:4, 2), diag(3))
## combine "Matrix" class and traditional matrices:
bdiag(Diagonal(2), matrix(1:3, 3,4), diag(3:2))

m1ist <- list(1, 2:3, diag(x=5:3), 27, cbind(1,3:6), 100:101)
bdiag(m1ist)

stopifnot(identical(bdiag(m1ist),
                    bdiag(lapply(m1ist, as.matrix))))
```

---

 BunchKaufman-methods

*Bunch-Kaufman Decomposition Methods*


---

**Description**

The Bunch-Kaufman Decomposition of a square symmetric matrix  $A$  is  $A = PLDL'P'$  where  $P$  is a permutation matrix,  $L$  is *unit*-lower triangular and  $D$  is *block*-diagonal with blocks of dimension  $1 \times 1$  or  $2 \times 2$ .

**Usage**

```
BunchKaufman(x, ...)
```

**Arguments**

`x`                    a symmetric square matrix.  
`...`                potentially further arguments passed to methods.

**Methods**

Currently, only methods for **dense** numeric symmetric matrices are implemented.

```
x = "dspMatrix" ...
```

```
x = "dsyMatrix" ...
```

These rely on the Lapack routines `dsptrf` and `dsytrf`, respectively.

**See Also**

The resulting class, [BunchKaufman](#). Related decompositions are the LU, [lu](#), and the Cholesky, [chol](#) (and for *sparse* matrices, [Cholesky](#)).

**Examples**

```
data(CAex)
dim(CAex)
isSymmetric(CAex) # TRUE
CAs <- as(CAex, "symmetricMatrix")
if(FALSE) # no method defined yet for *sparse* :
  bk. <- BunchKaufman(CAs)
## does apply to *dense* symmetric matrices:
bkCA <- BunchKaufman(as(CAs, "denseMatrix"))
bkCA
```

CAex

*Albers' example Matrix with "Difficult" Eigen Factorization***Description**

An example of a sparse matrix for which `eigen()` seemed to be difficult, an unscaled version of this has been posted to the web, accompanying an E-mail to R-help (<https://stat.ethz.ch/mailman/listinfo/r-help>), by Casper J Albers, Open University, UK.

**Usage**

```
data(CAex)
```

**Format**

This is a  $72 \times 72$  symmetric matrix with 216 non-zero entries in five bands, stored as sparse matrix of class `dgCMatrix`.

**Details**

In some versions of R, `eigen(CAex)` fell into an infinite loop (whereas `eigen(CAex, EISPACK=TRUE)` has been okay).

**Examples**

```
data(CAex)
str(CAex) # of class "dgCMatrix"

image(CAex) # -> it's a simple band matrix with 5 bands
## and the eigen values are basically 1 (42 times) and 0 (30 x):
zapsmall(ev <- eigen(CAex, EISPACK=TRUE, only.values=TRUE)$values)
## i.e., the matrix is symmetric, hence
sCA <- as(CAex, "symmetricMatrix")
## and
stopifnot(class(sCA) == "dsCMatrix",
           as(sCA, "matrix") == as(CAex, "matrix"))
```

cBind

*Versions of 'cbind' and 'rbind' recursively built on cbind2/rbind2***Description**

The base functions `cbind` and `rbind` are defined for an arbitrary number of arguments and hence have the first formal argument `...`. For that reason, S4 methods cannot easily be defined for binding together matrices inheriting from `Matrix`.

For that reason, `cbind2` and `rbind2` have been provided for binding together *two* matrices, and we have defined methods for these and the `'Matrix'`-matrices.

As a substitute for *S4-enabled* versions of `cbind` and `rbind`, you can use `cBind` and `rBind` with identical syntax and semantic in order to bind together multiple matrices (`"matrix"` or `"Matrix"`) and vectors.

**Usage**

```
cBind(..., deparse.level = 1)
rBind(..., deparse.level = 1)
```

**Arguments**

`...` matrix-like R objects to be bound together, see [cbind](#) and [rbind](#).  
`deparse.level` integer determining under which circumstances column and row names are built from the actual arguments' 'expression', see [cbind](#).

**Details**

The implementation of these is *recursive*, calling [cbind2](#) or [rbind2](#) respectively, where these have methods defined and so should dispatch appropriately.

**Value**

typically a 'matrix-like' object of a similar [class](#) as the first argument in `...`

**Author(s)**

Martin Maechler

**See Also**

[cbind2](#), [cbind](#), [Methods](#).

**Examples**

```
(a <- matrix(c(2:1,1:2), 2,2))
cbind(0, rBind(a, 7)) # remains traditional matrix

D <- Diagonal(2)
cBind(4, a, D, -1, D, 0) # a sparse Matrix
```

---

CHMfactor-class      *CHOLMOD-based Cholesky Factorizations*

---

**Description**

The virtual class "CHMfactor" is a class of CHOLMOD-based Cholesky factorizations of symmetric, sparse, compressed, column-oriented matrices. Such a factorization is simplicial (virtual class "CHMsimpl") or supernodal (virtual class "CHMsuper"). Objects that inherit from these classes are either numeric factorizations (classes "dCHMsimpl" and "dCHMsuper") or symbolic factorizations (classes "nCHMsimpl" and "nCHMsuper").

**Usage**

```
## S4 method for signature 'CHMfactor':
update(object, parent, mult = 0, ...)
isLDL(x)
```



**Arguments**

<code>object, x</code>	a "CHMfactor" object.
<code>parent</code>	a "dsCMatrix" matrix or "dgCMatrix" object with the same nonzero pattern as the matrix that generated <code>object</code> . If <code>parent</code> is a symmetric matrix (class "dsCMatrix") then <code>object</code> should be a decomposition of a matrix with the same nonzero pattern as <code>parent</code> . If <code>parent</code> is not symmetric then <code>object</code> should be the decomposition of a matrix with the same nonzero pattern as <code>tcrossprod(parent)</code> .
<code>mult</code>	a numeric scalar (default 0). <code>mult</code> times the identity matrix is (implicitly) added to <code>parent</code> or <code>tcrossprod(parent)</code> before updating the decomposition <code>object</code> .
<code>...</code>	Optional additional arguments to the methods.

**Objects from the Class**

Objects can be created by calls of the form `new("dCHMsuper", ...)` but are more commonly created via `Cholesky()`, applied to `dsCMatrix` or `lsCMatrix` objects.

**Slots**

of "CHMfactor" and all classes inheriting from it:

`perm`: An integer vector giving the 0-based permutation of the rows and columns chosen to reduce fill-in and for post-ordering.

`colcount`: Object of class "integer" ....

`type`: Object of class "integer" ....

Slots of the non virtual classes "[dl]CHM(superlsimpl)":

`p`: Object of class "integer" of pointers, one for each column, to the initial (zero-based) index of elements in the column. Only present in classes that contain "CHMsimpl".

`i`: Object of class "integer" of length `nnzero` (number of non-zero elements). These are the row numbers for each non-zero element in the matrix. Only present in classes that contain "CHMsimpl".

`x`: For the "d\*" classes: "numeric" - the non-zero elements of the matrix.

**Methods**

**isLDL** (`x`) returns a `logical` indicating if `x` is an  $LDL'$  decomposition or (when `FALSE`) an  $LL'$  one.

**coerce** `signature(from = "CHMfactor", to = "sparseMatrix")` Returns the lower triangular factor  $L$  from the  $LL'$  form of the Cholesky factorization. Note that (currently) the factor from the  $LL'$  form is always returned, even if the "CHMfactor" object represents an  $LDL'$  decomposition. Furthermore, this is the factor after any fill-reducing permutation has been applied. See the `expand` method for obtaining both the permutation matrix,  $P$ , and the lower Cholesky factor,  $L$ .

**coerce** `signature(from = "CHMfactor", to = "pMatrix")` Returns the permutation matrix,  $P$ , representing the fill-reducing permutation used in the decomposition.

- expand** signature(`x = "CHMfactor"`) Returns a list with components `P`, the matrix representing the fill-reducing permutation, and `L`, the lower triangular Cholesky factor. The original positive-definite matrix corresponds to the product  $P'LL'P$ . Because of fill-in during the decomposition the product may apparently have more non-zeros than the original matrix, even after applying `drop0` to it. However, the extra "non-zeros" should be very small in magnitude.
- image** signature(`x = "CHMfactor"`) Plot the image of the lower triangular factor, `L`, from the decomposition. This method is equivalent to `image(as(x, "sparseMatrix"))` so the comments in the above description of the `coerce` method apply here too.
- solve** signature(`a = "CHMfactor"`, `b = "ddenseMatrix"`) The `solve` methods for a "CHMfactor" object take an optional third argument `system` whose value can be one of the character strings "A", "LDLt", "LD", "DLt", "L", "Lt", "D", "P" or "Pt". This argument describes the system to be solved. The default, "A", is to solve  $Ax = b$  for  $x$  where  $A$  is sparse, positive-definite matrix that was factored to produce `a`. Analogously, `system = "L"` returns the solution  $x$ , of  $Lx = b$ ; similarly, for all system codes but "P" and "Pt" where, e.g., `x <- solve(a, b, system="P")` is equivalent to `x <- P %*% b`.
- solve** signature(`a = "CHMfactor"`, `b = "matrix"`), and
- solve** signature(`a = "CHMfactor"`, `b = "numeric"`) call the above signature(`*`, `b = "ddenseMatrix"`) method.
- solve** signature(`a = "CHMfactor"`, `b = "dsparseMatrix"`) takes the same third argument `system` and calls the corresponding sparse CHOLMOD algorithm.
- determinant** signature(`x = "CHMfactor"`, `logarithm = "logical"`) returns the determinant (or the logarithm of the determinant, if `logarithm = TRUE`, the default) of the factor `L` from the  $LL'$  decomposition (even if the decomposition represented by `x` is of the  $LDL'$  form (!)). This is the square root of the determinant (half the logarithm of the determinant when `logarithm = TRUE`) of the positive-definite matrix that was decomposed.
- update** signature(`object = "CHMfactor"`). The `update` method requires an additional argument `parent`, which is a "dsCMatrix" object with the same structure of nonzeros as the matrix that was decomposed to produce `object`, and provides an optional argument `mult`, a numeric scalar. This method updates the numeric values in `object` to the decomposition of  $A + mI$  where  $A$  is the matrix represented by `parent` and  $m$  is the scalar `mult`. Because only the numeric values are updated this method should be faster than creating and decomposing  $A + mI$ . It is not uncommon to want, say, the determinant of  $A + mI$  for many different values of  $m$ . This method would be the preferred approach in such cases.

## See Also

[Cholesky](#), also for examples; class [dgCMatrix](#).

## Examples

```
## An example for the expand() method
n <- 1000; m <- 200; nnz <- 2000
set.seed(1)
M1 <- spMatrix(n, m,
               i = sample(n, nnz, replace = TRUE),
               j = sample(m, nnz, replace = TRUE),
               x = round(rnorm(nnz), 1))
XX <- crossprod(M1)
CX <- Cholesky(XX)
isLDL(CX)
str(CX) ## a "dCHMsimpl" object
```

```

r <- expand(CX)
L.P <- with(r, crossprod(L,P)) ## == L'P
PLLP <- crossprod(L.P)      ## == (L'P)' L'P == P'LL'P
b <- sample(m)
stopifnot(all.equal(PLLP, XX),
          all(as.vector(solve(CX, b, system="P" )) == r$P %*% b),
          all(as.vector(solve(CX, b, system="Pt")) == t(r$P) %*% b) )

## [ See help(Cholesky) for more examples ]

```

---

chol

*Choleski Decomposition - 'Matrix' S4 Generic*


---

### Description

Compute the Choleski factorization of a real symmetric positive-definite square matrix.

### Usage

```

chol(x, ...)
## S4 method for signature 'dsCMatrix':
chol(x, pivot = FALSE, ...)

```

### Arguments

<code>x</code>	a (sparse or dense) square matrix, here inheriting from class <code>Matrix</code> ; if <code>x</code> is not positive definite, an error is signalled.
<code>pivot</code>	logical indicating if pivoting is used.
<code>...</code>	potentially further arguments passed to methods.

### Value

a matrix of class `Cholesky`, i.e., upper triangular:  $RR' = x$ .

### Methods

Use `showMethods(chol)` to see all; some are worth mentioning here:

- chol** signature(`x = "dgeMatrix"`): works via `"dpoMatrix"`, see class `dpoMatrix`.
- chol** signature(`x = "dpoMatrix"`): Returns (and stores) the Cholesky decomposition of `x`, via LAPACK routines `dlacpy` and `dpotrf`.
- chol** signature(`x = "dppMatrix"`): Returns (and stores) the Cholesky decomposition via LAPACK routine `dpptrf`.
- chol** signature(`x = "dsCMatrix"`, `pivot = "logical"`): Returns (and stores) the Cholesky decomposition of `x`. If `pivot` is `TRUE` (the default) the Approximate Minimal Degree (AMD) algorithm is used to create a reordering of the rows and columns of `x` so as to reduce fill-in.

## References

Timothy A. Davis (2006) *Direct Methods for Sparse Linear Systems*, SIAM Series “Fundamentals of Algorithms”.

Tim Davis (1996), An approximate minimal degree ordering algorithm, *SIAM J. Matrix Analysis and Applications*, **17**, 4, 886–905.

## See Also

The default from **base**, [chol](#).

## Examples

```
showMethods(chol, inherited = FALSE) # show different methods

sy2 <- new("dsyMatrix", Dim = as.integer(c(2,2)), x = c(14, NA, 32, 77))
(c2 <- chol(sy2))#-> "Cholesky" matrix
stopifnot(all.equal(c2, chol(as(sy2, "dpoMatrix")), tol= 1e-13))
str(c2)

## An example where chol() can't work
(sy3 <- new("dsyMatrix", Dim = as.integer(c(2,2)), x = c(14, -1, 2, -7)))
try(chol(sy3)) # error, since it is not positive definite
```

---

chol2inv-methods     *Inverse from Choleski or QR Decomposition – Matrix Methods*

---

## Description

Invert a symmetric, positive definite square matrix from its Choleski decomposition. Equivalently, compute  $(X'X)^{-1}$  from the ( $R$  part) of the QR decomposition of  $X$ .

Even more generally, given an upper triangular matrix  $R$ , compute  $(R'R)^{-1}$ .

## Methods

**x = "ANY"** the default method from **base**, see [chol2inv](#), for traditional matrices.

**x = "dtrMatrix"** method for the numeric triangular matrices, built on the same LAPACK DPOTRI function as the base method.

**x = "denseMatrix"** if  $x$  is coercable to a [triangularMatrix](#), call the "dtrMatrix" method above.

**x = "sparseMatrix"** if  $x$  is coercable to a [triangularMatrix](#), use [solve\(\)](#) currently.

## See Also

[chol](#) (for [Matrix](#) objects); further, [chol2inv](#) (from the **base** package), [solve](#).

## Examples

```
(M <- Matrix(cbind(1, 1:3, c(1,3,7))))
(cM <- chol(M)) # a "Cholesky" object, inheriting from "dtrMatrix"
chol2inv(cM) %**% M # the identity
stopifnot(all(chol2inv(cM) %**% M - Diagonal(nrow(M))) < 1e-10)
```

**Description**

Computes the Cholesky decomposition of a sparse, symmetric, positive-definite matrix. However, typically `chol()` should rather be used unless you are interested in the different kinds of sparse Cholesky decompositions.

**Usage**

```
Cholesky(A, perm = TRUE, LDL = !super, super = FALSE, Imult = 0, ...)
```

**Arguments**

A	sparse symmetric matrix. No missing values or IEEE special values are allowed.
perm	logical scalar indicating if a fill-reducing permutation should be computed and applied to the rows and columns of A. Default is TRUE.
LDL	logical scalar indicating if the decomposition should be computed as LDL' where L is a unit lower triangular matrix. The alternative is LL' where L is lower triangular with arbitrary diagonal elements. Default is TRUE. Setting it to NA leaves the choice to a CHOLMOD-internal heuristic.
super	logical scalar indicating if a supernodal decomposition should be created. The alternative is a simplicial decomposition. Default is FALSE. Setting it to NA leaves the choice to a CHOLMOD-internal heuristic.
Imult	numeric scalar which defaults to zero. The matrix that is decomposed is $A+m*I$ where $m$ is the value of Imult and I is the identity matrix of order <code>ncol(A)</code> .
...	further arguments passed to or from other methods.

**Details**

This is a generic function with special methods for different types of matrices. Use `showMethods("Cholesky")` to list all the methods for the `Cholesky` generic.

The method for class `dsCMatrix` of sparse matrices — the only one available currently — is based on functions from the CHOLMOD library.

Again: If you just want the Cholesky decomposition of a matrix, you should probably rather use `chol(.)`.

**Value**

an object inheriting from either `"CHMsuper"`, or `"CHMsimpl"`, depending on the `super` argument; both classes extend `"CHMfactor"` which extends `"MatrixFactorization"`.

In other words, the result of `Cholesky()` is *not* a matrix, and if you want one, you should probably rather use `chol(.)`.

## References

Tim Davis (2005) *CHOLMOD: sparse supernodal Cholesky factorization and update/downdate*  
<http://www.cise.ufl.edu/research/sparse/cholmod/>

Timothy A. Davis (2006) *Direct Methods for Sparse Linear Systems*, SIAM Series “Fundamentals of Algorithms”.

## See Also

Class definitions `CHMfactor` and `dsCMatrix` and function `expand`. Note the extra `solve(*, system = . )` options in `CHMfactor`.

Note that `chol()` returns matrices (inheriting from "`Matrix`") whereas `Cholesky()` returns a "`CHMfactor`" object, and hence a typical user will rather use `chol(A)`.

## Examples

```
data(KNex)
mtm <- with(KNex, crossprod(mm))
str(mtm@factors) # empty list()
(C1 <- Cholesky(mtm)) # uses show(<MatrixFactorization>)
str(mtm@factors) # 'SPDCholesky' (simpl)
(Cm <- Cholesky(mtm, super = TRUE))
c(C1 = isLDL(C1), Cm = isLDL(Cm))
str(mtm@factors) # 'SPDCholesky' *and* 'SPdCholesky'
str(cml <- as(C1, "sparseMatrix"))
str(cmat <- as(Cm, "sparseMatrix")) # hmm: super is *less* sparse here
cml[1:20, 1:20]

b <- matrix(c(rep(0, 711), 1), nc = 1)
## solve(Cm, b) by default solves Ax = b, where A = Cm'Cm !
## hence, the identical() check *should* work, but fails on some GOTOblas:
x <- solve(Cm, b)
stopifnot(identical(x, solve(Cm, b, system = "A")),
           all.equal(x, solve(mtm, b)))

Cn <- Cholesky(mtm, perm = FALSE) # no permutation -- much worse:
sizes <- c(simple = object.size(C1),
           super = object.size(Cm),
           noPerm = object.size(Cn))
format(cbind(100 * sizes / sizes[1]), digits=4)

## Visualize the sparseness:
dq <- function(ch) paste('"' , ch, '"' , sep="") ## dQuote(<UTF-8>) gives bad plots
image(mtm, main=paste("crossprod(mm) : Sparse", dq(class(mtm))))
image(cml, main= paste("as(Cholesky(crossprod(mm)), \"sparseMatrix\") : ",
                      dq(class(cml))))
```

## Description

The "Cholesky" class is the class of Cholesky decompositions of positive-semidefinite, real dense matrices. The "BunchKaufman" class is the class of Bunch-Kaufman decompositions of symmetric, real matrices. The "pCholesky" and "pBunchKaufman" classes are their *packed* storage versions.

## Objects from the Class

Objects can be created by calls of the form `new("Cholesky", ...)` or `new("BunchKaufman", ...)`, etc, or rather by calls of the form `chol(pm)` or `BunchKaufman(pm)` where `pm` inherits from the "dpoMatrix" or "dsyMatrix" class or as a side-effect of other functions applied to "dpoMatrix" objects (see `dpoMatrix`).

## Slots

A Cholesky decomposition extends class `MatrixFactorization` but is basically a triangular matrix extending the "dtrMatrix" class.

`uplo`: inherited from the "dtrMatrix" class.

`diag`: inherited from the "dtrMatrix" class.

`x`: inherited from the "dtrMatrix" class.

`Dim`: inherited from the "dtrMatrix" class.

`Dimnames`: inherited from the "dtrMatrix" class.

A Bunch-Kaufman decomposition also extends the "dtrMatrix" class and has a `perm` slot representing a permutation matrix. The packed versions extend the "dtpMatrix" class.

## Extends

Class "MatrixFactorization" and "dtrMatrix", directly. Class "dgeMatrix", by class "dtrMatrix". Class "Matrix", by class "dtrMatrix".

## Methods

There are currently no methods defined with class "Cholesky" in the signature. Of course methods for "dtrMatrix" or "MatrixFactorization" do apply.

## Note

1. Objects of class "Cholesky" typically stem from `chol(D)`, applied to a *dense* matrix `D`. On the other hand, the *function* `Cholesky(S)` applies to a *sparse* matrix `S`, and results in objects inheriting from class `CHMfactor`.
2. For traditional matrices `m`, `chol(m)` is a traditional matrix as well, triangular, but simply an  $n \times n$  numeric *matrix*. Hence, for compatibility, the "Cholesky" and "BunchKaufman" classes (and their "p\*" packed versions) also extend triangular Matrix classes (such as "dtrMatrix").

Consequently, `determinant(R)` for `R <- chol(A)` returns the determinant of `R`, not of `A`. This is in contrast to class `CHMfactor` objects `C`, where `determinant(C)` gives the determinant of the *original* matrix `A`, for `C <- Cholesky(A)`, see also the determinant method documentation on the class `CHMfactor` page.

**See Also**

Classes [dtrMatrix](#), [dpoMatrix](#); function [chol](#).

Function [Cholesky](#) resulting in class [CHMfactor](#) objects, *not* class "Cholesky" ones, see the section 'Note'.

**Examples**

```
(sm <- as(as(Matrix(diag(5) + 1), "dsyMatrix"), "dspMatrix"))
signif(csm <- chol(sm), 4)

(pm <- crossprod(Matrix(rnorm(18), nrow = 6, ncol = 3)))
(ch <- chol(pm))
if (toupper(ch@uplo) == "U") # which is TRUE
  crossprod(ch)
stopifnot(all.equal(as(crossprod(ch), "matrix"),
                    as(pm, "matrix"), tol=1e-14))
```

colSums

*Form Row and Column Sums and Means***Description**

Form row and column sums and means for [Matrix](#) objects.

**Usage**

```
colSums(x, na.rm = FALSE, dims = 1, ...)
rowSums(x, na.rm = FALSE, dims = 1, ...)
colMeans(x, na.rm = FALSE, dims = 1, ...)
rowMeans(x, na.rm = FALSE, dims = 1, ...)

## S4 method for signature 'CsparseMatrix':
colSums(x, na.rm = FALSE,
        dims = 1, sparseResult = FALSE)
## S4 method for signature 'CsparseMatrix':
rowSums(x, na.rm = FALSE,
        dims = 1, sparseResult = FALSE)
## S4 method for signature 'CsparseMatrix':
colMeans(x, na.rm = FALSE,
         dims = 1, sparseResult = FALSE)
## S4 method for signature 'CsparseMatrix':
rowMeans(x, na.rm = FALSE,
         dims = 1, sparseResult = FALSE)
```

**Arguments**

<code>x</code>	a <a href="#">Matrix</a> , i.e., inheriting from <a href="#">Matrix</a> .
<code>na.rm</code>	logical. Should missing values (including <code>NaN</code> ) be omitted from the calculations?
<code>dims</code>	completely ignored by the <a href="#">Matrix</a> methods.
<code>...</code>	potentially further arguments, for method <code>&lt;-&gt;</code> generic compatibility.



`sparseResult` logical indicating if the result should be sparse, i.e., inheriting from class `sparseVector`.

### Value

returns a numeric vector if `sparseResult` is FALSE as per default. Otherwise, returns a `sparseVector`.

### See Also

`colSums` and the `sparseVector` classes.

### Examples

```
(M <- bdiag(Diagonal(2), matrix(1:3, 3,4), diag(3:2))) # 7 x 8
colSums(M)
d <- Diagonal(10, c(0,0,10,0,2,rep(0,5)))
MM <- kronecker(d, M)
dim(MM) # 70 80
length(MM@x) # 160, but many are '0' ; drop those:
MM <- drop0(MM)
length(MM@x) # 32
cm <- colSums(MM)
(scm <- colSums(MM, sparseResult = TRUE))
stopifnot(is(scm, "sparseVector"),
           identical(cm, as.numeric(scm)))
rowSums(MM, sparseResult = TRUE) # 16 of 70 are not zero
colMeans(MM, sparseResult = TRUE)
## Since we have no 'NA's, these two are equivalent :
stopifnot(identical(rowMeans(MM, sparseResult = TRUE),
                    rowMeans(MM, sparseResult = TRUE, na.rm = TRUE)),
           rowMeans(Diagonal(16)) == 1/16,
           colSums(Diagonal(7)) == 1)
```

---

compMatrix-class    *Class "compMatrix" of Composite (Factorizable) Matrices*

---

### Description

Virtual class of *composite* matrices; i.e., matrices that can be *factorized*, typically as a product of simpler matrices.

### Objects from the Class

A virtual Class: No objects may be created from it.

### Slots

**factors:** Object of class "list" - a list of factorizations of the matrix. Note that this is typically empty, i.e. `list()`, initially and is updated automatically whenever a matrix factorization is computed.

**Dim,**

**Dimnames:** inherited from the `Matrix` class, see there.

**Extends**

Class "Matrix", directly.

---

condest	<i>Compute Approximate CONDition number and 1-Norm of (Large) Matrices</i>
---------	--

---

**Description**

“Estimate”, i.e. compute approximately the CONDition number of a (potentially large, often sparse) matrix  $A$ . It works by apply a fast approximation of the 1-norm, `norm(A, "1")`, through `onenormest(.)`.

**Usage**

```
condest(A, t = min(n, 5), normA = norm(A, "1"),
        silent = FALSE, quiet = TRUE)

onenormest(A, t = min(n, 5), A.x, At.x, n,
           silent = FALSE, quiet = silent,
           iter.max = 10, eps = 4 * .Machine$double.eps)
```

**Arguments**

A	a square matrix, optional for <code>onenormest()</code> , where instead of $A$ , $A.x$ and $At.x$ can be specified, see there.
t	number of columns to use in the iterations.
normA	number; (an estimate of) the 1-norm of $A$ , by default <code>norm(A, "1")</code> ; may be replaced by an estimate.
silent	logical indicating if warning and (by default) convergence messages should be displayed.
quiet	logical indicating if convergence messages should be displayed.
A.x, At.x	when $A$ is missing, these two must be given as functions which compute $A \% \% x$ , or $t(A) \% \% x$ , respectively.
n	<code>== nrow(A)</code> , only needed when $A$ is not specified.
iter.max	maximal number of iterations for the 1-norm estimator.
eps	the relative change that is deemed irrelevant.

**Value**

Both functions return a `list`; `onenormest()` with components,

est	a number $> 0$ , the estimated <code>norm(A, "1")</code> .
v	the maximal $AX$ column.

The function `condest()` returns a list with components,

est	a number $> 0$ , the estimated condition number $\hat{\kappa}$ ; when $r := rcond(A)$ , $1/\hat{\kappa} \approx r$ .
-----	--

<code>v</code>	integer vector length $n$ , with an 1 at the index $j$ with maximal column $A[, j]$ in $A$ .
<code>w</code>	numeric vector, the largest $Ax$ found.
<code>iter</code>	the number of iterations used.

**Author(s)**

This is based on octave's `condest()` and `onenormest()` implementations with original author Jason Riedy, U Berkeley; translation to R and adaption by Martin Maechler.

**References**

Nicholas J. Higham and Françoise Tisseur (2000). A Block Algorithm for Matrix 1-Norm Estimation, with an Application to 1-Norm Pseudospectra. *SIAM J. Matrix Anal. Appl.* **21**, 4, 1185–1201. <http://dx.doi.org/10.1137/S0895479899356080>

William W. Hager (1984). Condition Estimates. *SIAM J. Sci. Stat. Comput.* **5**, 311–316.

**See Also**

[norm](#), [rcond](#).

**Examples**

```
data(KNex)
mtm <- with(KNex, crossprod(mm))
system.time(ce <- condest(mtm))
## reciprocal
1 / ce$est
system.time(rc <- rcond(mtm)) # takes ca 3 x longer
rc
all.equal(rc, 1/ce$est) # TRUE -- the approximation was good
```

---

contrast

*Contrast Matrices, Optionally Sparse*

---

**Description**

Return a matrix of contrasts.

This help file for package **Matrix** is only needed for R versions < 2.10.0.

**Usage**

```
contr.helmert(n, contrasts = TRUE, sparse = FALSE)
contr.poly(n, scores = 1:n, contrasts = TRUE, sparse = FALSE)
contr.sum(n, contrasts = TRUE, sparse = FALSE)
contr.treatment(n, base = 1, contrasts = TRUE, sparse = FALSE)
contr.SAS(n, contrasts = TRUE, sparse = FALSE)
```

**Arguments**

<code>n</code>	a vector of levels for a factor, or the number of levels.
<code>contrasts</code>	a logical indicating whether contrasts should be computed.
<code>sparse</code>	logical indicating if the result should be sparse, using <a href="#">Matrix</a> from package <b>Matrix</b> .
<code>scores</code>	the set of values over which orthogonal polynomials are to be computed.
<code>base</code>	an integer specifying which group is considered the baseline group. Ignored if <code>contrasts</code> is <code>FALSE</code> .

**Details**

These functions are used for creating contrast matrices for use in fitting analysis of variance and regression models. The columns of the resulting matrices contain contrasts which can be used for coding a factor with `n` levels. The returned value contains the computed contrasts. If the argument `contrasts` is `FALSE` a square indicator matrix (the dummy coding) is returned **except** for `contr.poly` (which include the 0-degree, i.e. constant, polynomial when `contrasts = FALSE`).

`contr.helmert` returns Helmert contrasts, which contrast the second level with the first, the third with the average of the first two, and so on. `contr.poly` returns contrasts based on orthogonal polynomials. `contr.sum` uses 'sum to zero contrasts'.

`contr.treatment` contrasts each level with the baseline level (specified by `base`): the baseline level is omitted. Note that this does not produce 'contrasts' as defined in the standard theory for linear models as they are not orthogonal to the intercept.

`contr.SAS` is a wrapper for `contr.treatment` that sets the base level to be the last level of the factor. The coefficients produced when using these contrasts should be equivalent to those produced by many (but not all) SAS procedures.

For consistency, `sparse` is an argument to all contrast functions, however `sparse = TRUE` for `contr.poly` is nonsense (and hence an error), and also is rarely sensible for `contr.helmert`.

**Value**

A matrix with `n` rows and `k` columns, with `k=n-1` if `contrasts` is `TRUE` and `k=n` if `contrasts` is `FALSE`.

**References**

Chambers, J. M. and Hastie, T. J. (1992) *Statistical models*. Chapter 2 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

[contrasts](#), [C](#), and [aov](#), [glm](#), [lm](#).

**Examples**

```
(cH <- contr.helmert(4))
apply(cH, 2, sum) # column sums are 0!
crossprod(cH) # diagonal -- columns are orthogonal
contr.helmert(4, contrasts = FALSE) # just the 4 x 4 identity matrix

(cT <- contr.treatment(5))
```

```

all(crossprod(cT) == diag(4)) # TRUE: even orthonormal

cT. <- contr.SAS(5)
all(crossprod(cT.) == diag(4)) # TRUE
(cS. <- contr.SAS(5, sparse = TRUE))
all(cT. == cS.)

(cP <- contr.poly(3)) # Linear and Quadratic
zapsmall(crossprod(cP), digits=15) # orthonormal up to fuzz

```

---

CsparseMatrix-class

*Class "CsparseMatrix" of Sparse Matrices in Column-compressed Form*

---

### Description

The "CsparseMatrix" class is the virtual class of all sparse matrices coded in sorted compressed column-oriented form. Since it is a virtual class, no objects may be created from it. See `showClass("CsparseMatrix")` for its subclasses.

### Slots

- i:** Object of class "integer" of length `nnzero` (number of non-zero elements). These are the *0-based* row numbers for each non-zero element in the matrix, i.e., `i` must be in `0:(nrow(.) - 1)`.
- p:** Object of class "integer" for providing pointers, one for each column, to the initial (zero-based) index of elements in the column. `.@p` is of length `ncol(.) + 1`, with `p[1] == 0` and `p[length(p)] == nnzero`, such that in fact, `diff(.@p)` are the number of non-zero elements for each column.

**Dim, Dimnames:** inherited from the superclass, see the [sparseMatrix](#) class.

### Extends

Class "sparseMatrix", directly. Class "Matrix", by class "sparseMatrix".

### Methods

```

Arith signature(e1 = "CsparseMatrix", e2 = "numeric"):...
Arith signature(e1 = "numeric", e2 = "CsparseMatrix"):...
Math signature(x = "CsparseMatrix"):...
band signature(x = "CsparseMatrix"):...
- signature(e1 = "CsparseMatrix", e2 = "numeric"):...
- signature(e1 = "numeric", e2 = "CsparseMatrix"):...
[<- signature(x = "CsparseMatrix", i = "index", j = "missing",
  value = "replValue"):...
[<- signature(x = "CsparseMatrix", i = "index", j = "index", value
  = "replValue"):...

```

```

[<- signature(x = "CsparseMatrix", i = "missing", j = "index",
  value = "replValue"):...
%% signature(x = "CsparseMatrix", y = "CsparseMatrix"):...
%% signature(x = "CsparseMatrix", y = "denseMatrix"):...
%% signature(x = "CsparseMatrix", y = "matrix"):...
+ signature(e1 = "CsparseMatrix", e2 = "numeric"):...
+ signature(e1 = "numeric", e2 = "CsparseMatrix"):...
coerce signature(from = "CsparseMatrix", to = "TsparseMatrix"):...
coerce signature(from = "CsparseMatrix", to = "denseMatrix"):...
coerce signature(from = "CsparseMatrix", to = "matrix"):...
coerce signature(from = "CsparseMatrix", to = "lsparseMatrix"):...
coerce signature(from = "CsparseMatrix", to = "nsparseMatrix"):...
coerce signature(from = "TsparseMatrix", to = "CsparseMatrix"):...
coerce signature(from = "denseMatrix", to = "CsparseMatrix"):...
crossprod signature(x = "CsparseMatrix", y = "CsparseMatrix"):...
crossprod signature(x = "CsparseMatrix", y = "missing"):...
crossprod signature(x = "CsparseMatrix", y = "dgeMatrix"):...
crossprod signature(x = "CsparseMatrix", y = "matrix"):...
diag signature(x = "CsparseMatrix"):...
gamma signature(x = "CsparseMatrix"):...
lgamma signature(x = "CsparseMatrix"):...
log signature(x = "CsparseMatrix"):...
t signature(x = "CsparseMatrix"):...
tcrossprod signature(x = "CsparseMatrix", y = "CsparseMatrix"):...
tcrossprod signature(x = "CsparseMatrix", y = "missing"):...
tril signature(x = "CsparseMatrix"):...
triu signature(x = "CsparseMatrix"):...

```

### Note

All classes extending `CsparseMatrix` have a common validity (see `validObject`) check function. That function additionally checks the `i` slot for each column to contain increasing row numbers.

In earlier versions of **Matrix** ( $\leq 0.999375-16$ ), `validObject` automatically re-sorted the entries when necessary, and hence `new()` calls with somewhat permuted `i` and `x` slots worked, as `new(...)` (*with* slot arguments) automatically checks the validity.

Now, you have to use `sparseMatrix` to achieve the same functionality or know how to use `.validateCsparse()` to do so.

### See Also

`colSums`, `kronecker`, and other such methods with own help pages.

Further, the super class of `CsparseMatrix`, `sparseMatrix`, and, e.g., class `dgCMatrix` for the links to other classes.

**Examples**

```

getClass("CsparseMatrix")

## The common validity check function (based on C code):
getValidity(getClass("CsparseMatrix"))

## This behavior has been changed
# un-sorted i-slot on input is automatically "sorted" :
#M <- new("dgCMatrix", Dim = 2:3, p = as.integer(c(0,1,1,3)),
#         i = c(1L, 1:0), x= c(2,2,1))
#stopifnot(M@i == c(1L, 0:1), M@x == c(2,1,2))

```

---

ddenseMatrix-class *Virtual Class "ddenseMatrix" of Numeric Dense Matrices*

---

**Description**

This is the virtual class of all dense numeric (i.e., **double**, hence “*ddense*”) S4 matrices.

Its most important subclass is the [dgeMatrix](#) class.

**Extends**

Class "dMatrix" directly; class "Matrix", by the above.

**Slots**

the same slots at its subclass [dgeMatrix](#), see there.

**Methods**

Most methods are implemented via `as(*, "dgeMatrix")` and are mainly used as “fallbacks” when the subclass doesn’t need its own specialized method.

Use `showMethods(class = "ddenseMatrix", where = "package:Matrix")` for an overview.

**See Also**

The virtual classes [Matrix](#), [dMatrix](#), and [dsparseMatrix](#).

**Examples**

```

showClass("ddenseMatrix")

showMethods(class = "ddenseMatrix", where = "package:Matrix")

```

---

 ddiMatrix-class      *Class "ddiMatrix" of Diagonal Numeric Matrices*


---

### Description

The class "ddiMatrix" of numerical diagonal matrices.

Note that diagonal matrices now extend `sparseMatrix`, whereas they did extend dense matrices earlier.

### Objects from the Class

Objects can be created by calls of the form `new("ddiMatrix", ...)` but typically rather via [Diagonal](#).

### Slots

**x:** numeric vector. For an  $n \times n$  matrix, the x slot is of length  $n$  or 0, depending on the `diag` slot:  
**diag:** "character" string, either "U" or "N" where "U" denotes unit-diagonal, i.e., identity matrices.

**Dim,Dimnames:** matrix dimension and `dimnames`, see the [Matrix](#) class description.

### Extends

Class "[diagonalMatrix](#)", directly. Class "[dMatrix](#)", directly. Class "[sparseMatrix](#)", indirectly, see `showClass("ddiMatrix")`.

### Methods

```
%% signature(x = "ddiMatrix", y = "ddiMatrix"):...
```

### See Also

Class [diagonalMatrix](#) and function [Diagonal](#).

### Examples

```
(d2 <- Diagonal(x = c(10,1)))
str(d2)
## slightly larger in internal size:
str(as(d2, "sparseMatrix"))

M <- Matrix(cbind(1,2:4))
M %*% d2 #> `fast' multiplication

chol(d2) # trivial
stopifnot(is(cd2 <- chol(d2), "ddiMatrix"),
          all.equal(cd2@x, c(sqrt(10),1)))
```



---

denseMatrix-class    *Virtual Class "denseMatrix" of All Dense Matrices*

---

### Description

This is the virtual class of all dense (S4) matrices. It is the direct superclass of [ddenseMatrix](#), [ldenseMatrix](#)

### Extends

class "Matrix" directly.

### Slots

exactly those of its superclass "Matrix".

### Methods

Use [showMethods](#)(class = "denseMatrix", where = "package:Matrix") for an overview of methods.

Extraction ("[") methods, see [\[-methods](#).

### See Also

[colSums](#), [kronecker](#), and other such methods with own help pages.

Its superclass [Matrix](#), and main subclasses, [ddenseMatrix](#) and [sparseMatrix](#).

### Examples

```
showClass("denseMatrix")
```

---

dgCMatrix-class    *Compressed, sparse, column-oriented numeric matrices*

---

### Description

The `dgCMatrix` class is a class of sparse numeric matrices in the compressed, sparse, column-oriented format. In this implementation the non-zero elements in the columns are sorted into increasing row order. `dgCMatrix` is the “*standard*” class for sparse numeric matrices in the **Matrix** package.

### Objects from the Class

Objects can be created by calls of the form `new("dgCMatrix", ...)` or often more easily via `Matrix(*, sparse = TRUE)`.

### Slots

`x`: Object of class "numeric" - the non-zero elements of the matrix.

`...` all other slots are inherited from the superclass "[CsparseMatrix](#)".

**Methods**

**coerce** signature(from = "matrix", to = "dgCMatrix")  
**coerce** signature(from = "dgCMatrix", to = "matrix")  
**coerce** signature(from = "dgCMatrix", to = "dgTMatrix")  
**crossprod** signature(x = "dgCMatrix", y = "missing") returns  $t(x) \%*\% x$  as an `dsCMatrix` object.  
**crossprod** signature(x = "dgCMatrix", y = "matrix"): ...  
**crossprod** signature(x = "dgCMatrix", y = "numeric"): ...  
**diag** signature(x = "dgCMatrix"): returns the diagonal of x  
**dim** signature(x = "dgCMatrix"): returns the dimensions of x  
**image** signature(x = "dgCMatrix"): plots an image of x using the `levelplot` function  
**lu** signature(x = "dgCMatrix"): computes the LU decomposition of a square `dgCMatrix` object

**See Also**

Classes `dsCMatrix`, `dtCMatrix`, `lu`

**Examples**

```
(m <- Matrix(c(0,0,2:0), 3,5))
str(m)
m[,1]
```

---

dgeMatrix-class      *Class "dgeMatrix" of Dense Numeric (S4 Class) Matrices*

---

**Description**

A general numeric dense matrix in the S4 Matrix representation. `dgeMatrix` is the “*standard*” class for dense numeric matrices in the **Matrix** package.

**Objects from the Class**

Objects can be created by calls of the form `new("dgeMatrix", ...)` or, more commonly, by coercion from the `Matrix` class (see `Matrix`) or by `Matrix(...)`.

**Slots**

**x**: Object of class "numeric" - the numeric values contained in the matrix, in column-major order.  
**Dim**: Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.  
**Dimnames**: a list of length two - inherited from class `Matrix`.  
**factors**: Object of class "list" - a list of factorizations of the matrix.

## Methods

The are group methods (see, e.g., [Arith](#))

**Arith** signature(e1 = "dgeMatrix", e2 = "dgeMatrix"):...

**Arith** signature(e1 = "dgeMatrix", e2 = "numeric"):...

**Arith** signature(e1 = "numeric", e2 = "dgeMatrix"):...

**Math** signature(x = "dgeMatrix"):...

**Math2** signature(x = "dgeMatrix", digits = "numeric"):...

and other matrix methods available:

**%\*%** signature(x = "dgeMatrix", y = "dgeMatrix"): **Matrix multiplication**;  
ditto for several other signature combinations, see `showMethods("%*%", class = "dgeMatrix")`.

**Schur** signature(x = "dgeMatrix", vectors = "logical"):...

**Schur** signature(x = "dgeMatrix", vectors = "missing"):...

**chol** signature(x = "dgeMatrix"): see [chol](#).

**coerce** signature(from = "dgeMatrix", to = "lgeMatrix"):...

**coerce** signature(from = "dgeMatrix", to = "matrix"):...

**coerce** signature(from = "matrix", to = "dgeMatrix"):...

**colMeans** signature(x = "dgeMatrix"): columnwise means (averages)

**colSums** signature(x = "dgeMatrix"): columnwise sums

**crossprod** signature(x = "dgeMatrix", y = "dgeMatrix"): ditto for several other signatures, use `showMethods("crossprod", class = "dgeMatrix")`, matrix crossproduct, an efficient version of `t(x) %*% y`.

**diag** signature(x = "dgeMatrix"):...

**dim** signature(x = "dgeMatrix"):...

**dimnames** signature(x = "dgeMatrix"):...

**eigen** signature(x = "dgeMatrix", only.values= "logical"):...

**eigen** signature(x = "dgeMatrix", only.values= "missing"):...

**norm** signature(x = "dgeMatrix", type = "character"):...

**norm** signature(x = "dgeMatrix", type = "missing"):...

**rcond** signature(x = "dgeMatrix", norm = "character"):...

**rcond** signature(x = "dgeMatrix", norm = "missing"):...

**rowMeans** signature(x = "dgeMatrix"): rowwise means (averages)

**rowSums** signature(x = "dgeMatrix"): rowwise sums

**solve** signature(a = "dgeMatrix", b = "dgeMatrix"):...

**solve** signature(a = "dgeMatrix", b = "missing"):...

**t** signature(x = "dgeMatrix"):...

## See Also

Classes [Matrix](#), [dtrMatrix](#), and [dsyMatrix](#).

---

dgRMatrix-class      *Sparse Compressed, Row-oriented Numeric Matrices*

---

## Description

The `dgRMatrix` class is a class of sparse numeric matrices in the compressed, sparse, row-oriented format. In this implementation the non-zero elements in the rows are sorted into increasing column order.

**Note:** Currently, the column-oriented sparse classes, e.g., `dgCMatrix`, are preferred and better supported in the **Matrix** package.

## Objects from the Class

Objects can be created by calls of the form `new("dgRMatrix", ...)`.

## Slots

**j:** Object of class "integer" of length `nnzero` (number of non-zero elements). These are the column numbers for each non-zero element in the matrix.

**p:** Object of class "integer" of pointers, one for each row, to the initial (zero-based) index of elements in the row.

**x:** Object of class "numeric" - the non-zero elements of the matrix.

**Dim:** Object of class "integer" - the dimensions of the matrix.

## Methods

**coerce** signature(`from` = "matrix", `to` = "dgRMatrix")

**coerce** signature(`from` = "dgRMatrix", `to` = "matrix")

**coerce** signature(`from` = "dgRMatrix", `to` = "dgTMatrix")

**diag** signature(`x` = "dgRMatrix"): returns the diagonal of `x`

**dim** signature(`x` = "dgRMatrix"): returns the dimensions of `x`

**image** signature(`x` = "dgRMatrix"): plots an image of `x` using the `levelplot` function

## See Also

the `dgCMatrix` class.

---

 dgTMatrix-class      *Sparse matrices in triplet form*


---

### Description

The "dgTMatrix" class is the class of sparse matrices stored as (possibly redundant) triplets. The internal representation is not at all unique, contrary to the one for class [dgCMatrix](#).

### Objects from the Class

Objects can be created by calls of the form `new("dgTMatrix", ...)`, but more typically via `as(*, "dgTMatrix")`.

### Slots

- i**: Object of class "integer" - the row indices of non-zero entries *in 0-base*, i.e., must be in `0:(nrow(.)-1)`.
- j**: Object of class "integer" - the column indices of non-zero entries. Must be the same length as slot **i** and *0-based* as well, i.e., in `0:(ncol(.)-1)`.
- x**: Object of class "numeric" - the (non-zero) entry at position `(i, j)`. Must be the same length as slot **i**. If an index pair occurs more than once the corresponding values of slot **x** are added to form the element of the matrix.
- Dim**: Object of class "integer" of length 2 - the dimensions of the matrix.

### Methods

- +** signature(`e1 = "dgTMatrix"`, `e2 = "dgTMatrix"`)
- coerce** signature(`from = "dgTMatrix"`, `to = "dgCMatrix"`)
- coerce** signature(`from = "dgTMatrix"`, `to = "dgeMatrix"`)
- coerce** signature(`from = "dgTMatrix"`, `to = "matrix"`), and typically coercion methods for more specific signatures, we are not mentioning here.  
Note that these are not guaranteed to continue to exist, but rather you should use calls like `as(x, "CsparseMatrix")`, `as(x, "generalMatrix")`, `as(x, "dMatrix")`, i.e. coercion to higher level virtual classes.
- coerce** signature(`from = "matrix"`, `to = "dgTMatrix"`), (direct coercion from tradition matrix).
- crossprod** signature(`x = "dgTMatrix"`, `y = "missing"`) returns `t(x) %*% x` as an `dsCMatrix` object.
- crossprod** signature(`x = "dgTMatrix"`, `y = "matrix"`): ...
- crossprod** signature(`x = "dgTMatrix"`, `y = "numeric"`): ...
- image** signature(`x = "dgTMatrix"`): plots an image of `x` using the [levelplot](#) function
- t** signature(`x = "dgTMatrix"`): returns the transpose of `x`

### Note

Triplet matrices are a convenient form in which to construct sparse matrices after which they can be coerced to [dgCMatrix](#) objects.

**See Also**

Class [dgCMatrix](#) or the superclasses [dsparseMatrix](#) and [TsparseMatrix](#);

**Examples**

```
m <- Matrix(0+1:28, nrow = 4)
m[-3,c(2,4:5,7)] <- m[ 3, 1:4] <- m[1:3, 6] <- 0
(mT <- as(m, "dgTMatrix"))
str(mT)
mT[1,]
mT[4, drop = FALSE]
stopifnot(identical(mT[lower.tri(mT)],
                    m [lower.tri(m) ]))
mT[lower.tri(mT,diag=TRUE)] <- 0
mT
```

---

 Diagonal

---

*Create Diagonal Matrix Object*


---

**Description**

Create a diagonal matrix object, i.e., an object inheriting from [diagonalMatrix](#).

**Usage**

```
Diagonal(n, x = NULL)

.symDiagonal(n, x = rep.int(1,n), uplo = "U")
.sparseDiagonal(n, x = rep.int(1,m), uplo = "U",
                shape = if(missing(cols)) "t" else "g",
                kind, cols = if(n) 0:(n - 1L) else integer(0))
```

**Arguments**

<code>n</code>	integer specifying the dimension of the (square) matrix. If missing, <code>length(x)</code> is used.
<code>x</code>	numeric or logical; if missing, a <i>unit</i> diagonal $n \times n$ matrix is created.
<code>uplo</code>	for <code>.symDiagonal</code> , the resulting sparse <a href="#">symmetricMatrix</a> will have slot <code>uplo</code> set from this argument, either "U" or "L". Only rarely will it make sense to change this from the default.
<code>shape</code>	string of 1 character, one of <code>c("t", "s", "g")</code> , to chose a triangular, symmetric or general result matrix.
<code>kind</code>	string of 1 character, one of <code>c("d", "l", "n")</code> , to chose the storage mode of the result, from classes <a href="#">dsparseMatrix</a> , <a href="#">lsparseMatrix</a> , or <a href="#">nsparseMatrix</a> , respectively.
<code>cols</code>	integer vector with values from <code>0:(n-1)</code> , denoting the <i>columns</i> to subselect conceptually, i.e., get the equivalent of <code>Diagonal(n, *)[, cols + 1]</code> .

**Value**

`Diagonal()` returns an object of class `ddiMatrix` or `ldiMatrix` (with “superclass” `diagonalMatrix`).

`.symDiagonal()` returns an object of class `dsCMatrix` or `lsCMatrix`, i.e., a *sparse symmetric* matrix. This can be more efficient than `Diagonal(n)` when the result is combined with further symmetric (sparse) matrices, however *not* for matrix multiplications where `Diagonal()` is clearly preferred.

`.sparseDiagonal()`, the workhorse of `.symDiagonal` returns a `CsparseMatrix` (the resulting class depending on `shape` and `kind`) representation of `Diagonal(n)`, or, when `cols` are specified, of `Diagonal(n)[, cols+1]`.

**Author(s)**

Martin Maechler

**See Also**

the generic function `diag` for *extraction* of the diagonal from a matrix works for all “Matrices”.

`bandSparse` constructs a *banded* sparse matrix from its non-zero sub-/super - diagonals.

`Matrix` for general matrix construction; further, class `diagonalMatrix`.

**Examples**

```
Diagonal(3)
Diagonal(x = 10^(3:1))
Diagonal(x = (1:4) >= 2) #-> "ldiMatrix"

## Use Diagonal() + kronecker() for "repeated-block" matrices:
M1 <- Matrix(0+0:5, 2, 3)
(M <- kronecker(Diagonal(3), M1))

(S <- crossprod(Matrix(rbinom(60, size=1, prob=0.1), 10, 6)))
(SI <- S + 10*.symDiagonal(6)) # sparse symmetric still
stopifnot(is(SI, "dsCMatrix"))
```

---

diagonalMatrix-class

*Class "diagonalMatrix" of Diagonal Matrices*

---

**Description**

Class "diagonalMatrix" is the virtual class of all diagonal matrices.

**Objects from the Class**

A virtual Class: No objects may be created from it.

**Slots**

**diag:** code"character" string, either "U" or "N", where "U" means ‘unit-diagonal’.

**Dim:** matrix dimension, and

**Dimnames:** the `dimnames`, a `list`, see the `Matrix` class description. Typically `list(NULL, NULL)` for diagonal matrices.

**Extends**

Class "`sparseMatrix`", directly.

**Methods**

These are just a subset of the signature for which defined methods. Currently, there are (too) many explicit methods defined in order to ensure efficient methods for diagonal matrices.

**coerce** signature(from = "matrix", to = "diagonalMatrix"):...

**coerce** signature(from = "Matrix", to = "diagonalMatrix"):...

**coerce** signature(from = "diagonalMatrix", to = "generalMatrix"):...

**coerce** signature(from = "diagonalMatrix", to = "triangularMatrix"):...

...

**coerce** signature(from = "diagonalMatrix", to = "nMatrix"):...

**coerce** signature(from = "diagonalMatrix", to = "matrix"):...

**coerce** signature(from = "diagonalMatrix", to = "sparseVector"):...

**t** signature(x = "diagonalMatrix"):...

**%\*%** signature(x = "dgeMatrix", y = "diagonalMatrix"):...

**%\*%** signature(x = "matrix", y = "diagonalMatrix"):...

**%\*%** signature(x = "diagonalMatrix", y = "matrix"):...

**%\*%** signature(x = "diagonalMatrix", y = "dgeMatrix"):...

**crossprod** signature(x = "diagonalMatrix", y = "dgeMatrix"):...

and many more methods

**solve** signature(a = "diagonalMatrix", b, ...): is trivially implemented, of course.

**which** signature(x = "nMatrix"), semantically equivalent to **base** function `which(x, arr.ind)`.

**\*** signature(e1 = "ddiMatrix", e2="denseMatrix"): arithmetic and other operators from the `Ops` group have a few dozen explicit method definitions, in order to keep the results *diagonal* in many cases, including the following:

**/** signature(e1 = "ddiMatrix", e2="denseMatrix"): the result is from class `ddiMatrix` which is typically very desirable. Note that when e2 contains off-diagonal zeros or NAs, we implicitly use  $0/x = 0$ , hence differing from traditional R arithmetic (where  $0/0 \mapsto \text{NaN}$ ), in order to preserve sparsity.

**See Also**

`ddiMatrix` and `ldiMatrix` are “actual” classes extending "diagonalMatrix".



**Examples**

```

I5 <- Diagonal(5)
D5 <- Diagonal(x = 10*(1:5))
## trivial (but explicitly defined) methods:
stopifnot(identical(crossprod(I5), I5),
           identical(tcrossprod(I5), I5),
           identical(crossprod(I5, D5), D5),
           identical(tcrossprod(D5, I5), D5),
           identical(solve(D5), solve(D5, I5)),
           all.equal(D5, solve(solve(D5)), tol = 1e-12)
)
solve(D5)

```

---

dMatrix-class

*(Virtual) Class "dMatrix" of "double" Matrices*


---

**Description**

The `dMatrix` class is a virtual class contained by all actual classes of numeric matrices in the **Matrix** package. Similarly, all the actual classes of logical matrices inherit from the `lMatrix` class.

**Slots**

Common to *all* matrix object in the package:

**Dim:** Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

**Dimnames:** list of length two; each component containing NULL or a `character` vector length equal the corresponding `Dim` element.

**Methods**

There are (relatively simple) group methods (see, e.g., [Arith](#))

**Arith** signature(e1 = "dMatrix", e2 = "dMatrix"):...

**Arith** signature(e1 = "dMatrix", e2 = "numeric"):...

**Arith** signature(e1 = "numeric", e2 = "dMatrix"):...

**Math** signature(x = "dMatrix"):...

**Math2** signature(x = "dMatrix", digits = "numeric"): this group contains `round()` and `signif()`.

**Compare** signature(e1 = "numeric", e2 = "dMatrix"):...

**Compare** signature(e1 = "dMatrix", e2 = "numeric"):...

**Compare** signature(e1 = "dMatrix", e2 = "dMatrix"):...

**Summary** signature(x = "dMatrix"): The "Summary" group contains the seven functions `max()`, `min()`, `range()`, `prod()`, `sum()`, `any()`, and `all()`.

The following methods are also defined for all double matrices:

**coerce** signature(from = "dMatrix", to = "matrix"):...

**expm** signature(x = "dMatrix"): computes the “*Matrix Exponential*”, see [expm](#).

**zapsmall** signature(x = "dMatrix"): ...

The following methods are defined for all logical matrices:

**which** signature(x = "lMatrix"): as the **base** function [which](#)(x, arr.ind) returns the indices of the **TRUE** entries in x; if arr.ind is true, as a 2-column matrix of row and column indices.

### See Also

The nonzero-pattern matrix class [nMatrix](#), which can be used to store non-NA logical matrices even more compactly.

The numeric matrix classes [dgeMatrix](#), [dgCMatrix](#), and [Matrix](#).

### Examples

```
showClass("dMatrix")

set.seed(101)
round(Matrix(rnorm(28), 4, 7), 2)
(M <- zapsmall(Matrix(rlnorm(56, sd=10), 4, 14)))
table(as.logical(M == 0))
```

---

dpoMatrix-class      *Positive Semi-definite Dense Numeric Matrices*

---

### Description

The "dpoMatrix" class is the class of positive-semidefinite symmetric matrices in nonpacked storage. The "dppMatrix" class is the same except in packed storage. Only the upper triangle or the lower triangle is required to be available.

The "corMatrix" class extends "dpoMatrix" with a slot sd.

### Objects from the Class

Objects can be created by calls of the form `new("dpoMatrix", ...)` or from `crossprod` applied to an "dgeMatrix" object.

### Slots

**uplo**: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

**x**: Object of class "numeric". The numeric values that constitute the matrix, stored in column-major order.

**Dim**: Object of class "integer". The dimensions of the matrix which must be a two-element vector of non-negative integers.

**Dimnames**: inherited from class "Matrix"

**factors**: Object of class "list". A named list of factorizations that have been computed for the matrix.

**sd**: (for "corMatrix") a **numeric** vector of length n containing the (original)  $\sqrt{\text{var}(\cdot)}$  entries which allow reconstruction of a covariance matrix from the correlation matrix.

**Extends**

Class "dsyMatrix", directly.

Classes "dgeMatrix", "symmetricMatrix", and many more by class "dsyMatrix".

**Methods**

**chol** signature(x = "dpoMatrix"): Returns (and stores) the Cholesky decomposition of x, see [chol](#).

**rcond** signature(x = "dpoMatrix", norm = "character"): Returns (and stores) the reciprocal of the condition number of x. The norm can be "O" for the one-norm (the default) or "I" for the infinity-norm. For symmetric matrices the result does not depend on the norm.

**solve** signature(a = "dpoMatrix", b = "missing"): Return the inverse of a.

**solve** signature(a = "dpoMatrix", b = "numeric"): Solve the linear system defined by a and b, where b can be a numeric vector, or a matrix, or a dgeMatrix object. The Cholesky decomposition of a is calculated (if needed) while solving the system.

**Arith** signature(e1 = "dpoMatrix", e2 = "numeric") (and quite a few other signatures): The result of ("elementwise" defined) arithmetic operations is typically *not* positive-definite anymore. The only exceptions, currently, are multiplications, divisions or additions with *positive* length(.) == 1 numbers (or [logicals](#)).

**See Also**

Classes [dsyMatrix](#) and [dgeMatrix](#); further, [Matrix](#), [rcond](#), [chol](#), [solve](#), [crossprod](#).

**Examples**

```
h6 <- Hilbert(6)
rcond(h6)
str(h6)
h6 * 27720 # is ``integer``
solve(h6)
str(hp6 <- as(h6, "dppMatrix"))

### Note that as(*, "corMatrix") *scales* the matrix
(ch6 <- as(h6, "corMatrix"))
stopifnot(all.equal(h6 * 27720, round(27720 * h6), tol = 1e-14),
          all.equal(ch6@sd^(-2), 2*(1:6)-1, tol= 1e-12))
chch <- chol(ch6)
stopifnot(identical(chch, ch6@factors$Cholesky),
          all(abs(crossprod(chch) - ch6) < 1e-10))
```

---

drop0

*Drop "Explicit Zeroes" from a Sparse Matrix*

---

**Description**

Returns a sparse matrix with no "explicit zeroes", i.e., all zero or FALSE entries are dropped from the explicitly indexed matrix entries.

**Usage**

```
drop0(x, tol = 0, is.Csparse = NA)
```

**Arguments**

`x` a Matrix, typically sparse, i.e., inheriting from `sparseMatrix`.

`tol` non-negative number to be used as tolerance for checking if an entry  $x_{i,j}$  should be considered to be zero.

`is.Csparse` logical indicating prior knowledge about the “Cspareness” of `x`. This exists for possible speedup reasons only.

**Value**

a Matrix like `x` but with no explicit zeros, i.e., `!any(x@x == 0)`, always inheriting from `CsparseMatrix`.

**Note**

When a sparse matrix is the result of matrix multiplications, you may want to consider combining `drop0()` with `zapsmall()`, see the example.

**See Also**

`spMatrix`, class `sparseMatrix`

**Examples**

```
m <- spMatrix(10,20, i= 1:8, j=2:9,
              x = c(0:2,3:-1))
m
drop0(m)

## A larger example:
t5 <- new("dtCMatrix", Dim = c(5L, 5L), uplo = "L",
         x = c(10, 1, 3, 10, 1, 10, 1, 10, 10),
         i = c(0L,2L,4L, 1L, 3L,2L,4L, 3L, 4L),
         p = c(0L, 3L, 5L, 7:9))
TT <- kronecker(t5, kronecker(kronecker(t5,t5), t5))
IT <- solve(TT)
I. <- TT %*% IT ; nnzero(I.) # 697 ( = 625 + 72 )
I.0 <- drop0(zapsmall(I.))
stopifnot(all(I.0 == Diagonal(625)))
```

---

dsCMatrix-class      *Numeric Symmetric Sparse (column compressed) Matrices*

---

**Description**

The `dsCMatrix` class is a class of symmetric, sparse numeric matrices in the compressed, column-oriented format. In this implementation the non-zero elements in the columns are sorted into increasing row order.

The `dsTMatrix` class is the class of symmetric, sparse numeric matrices in triplet format.

## Objects from the Class

Objects can be created by calls of the form `new("dsCMatrix", ...)` or `new("dsTMatrix", ...)` or (for `dsCMatrix`) also automatically from `Matrix(.)`.

## Slots

- `uplo`: A character object indicating if the upper triangle ("U") or the lower triangle ("L") is stored.
- `i`: Object of class "integer" of length `nnZ` (*half* number of non-zero elements). These are the row numbers for each non-zero element in the lower triangle of the matrix.
- `p`: (only in class "dsCMatrix:") Object of class "integer" of pointers, one for each column, to the initial (zero-based) index of elements in the column.
- `j`: (only in class "dsTMatrix:") Object of class "integer" of length `nnZ` (as `i`). These are the column numbers for each non-zero element in the lower triangle of the matrix.
- `x`: Object of class "numeric" of length `nnZ` – the non-zero elements of the matrix (to be duplicated for full matrix).
- `factors`: Object of class "list" - a list of factorizations of the matrix.
- `Dim`: Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

## Extends

Both classes extend classes and `symmetricMatrix` `dsparseMatrix` directly; `dsCMatrix` further directly extends `CsparseMatrix`, where `dsTMatrix` does `TsparseMatrix`.

## Methods

- solve** signature(`a = "dsCMatrix"`, `b = "dsparseMatrix"`): Solve a linear system of equations defined by `x` using a Cholesky decomposition. All steps will be based on *sparse* representations.
- solve** signature(`a = "dsCMatrix"`, `b = "matrix"`): Solve a linear system of equations defined by `x` using a Cholesky decomposition.
- chol** signature(`x = "dsCMatrix"`, `pivot = "logical"`): Returns (and stores) the Cholesky decomposition of `x`, see `chol`.
- Cholesky** signature(`A = "dsCMatrix"`, ...): Computes more flexibly Cholesky decompositions, see `Cholesky`.
- determinant** signature(`x = "dsCMatrix"`, `logarithm = "missing"`): Evaluate the determinant of `x` on the logarithm scale. This creates and stores the Cholesky factorization.
- determinant** signature(`x = "dsCMatrix"`, `logarithm = "logical"`): Evaluate the determinant of `x` on the logarithm scale or not, according to the `logarithm` argument. This creates and stores the Cholesky factorization.
- t** signature(`x = "dsCMatrix"`): Transpose. As for all symmetric matrices, a matrix for which the upper triangle is stored produces a matrix for which the lower triangle is stored and vice versa, i.e., the `uplo` slot is swapped, and the row and column indices are interchanged.
- t** signature(`x = "dsTMatrix"`): Transpose. The `uplo` slot is swapped from "U" to "L" or vice versa, as for a "dsCMatrix", see above.
- coerce** signature(`from = "dsCMatrix"`, `to = "dgTMatrix"`)
- coerce** signature(`from = "dsCMatrix"`, `to = "dgeMatrix"`)

```

coerce signature(from = "dsCMatrix", to = "matrix")
coerce signature(from = "dsTMatrix", to = "dgeMatrix")
coerce signature(from = "dsTMatrix", to = "dsCMatrix")
coerce signature(from = "dsTMatrix", to = "dsyMatrix")
coerce signature(from = "dsTMatrix", to = "matrix")

```

### See Also

Classes [dgCMatrix](#), [dgTMatrix](#), [dgeMatrix](#) and those mentioned above.

### Examples

```

mm <- Matrix(toeplitz(c(10, 0, 1, 0, 3)), sparse = TRUE)
mm # automatically dsCMatrix
str(mm)

## how would we go from a manually constructed Tsparse* :
mT <- as(mm, "dgTMatrix")

## Either
(symM <- as(mT, "symmetricMatrix"))# dsT
(symC <- as(symM, "CsparseMatrix"))# dsC
## or
sC <- Matrix(mT, sparse=TRUE, forceCheck=TRUE)

sym2 <- as(symC, "TsparseMatrix")

```

---

dsparseMatrix-class

*Virtual Class "dsparseMatrix" of Numeric Sparse Matrices*

---

### Description

The Class "dsparseMatrix" is the virtual (super) class of all numeric sparse matrices.

### Slots

**Dim:** the matrix dimension, see class "[Matrix](#)".

**Dimnames:** see the "[Matrix](#)" class.

**x:** a [numeric](#) vector containing the (non-zero) matrix entries.

### Extends

Class "dMatrix" and "sparseMatrix", directly.

Class "Matrix", by the above classes.

### See Also

the documentation of the (non virtual) sub classes, see `showClass("dsparseMatrix")`; in particular, [dgTMatrix](#), [dgCMatrix](#), and [dGRMatrix](#).

**Examples**

```
showClass("dsparseMatrix")
```

---

```
dsRMatrix-class      Symmetric Sparse Compressed Row Matrices
```

---

**Description**

The `dsRMatrix` class is a class of symmetric, sparse matrices in the compressed, row-oriented format. In this implementation the non-zero elements in the rows are sorted into increasing column order.

**Objects from the Class**

These `..RMatrix` classes are currently still mostly unimplemented!

Objects can be created by calls of the form `new("dsRMatrix", ...)`.

**Slots**

**uplo:** A character object indicating if the upper triangle ("U") or the lower triangle ("L") is stored. At present only the lower triangle form is allowed.

**j:** Object of class "integer" of length `nnzero` (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.

**p:** Object of class "integer" of pointers, one for each row, to the initial (zero-based) index of elements in the row.

**factors:** Object of class "list" - a list of factorizations of the matrix.

**x:** Object of class "numeric" - the non-zero elements of the matrix.

**Dim:** Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

**Dimnames:** List of length two, see [Matrix](#).

**Extends**

Classes [RsparseMatrix](#), [dsparseMatrix](#) and [symmetricMatrix](#), directly.

Class "dMatrix", by class "dsparseMatrix", class "sparseMatrix", by class "dsparseMatrix" or "RsparseMatrix"; class "compMatrix" by class "symmetricMatrix" and of course, class "Matrix".

**Methods**

**forceSymmetric** signature(`x = "dsRMatrix"`, `uplo = "missing"`): a trivial method just returning `x`

**forceSymmetric** signature(`x = "dsRMatrix"`, `uplo = "character"`): if `uplo == x@uplo`, this trivially returns `x`; otherwise `t(x)`.

**coerce** signature(`from = "dsCMatrix"`, `to = "dsRMatrix"`)

**See Also**

the classes [dgCMatrix](#), [dgTMatrix](#), and [dgeMatrix](#).

**Examples**

```
(m0 <- new("dsRMatrix"))
m2 <- new("dsRMatrix", Dim = c(2L,2L),
         x = c(3,1), j = c(1L,1L), p = 0:2)
m2
stopifnot(colSums(as(m2, "TsparseMatrix")) == 3:4)
str(m2)
(ds2 <- forceSymmetric(diag(2))) # dsy*
dR <- as(ds2, "RsparseMatrix")
dR # dsRMatrix
```

---

dsyMatrix-class      *Symmetric Dense Numeric Matrices*

---

**Description**

The "dsyMatrix" class is the class of symmetric, dense matrices in non-packed storage and "dspMatrix" is the class of symmetric dense matrices in packed storage. Only the upper triangle or the lower triangle is stored.

**Objects from the Class**

Objects can be created by calls of the form `new("dsyMatrix", ...)`.

**Slots**

**uplo:** Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

**x:** Object of class "numeric". The numeric values that constitute the matrix, stored in column-major order.

**Dim,Dimnames:** The dimension (a length-2 "integer") and corresponding names (or NULL), see the [Matrix](#).

**factors:** Object of class "list". A named list of factorizations that have been computed for the matrix.

**Extends**

"dsyMatrix" extends class "dgeMatrix", directly, whereas

"dspMatrix" extends class "ddenseMatrix", directly.

Both extend class "symmetricMatrix", directly, and class "Matrix" and others, *indirectly*, use `showClass("dsyMatrix")`, e.g., for details.

**Methods**

**coerce** signature(from = "ddenseMatrix", to = "dgeMatrix")

**coerce** signature(from = "dspMatrix", to = "matrix")

**coerce** signature(from = "dsyMatrix", to = "matrix")

**coerce** signature(from = "dsyMatrix", to = "dspMatrix")

**coerce** signature(from = "dspMatrix", to = "dsyMatrix")



```

norm signature(x = "dspMatrix", type = "character")
norm signature(x = "dsyMatrix", type = "character")
norm signature(x = "dspMatrix", type = "missing")
norm signature(x = "dsyMatrix", type = "missing")
solve signature(a = "dspMatrix", b = "missing")
solve signature(a = "dsyMatrix", b = "missing")
solve signature(a = "dspMatrix", b = "matrix")
solve signature(a = "dsyMatrix", b = "matrix")
t signature(x = "dsyMatrix"): Transpose; swaps from upper triangular to lower triangular storage, i.e., the uplo slot from "U" to "L" or vice versa, the same as for all symmetric matrices.

```

### See Also

Classes [dgeMatrix](#) and [Matrix](#); [solve](#), [norm](#), [rcond](#), [t](#)

### Examples

```

## Only upper triangular part matters (when uplo == "U" as per default)
(sy2 <- new("dsyMatrix", Dim = as.integer(c(2,2)), x = c(14, NA, 32, 77))
str(t(sy2)) # uplo = "L", and the lower tri. (i.e. NA is replaced).

chol(sy2) #-> "Cholesky" matrix

## Coercing to dpoMatrix gives invalid object:
sy3 <- new("dsyMatrix", Dim = as.integer(c(2,2)), x = c(14, -1, 2, -7))
try(as(sy3, "dpoMatrix")) # -> error: not positive definite

```

---

dtCMatrix-class      *Triangular, (compressed) sparse column matrices*

---

### Description

The "dtCMatrix" class is a class of triangular, sparse matrices in the compressed, column-oriented format. In this implementation the non-zero elements in the columns are sorted into increasing row order. The "dtTMatrix" class is a class of triangular, sparse matrices in triplet format.

### Objects from the Class

Objects can be created by calls of the form `new("dtCMatrix", ...)` or calls of the form `new("dtTMatrix", ...)`, but more typically automatically via [Matrix\(\)](#) or coercion such as `as(x, "dtCMatrix")`.

**Slots**

- uplo:** Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.
- diag:** Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see [triangularMatrix](#).
- p:** Object of class "integer" of pointers, one for each column, to the initial (zero-based) index of elements in the column. (Only present in the dtCMatrix class.)
- i:** Object of class "integer" of length nnzero (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.
- j:** Object of class "integer" of length nnzero (number of non-zero elements). These are the column numbers for each non-zero element in the matrix. (Only present in the dtTMatrix class.)
- x:** Object of class "numeric" - the non-zero elements of the matrix.
- Dim,Dimnames:** The dimension (a length-2 "integer") and corresponding names (or NULL), inherited from the [Matrix](#), see there.

**Extends**

Class "dgCMatrix", directly. Class "triangularMatrix", directly. Class "dMatrix", "sparseMatrix", and more by class "dgCMatrix" etc, see the examples.

**Methods**

- coerce** signature(from = "dtCMatrix", to = "dgTMatrix")
- coerce** signature(from = "dtCMatrix", to = "dgeMatrix")
- coerce** signature(from = "dtTMatrix", to = "dgeMatrix")
- coerce** signature(from = "dtTMatrix", to = "dtrMatrix")
- coerce** signature(from = "dtTMatrix", to = "matrix")
- solve** signature(a = "dtCMatrix", b = "matrix")
- solve** signature(a = "dtCMatrix", b = "dgeMatrix")
- solve** signature(a = "dtCMatrix", b = "missing")
- solve** signature(a = "dtCMatrix", b = "numeric")
- solve** signature(a = "dtCMatrix", b = "CsparseMatrix"): fully sparse triangular solve, in traditional S/R\ aka [backsolve](#).
- t** signature(x = "dtCMatrix"): returns the transpose of x
- t** signature(x = "dtTMatrix"): returns the transpose of x

**See Also**

Classes [dgCMatrix](#), [dgTMatrix](#), [dgeMatrix](#), and [dtrMatrix](#).

**Examples**

```
showClass("dtCMatrix")

showClass("dtTMatrix")
t1 <- new("dtTMatrix", x= c(3,7), i= 0:1, j=3:2, Dim= as.integer(c(4,4)))
t1
```

```
## from 0-diagonal to unit-diagonal {low-level step}:
tu <- t1 ; tu@diag <- "U"
tu
(cu <- as(tu, "dtCMatrix"))
str(cu)# only two entries in @i and @x
stopifnot(cu@i == 1:0,
           all(2 * symmpart(cu) == Diagonal(4) + forceSymmetric(cu)))

t1[1,2:3] <- -1:-2
diag(t1) <- 10*c(1:2,3:2)
t1 # still triangular
(it1 <- solve(t1))
t1. <- solve(it1)
all(abs(t1 - t1.) < 10 * .Machine$double.eps)
```

---

dtpMatrix-class      *Packed triangular dense matrices*

---

### Description

The "dtpMatrix" class is the class of triangular, dense, numeric matrices in packed storage. The "dtrMatrix" class is the same except in nonpacked storage.

### Objects from the Class

Objects can be created by calls of the form `new("dtpMatrix", ...)` or by coercion from other classes of matrices.

### Slots

**uplo:** Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

**diag:** Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see [triangularMatrix](#).

**x:** Object of class "numeric". The numeric values that constitute the matrix, stored in column-major order. For a packed square matrix of dimension  $d \times d$ , `length(x)` is of length  $d(d+1)/2$  (also when `diag == "U"`!).

**Dim,Dimnames:** The dimension (a length-2 "integer") and corresponding names (or NULL), inherited from the [Matrix](#), see there.

### Extends

Class "ddenseMatrix", directly. Class "triangularMatrix", directly. Class "dMatrix" and more by class "ddenseMatrix" etc, see the examples.

### Methods

**%%%** signature(x = "dtpMatrix", y = "dgeMatrix"): Matrix multiplication; ditto for several other signature combinations, see `showMethods("%*%", class = "dtpMatrix")`.

**coerce** signature(from = "dtpMatrix", to = "dtrMatrix")

```

coerce signature(from = "dtpMatrix", to = "matrix")
determinant signature(x = "dtpMatrix", logarithm = "missing"):...
determinant signature(x = "dtpMatrix", logarithm = "logical"):...
diag signature(x = "dtpMatrix"):...
norm signature(x = "dtpMatrix", type = "character"):...
norm signature(x = "dtpMatrix", type = "missing"):...
rcond signature(x = "dtpMatrix", norm = "character"):...
rcond signature(x = "dtpMatrix", norm = "missing"):...
solve signature(a = "dtpMatrix", b = "missing"):...
solve signature(a = "dtpMatrix", b = "matrix"):...
t signature(x = "dtpMatrix"):...
unpack signature(x = "dtpMatrix"):...

```

**See Also**

Class [dtrMatrix](#)

**Examples**

```

showClass("dtrMatrix")

example("dtrMatrix-class")
(p1 <- as(T2, "dtpMatrix"))
str(p1)
(pp <- as(T, "dtpMatrix"))
stopifnot(length(p1@x) == 3, length(pp@x) == 3,
           p1 @ uplo == T2 @ uplo, pp @ uplo == T @ uplo)

```

**Description**

The `dtrMatrix` class is a class of triangular, sparse matrices in the compressed, row-oriented format. In this implementation the non-zero elements in the rows are sorted into increasing column order.

**Objects from the Class**

This class is currently still mostly unimplemented!

Objects can be created by calls of the form `new("dtRMatrix", ...)`.

**Slots**

- uplo:** Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular. At present only the lower triangle form is allowed.
- diag:** Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see [triangularMatrix](#).
- j:** Object of class "integer" of length `nnzero(.)` (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.
- p:** Object of class "integer" of pointers, one for each row, to the initial (zero-based) index of elements in the row. (Only present in the `dsRMatrix` class.)
- x:** Object of class "numeric" - the non-zero elements of the matrix.
- Dim:** The dimension (a length-2 "integer")
- Dimnames:** corresponding names (or NULL), inherited from the [Matrix](#), see there.

**Extends**

Class "dgRMatrix", directly. Class "dsparseMatrix", by class "dgRMatrix". Class "dMatrix", by class "dgRMatrix". Class "sparseMatrix", by class "dgRMatrix". Class "Matrix", by class "dgRMatrix".

**Methods**

No methods currently with class "dsRMatrix" in the signature.

**See Also**

Classes [dgCMatrix](#), [dgTMatrix](#), [dgeMatrix](#)

**Examples**

```
(m0 <- new("dtRMatrix"))
(m2 <- new("dtRMatrix", Dim = c(2L, 2L),
          x = c(5, 1:2), p = c(0L, 2:3), j = c(0:1, 1L)))
str(m2)
(m3 <- as(Diagonal(2), "RsparseMatrix"))# --> dtRMatrix
```

---

dtrMatrix-class      *Triangular, dense, numeric matrices*

---

**Description**

The "dtrMatrix" class is the class of triangular, dense, numeric matrices in nonpacked storage. The "dtpMatrix" class is the same except in packed storage.

**Objects from the Class**

Objects can be created by calls of the form `new("dtrMatrix", ...)`.

**Slots**

- uplo:** Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.
- diag:** Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see [triangularMatrix](#).
- x:** Object of class "numeric". The numeric values that constitute the matrix, stored in column-major order.
- Dim:** Object of class "integer". The dimensions of the matrix which must be a two-element vector of non-negative integers.

**Extends**

Class "ddenseMatrix", directly. Class "triangularMatrix", directly. Class "Matrix" and others, by class "ddenseMatrix".

**Methods**

- %%** signature(x = "dtrMatrix", y = "matrix") and other signatures (use `showMethods("%*%", class="dtrMatrix")`): matrix multiplication.
- coerce** signature(from = "dgeMatrix", to = "dtrMatrix")
- coerce** signature(from = "dtrMatrix", to = "matrix")
- coerce** signature(from = "dtrMatrix", to = "ltrMatrix")
- coerce** signature(from = "dtrMatrix", to = "matrix")
- coerce** signature(from = "matrix", to = "dtrMatrix")
- norm** signature(x = "dtrMatrix", type = "character")
- rcond** signature(x = "dtrMatrix", norm = "character")
- solve** signature(a = "dtrMatrix", b = "missing")
- solve** signature(a = "dtrMatrix", b = "matrix")

**See Also**

Classes [ddenseMatrix](#), [dtpMatrix](#), [triangularMatrix](#)

**Examples**

```
(m <- rbind(2:3, 0:-1))
(M <- as(m, "dgeMatrix"))

(T <- as(M, "dtrMatrix")) ## upper triangular is default
(T2 <- as(t(M), "dtrMatrix"))
stopifnot(T@uplo == "U", T2@uplo == "L", identical(T2, t(T)))
```

---

expand	<i>Expand a Decomposition into Factors</i>
--------	--

---

### Description

Expands decompositions stored in compact form into factors.

### Usage

```
expand(x, ...)
```

### Arguments

x	a matrix decomposition.
...	further arguments passed to or from other methods.

### Details

This is a generic function with special methods for different types of decompositions, see [showMethods](#)(expand) to list them all.

### Value

The expanded decomposition, typically a list of matrix factors.

### Note

Factors for decompositions such as `lu` and `qr` can be stored in a compact form. The function `expand` allows all factors to be fully expanded.

### See Also

The LU decomposition [lu](#), for which there *is* an `expand` method; [facmul](#).

### Examples

```
(x <- Matrix(round(rnorm(9),2), 3, 3))
(ex <- expand(lux <- lu(x)))
```

---

`expm`*Matrix Exponential*

---

**Description**

Compute the exponential of a matrix.

**Usage**

```
expm(x)
```

**Arguments**

`x` a matrix, typically inheriting from the `dMatrix` class.

**Details**

The exponential of a matrix is defined as the infinite Taylor series  $\text{expm}(A) = I + A + A^2/2! + A^3/3! + \dots$  (although this is definitely not the way to compute it). The method for the `dgeMatrix` class uses Ward's diagonal Pade' approximation with three step preconditioning.

**Value**

The matrix exponential of `x`.

**Author(s)**

This is a translation of the implementation of the corresponding Octave function contributed to the Octave project by A. Scottedward Hodel <A.S.Hodel@Eng.Auburn.EDU>. A bug in there has been fixed by Martin Maechler.

**References**

[http://en.wikipedia.org/wiki/Matrix\\_exponential](http://en.wikipedia.org/wiki/Matrix_exponential)

Cleve Moler and Charles Van Loan (2003) Nineteen dubious ways to compute the exponential of a matrix, twenty-five years later. *SIAM Review* **45**, 1, 3–49.

Eric W. Weisstein et al. (1999) *Matrix Exponential*. From MathWorld, <http://mathworld.wolfram.com/MatrixExponential.html>

**See Also**

[Schur](#)

**Examples**

```
(m1 <- Matrix(c(1,0,1,1), nc = 2))
(e1 <- expm(m1)) ; e <- exp(1)
stopifnot(all.equal(e1@x, c(e,0,e,e), tol = 1e-15))
(m2 <- Matrix(c(-49, -64, 24, 31), nc = 2))
(e2 <- expm(m2))
(m3 <- Matrix(cbind(0, rbind(6*diag(3), 0))) # sparse!
(e3 <- expm(m3)) # upper triangular
```





```
## NOTE: The following examples take quite some time
## ---- even on a fast internet connection:
if(FALSE) # the URL has been corrected, but we need an un-tar step!
str(sm <-
  readHB(gzcon(url("http://www.cise.ufl.edu/research/sparse/RB/Boeing/msc00726.tar.gz")))

str(jgl009 <-
  readMM(gzcon(url("ftp://math.nist.gov/pub/MatrixMarket2/Harwell-Boeing/counterx/jgl009.m

## End(Not run)
data(KNex)
writeMM(KNex$mm, "mmMM.mtx")
```

---

 facmul

---

*Multiplication by Decomposition Factors*


---

### Description

Performs multiplication by factors for certain decompositions (and allows explicit formation of those factors).

### Usage

```
facmul(x, factor, y, transpose, left, ...)
```

### Arguments

<code>x</code>	a matrix decomposition. No missing values or IEEE special values are allowed.
<code>factor</code>	an indicator for selecting a particular factor for multiplication.
<code>y</code>	a matrix or vector to be multiplied by the factor or its transpose. No missing values or IEEE special values are allowed.
<code>transpose</code>	a logical value. When <code>FALSE</code> (the default) the factor is applied. When <code>TRUE</code> the transpose of the factor is applied.
<code>left</code>	a logical value. When <code>TRUE</code> (the default) the factor is applied from the left. When <code>FALSE</code> the factor is applied from the right.
<code>...</code>	the method for <code>"qr.Matrix"</code> has additional arguments.

### Value

the product of the selected factor (or its transpose) and `y`

### NOTE

Factors for decompositions such as `lu` and `qr` can be stored in a compact form. The function `facmul` allows multiplication without explicit formation of the factors, saving both storage and operations.

### References

Golub, G., and Van Loan, C. F. (1989). *Matrix Computations*, 2nd edition, Johns Hopkins, Baltimore.

**Examples**

```

library(Matrix)
x <- Matrix(rnorm(9), 3, 3)
## Not run:
qrx <- qr(x) # QR factorization of x
y <- rnorm(3)
facmul( qr(x), factor = "Q", y) # form Q y

## End(Not run)

```

---

forceSymmetric

*Force a Matrix to 'symmetricMatrix' Without Symmetry Checks*


---

**Description**

Force `x` (inheriting from `Matrix` class) to `symmetricMatrix`, **without** a symmetry check (which is applied for all as (`x`, "symmetricMatrix") alike).

**Usage**

```
forceSymmetric(x, uplo)
```

**Arguments**

<code>x</code>	a (classed) square matrix.
<code>uplo</code>	optional string, "U" or "L". The default is "U" unless <code>x</code> already has a <code>uplo</code> slot (i.e., when it is <code>symmetricMatrix</code> , or <code>triangularMatrix</code> ), where the default will be <code>x@uplo</code> .

**Value**

a square matrix inheriting from class `symmetricMatrix`.

**See Also**

[symmpart](#) for the symmetric part, or the coercions `as(x, <symmetricMatrix class>)`.

**Examples**

```

## Hilbert matrix
i <- 1:6
h6 <- 1/outer(i - 1L, i, "+")
sd <- sqrt(diag(h6))
hh <- t(h6/sd)/sd # theoretically symmetric
isSymmetric(hh, tol=0) # FALSE; hence
try( as(hh, "symmetricMatrix") ) # fails, but this works fine:
H6 <- forceSymmetric(hh)

## result can be pretty surprising:
(M <- Matrix(1:36, 6))
forceSymmetric(M) # symmetric, hence very different in lower triangle
(tm <- tril(M))
forceSymmetric(tm)

```

---

 generalMatrix-class

*Class "generalMatrix" of General Matrices*


---

### Description

Virtual class of “general” matrices; i.e., matrices that do not have a known property such as symmetric, triangular, or diagonal.

### Objects from the Class

A virtual Class: No objects may be created from it.

### Slots

factors ,

Dim ,

Dimnames: all slots inherited from [compMatrix](#); see its description.

### Extends

Class "compMatrix", directly. Class "Matrix", by class "compMatrix".

### See Also

Classes [compMatrix](#), and the non-general virtual classes: [symmetricMatrix](#), [triangularMatrix](#), [diagonalMatrix](#).

---

 Hilbert

*Generate a Hilbert matrix*


---

### Description

Generate the  $n$  by  $n$  symmetric Hilbert matrix. Because these matrices are ill-conditioned for moderate to large  $n$ , they are often used for testing numerical linear algebra code.

### Usage

```
Hilbert(n)
```

### Arguments

$n$  a non-negative integer.

### Value

the  $n$  by  $n$  symmetric Hilbert matrix as a "dpoMatrix" object.

**See Also**

the class [dpoMatrix](#)

**Examples**

```
Hilbert(6)
```

---

image-methods

*Methods for image() in Package 'Matrix'*

---

**Description**

Methods for function [image](#) in package **Matrix**. An image of a matrix simply color codes all matrix entries and draws the  $n \times m$  matrix using an  $n \times m$  grid of (colored) rectangles.

**Usage**

```
## S4 method for signature 'dgTMatrix':
image(x,
      xlim = .5 + c(0, di[2]),
      ylim = .5 + c(di[1], 0), aspect = "iso",
      sub = sprintf("Dimensions: %d x %d", di[1], di[2]),
      xlab = "Column", ylab = "Row",
      useAbs = NULL, colorkey = !useAbs,
      col.regions = NULL,
      lwd = NULL, ...)
```

**Arguments**

<code>x</code>	a Matrix object, i.e., fulfilling <code>is(x, "Matrix")</code> .
<code>xlim, ylim</code>	x- and y-axis limits; may be used to “zoom into” matrix.
<code>aspect</code>	aspect ratio specified as number (y/x) or string; see <a href="#">levelplot</a> .
<code>sub, xlab, ylab</code>	axis annotation with sensible defaults; see <a href="#">plot.default</a> .
<code>useAbs</code>	logical indicating if <code>abs(x)</code> should be shown; if TRUE, the former (implicit) default, the default <code>col.regions</code> will be <a href="#">grey</a> colors (and no <code>colorkey</code> drawn). The default is FALSE unless the matrix has no negative entries.
<code>colorkey</code>	logical indicating if a color key aka ‘legend’ should be produced. Default is to draw one, unless <code>useAbs</code> is true.
<code>col.regions</code>	vector of gradually varying colors; see <a href="#">levelplot</a> .
<code>lwd</code>	non-negative number or NULL (default), specifying the line-width of the rectangles of each non-zero matrix entry (drawn by <a href="#">grid.rect</a> ). The default depends on the matrix dimension and the device size.
<code>...</code>	further arguments passed to methods and <a href="#">levelplot</a> .

**Methods**

All methods currently end up calling the method for the [dgTMatrix](#) class. Use `showMethods(image)` to list them all.

**Examples**

```

showMethods(image)
## If you want to see all the methods' implementations:
showMethods(image, incl=TRUE, inherit=FALSE)

data(CAex)
image(CAex, main = "image(CAex)")
image(CAex, useAbs=TRUE, main = "image(CAex, useAbs=TRUE)")

cCA <- Cholesky(crossprod(CAex), Imult = .01)
image(cCA, main="Cholesky(crossprod(CAex), Imult = .01)")
image(cCA, useAbs=TRUE)

data(USCounties)
image(USCounties)# huge
image(sign(USCounties))## just the pattern
# how the result looks, may depend heavily on
# the device, screen resolution, antialiasing etc
# e.g. x11(type="Xlib") may show very differently than cairo-based

## Drawing borders around each rectangle;
# again, viewing depends very much on the device:
image(USCounties[1:400,1:200], lwd=.1)
image(USCounties[1:200,1:200], lwd=.5)
image(USCounties[1:200,1:200], lwd=.01)

```

---

index-class

*Virtual Class "index" - Simple Class for Matrix Indices*


---

**Description**

The class "index" is a virtual class used for indices (in signatures) for matrix indexing and sub-assignment of "**Matrix**" matrices.

In fact, it is currently implemented as a simple class union ([setClassUnion](#)) of "numeric", "logical" and "character".

**Objects from the Class**

Since it is a virtual Class, no objects may be created from it.

**See Also**

[\[-methods\]](#), and  
[Subassign-methods](#), also for examples.

**Examples**

```
showClass("index")
```

---

 is.na-methods

*is.na() Methods for 'Matrix' Objects*


---

### Description

Methods for function `is.na()` for all Matrices (objects extending the `Matrix` class):

`x = "denseMatrix"` returns a `nMatrix` object of same dimension as `x`, with TRUE's whenever `x` was NA.

`x = "sparseMatrix"` ditto.

### Usage

```
## S4 method for signature 'sparseMatrix':
is.na(x)
```

### Arguments

`x` sparse or dense matrix.

### See Also

[NA](#), [is.na.nMatrix](#), [denseMatrix](#), [sparseMatrix](#).

### Examples

```
M <- Matrix(1:6, nrow=4, ncol=3,
            dimnames = list(c("a", "b", "c", "d"), c("A", "B", "C")))
stopifnot(all(!is.na(M)))
M[2:3,2] <- NA
is.na(M)

A <- spMatrix(10,20, i = c(1,3:8),
              j = c(2,9,6:10),
              x = 7 * (1:7))
stopifnot(all(!is.na(A)))
A[2,3] <- A[1,2] <- A[5, 5:9] <- NA
inA <- is.na(A)
stopifnot(sum(inA) == 1+1+5)
```

---

 isSymmetric-methods

*Methods for Function isSymmetric in Package 'Matrix'*


---

### Description

`isSymmetric(M)` returns a `logical` indicating `M` is a symmetric matrix. The methods are defined for virtual Matrix classes such that it works for all objects inheriting from class `Matrix`.

## Methods

**object = "symmetricMatrix" ...**

**object = "triangularMatrix" ...**

**object = "denseMatrix" ...**

**object = "diagonalMatrix" ...**

**object = "sparseMatrix" ...**

---

KNex

*Koenker-Ng Example Sparse Model Matrix and Response Vector*

---

## Description

A model matrix `mm` and corresponding response vector `y` used in an example by Koenker and Ng. The matrix `mm` is a sparse matrix with 1850 rows and 712 columns but only 8758 non-zero entries. It is a `"dgCMatrix"` object. The vector `y` is just `numeric` of length 1850.

## Usage

```
data(KNex)
```

## References

Roger Koenker and Pin Ng (2003). SparseM: A sparse matrix package for R; *J. of Statistical Software*, **8** (6), <http://www.jstatsoft.org/>

## Examples

```
data(KNex)
class(KNex$mm)
dim(KNex$mm)
image(KNex$mm)
str(KNex)

system.time( # a fraction of a second
  sparse.sol <- with(KNex, solve(crossprod(mm), crossprod(mm, y))))

head(round(sparse.sol, 3))

## Compare with QR-based solution ("more accurate, but slightly slower"):
system.time(
  sp.sol2 <- with(KNex, qr.coef(qr(mm), y)) )

all.equal(sparse.sol, sp.sol2, tol = 1e-13) # TRUE
```



---

kronecker-methods *Methods for Function 'kronecker()' in Package 'Matrix'*

---

### Description

Computes Kronecker products for objects inheriting from "Matrix".

In order to preserve sparseness, we treat  $0 * NA$  as 0, not as NA as usually in R (and as used for the base function `kronecker`).

### Methods

**kronecker** signature(X = "Matrix", Y = "ANY") .....

**kronecker** signature(X = "ANY", Y = "Matrix") .....

**kronecker** signature(X = "diagonalMatrix", Y = "ANY") .....

**kronecker** signature(X = "sparseMatrix", Y = "ANY") .....

**kronecker** signature(X = "TsparseMatrix", Y = "TsparseMatrix") .....

**kronecker** signature(X = "dgTMatrix", Y = "dgTMatrix") .....

**kronecker** signature(X = "dtTMatrix", Y = "dtTMatrix") .....

### Examples

```
(t1 <- spMatrix(5,4, x= c(3,2,-7,11), i= 1:4, j=4:1)) # 5 x 4
(t2 <- kronecker(Diagonal(3, 2:4), t1)) # 15 x 12

## should also work with special-cased logical matrices
l3 <- upper.tri(matrix(,3,3))
M <- Matrix(l3)
(N <- as(M, "nsparseMatrix"))
N2 <- as(N, "generalMatrix")
MM <- kronecker(M,M)
NN <- kronecker(N,N)
NN2 <- kronecker(N2,N2)
stopifnot(identical(NN,MM),
           is(NN, "triangularMatrix"))
```

---

ldenseMatrix-class *Virtual Class "ldenseMatrix" of Dense Logical Matrices*

---

### Description

`ldenseMatrix` is the virtual class of all dense logical (S4) matrices. It extends both `denseMatrix` and `lMatrix` directly.

### Slots

**x:** logical vector containing the entries of the matrix.

**Dim, Dimnames:** see `Matrix`.

**Extends**

Class "lMatrix", directly. Class "denseMatrix", directly. Class "Matrix", by class "lMatrix". Class "Matrix", by class "denseMatrix".

**Methods**

```
%% signature(x = "lsparseMatrix", y = "ldenseMatrix"):...
%% signature(x = "ldenseMatrix", y = "lsparseMatrix"):...
coerce signature(from = "matrix", to = "ldenseMatrix"):...
coerce signature(from = "ldenseMatrix", to = "matrix"):...
crossprod signature(x = "lsparseMatrix", y = "ldenseMatrix"):...
crossprod signature(x = "ldenseMatrix", y = "lsparseMatrix"):...
as.vector signature(x = "ldenseMatrix", mode = "missing"):...
```

**See Also**

Class [lgeMatrix](#) and the other subclasses.

**Examples**

```
showClass("ldenseMatrix")
as(diag(3) > 0, "ldenseMatrix")
```

---

ldiMatrix-class	<i>Class "ldiMatrix" of Diagonal Logical Matrices</i>
-----------------	---

---

**Description**

The class "ldiMatrix" of logical diagonal matrices.

**Objects from the Class**

Objects can be created by calls of the form `new("ldiMatrix", ...)` but typically rather via [Diagonal](#).

**Slots**

**x**: "logical" vector.  
**diag**: "character" string, either "U" or "N", see [ddiMatrix](#).  
**Dim,Dimnames**: matrix dimension and [dimnames](#), see the [Matrix](#) class description.

**Extends**

Class "[diagonalMatrix](#)" and class "lMatrix", directly.  
 Class "[sparseMatrix](#)", by class "diagonalMatrix".

**See Also**

Classes [ddiMatrix](#) and [diagonalMatrix](#); function [Diagonal](#).

**Examples**

```

(lM <- Diagonal(x = c(TRUE,FALSE,FALSE)))
str(lM)#> gory details (slots)

crossprod(lM) # numeric
(nM <- as(lM, "nMatrix"))# -> sparse (not formally ``diagonal'')
crossprod(nM) # logical sparse

```

---

lgeMatrix-class      *Class "lgeMatrix" of General Dense Logical Matrices*

---

**Description**

This is the class of general dense [logical](#) matrices.

**Slots**

**x:** Object of class "logical". The logical values that constitute the matrix, stored in column-major order.

**Dim,Dimnames:** The dimension (a length-2 "integer") and corresponding names (or NULL), see the [Matrix](#) class.

**factors:** Object of class "list". A named list of factorizations that have been computed for the matrix.

**Extends**

Class "ldenseMatrix", directly. Class "lMatrix", by class "ldenseMatrix". Class "denseMatrix", by class "ldenseMatrix". Class "Matrix", by class "ldenseMatrix". Class "Matrix", by class "ldenseMatrix".

**Methods**

Currently, mainly [t\(\)](#) and coercion methods (for [as\(.\)](#)); use, e.g., [showMethods\(class="lgeMatrix"\)](#) for details.

**See Also**

Non-general logical dense matrix classes such as [ltrMatrix](#), or [lsyMatrix](#); *sparse* logical classes such as [lgCMatrix](#).

**Examples**

```

showClass("lgeMatrix")
str(new("lgeMatrix"))
set.seed(1)
(lM <- Matrix(matrix(rnorm(28), 4,7) > 0))# a simple random lgeMatrix
set.seed(11)
(lC <- Matrix(matrix(rnorm(28), 4,7) > 0))# a simple random lgCMatrix
as(lM, "lgCMatrix")

```

---

lm.fit.sparse      *Fitter Function for Sparse Linear Models*


---

### Description

The basic computing engine for sparse linear least squares regression.

Note that the exact interface (arguments, return value) currently is **experimental**, and is bound to change. Use at your own risk!

### Usage

```
lm.fit.sparse(x, y, w = NULL, offset = NULL,
             method = c("qr", "cholesky"),
             tol = 1e-7, singular.ok = TRUE, order = NULL,
             transpose = FALSE)
```

### Arguments

x	<i>sparse</i> design matrix of dimension $n * p$ , i.e., an R object of a <code>class</code> extending <code>dsparseMatrix</code> ; typically the result of <code>sparse.model.matrix</code> .
y	vector of observations of length $n$ , or a matrix with $n$ rows.
w	vector of weights (length $n$ ) to be used in the fitting process. Weighted least squares is used with weights $w$ , i.e., $\sum(w * e^2)$ is minimized. <b>Not yet implemented !</b>
offset	numeric of length $n$ ). This can be used to specify an <i>a priori</i> known component to be included in the linear predictor during fitting.
method	a character string specifying the (factorization) method. Currently, "qr" or "cholesky".
tol	[for back-compatibility only; unused:] tolerance for the <code>qr</code> decomposition. Default is $1e-7$ .
singular.ok	[for back-compatibility only; unused:] logical. If FALSE, a singular model is an error.
order	integer or NULL, for <code>method == "qr"</code> , will determine how the fill-reducing ordering (aka permutation) for the "symbolic" part is determined (in <code>cs_amd()</code> ), with the options 0: natural, 1: Chol, 2: LU, and 3: QR, where 3 is the default.
transpose	logical; if true, use the transposed matrix $t(x)$ instead of $x$ .

### See Also

`sparse.model.matrix`; the non-sparse function in standard R's package `stats`: `lm.fit()`.

### Examples

```
dd <- expand.grid(a = as.factor(1:3),
                b = as.factor(1:4),
                c = as.factor(1:2),
                d = as.factor(1:8))
n <- nrow(dd)
dd[rep(seq_len(nrow(dd)), each = 10), ]
```

```

set.seed(17)
dM <- cbind(dd, x = round(rnorm(n), 1))
## randomly drop some
n <- nrow(dM <- dM[- sample(n, 50),])
dM <- within(dM, { A <- c(2,5,10)[a]
                  B <- c(-10,-1, 3:4)[b]
                  C <- c(-8,8)[c]
                  D <- c(10*(-5:-2), 20*c(0, 3:5))[d]
                  Y <- A + B + A*B + C + D + A*D + C*x + rnorm(n)/10
                  wts <- sample(1:10, n, replace=TRUE)
                  rm(A,B,C,D)
})
str(dM) # 1870 x 7

X <- sparse.model.matrix( ~ (a+b+c+d)^2 + c*x, data = dM)
dim(X) # 1870 x 69
X[1:10, 1:20]

## For now, use 'Matrix:::' --- TODO : export once interface is clear!

Xd <- as(X,"matrix")
system.time(fmDense <- lm.fit(Xd, y = dM[,"Y"]))
system.time( r1 <- Matrix:::lm.fit.sparse(X, y = dM[,"Y"]) ) # *is* faster
stopifnot(all.equal(r1, unname(fmDense$coeff), tol = 1e-12))
system.time(
  r2 <- Matrix:::lm.fit.sparse(X, y = dM[,"Y"], method = "chol" )
stopifnot(all.equal(r1, r2$coef, tol = 1e-12),
          all.equal(fmDense$residuals, r2$residuals, tol=1e-9)
          )

## with weights:
system.time(fmD.w <- with(dM, lm.wfit(Xd, Y, w = wts)))
system.time(fm.w1 <- with(dM, Matrix:::lm.fit.sparse(X, Y, w = wts)))
system.time(fm.w2 <- with(dM, Matrix:::lm.fit.sparse(X, Y, w = wts,
                                                    method = "chol" ) )
stopifnot(all.equal(fm.w1, unname(fmD.w$coeff), tol = 1e-12),
          all.equal(fm.w2$coef, fm.w1, tol = 1e-12),
          all.equal(fmD.w$residuals, fm.w2$residuals, tol=1e-9)
          )

```

---

lsparseMatrix-classes

*Sparse logical matrices*


---

## Description

The `lsparseMatrix` class is a virtual class of sparse matrices with TRUE/FALSE entries. Only the positions of the elements that are TRUE are stored. These can be stored in the “triple” form (classes `lgTMatrix`, `lsTMatrix`, and `ltTMatrix` which really contain pairs, not triplets) or in compressed column-oriented form (classes `lgCMatrix`, `lsCMatrix`, and `ltCMatrix`) or in compressed row-oriented form (classes `lgRMatrix`, `lsRMatrix`, and `ltRMatrix`). The second letter in the name of these non-virtual classes indicates general, symmetric, or triangular.

## Objects from the Class

Objects can be created by calls of the form `new("lgCMatrix", ...)` and so on. More frequently objects are created by coercion of a numeric sparse matrix to the logical form for use in the symbolic analysis phase of an algorithm involving sparse matrices. Such algorithms often involve two phases: a symbolic phase wherein the positions of the non-zeros in the result are determined and a numeric phase wherein the actual results are calculated. During the symbolic phase only the positions of the non-zero elements in any operands are of interest, hence any numeric sparse matrices can be treated as logical sparse matrices.

## Slots

- x:** Object of class "logical", i.e., either TRUE, NA, or FALSE.
- uplo:** Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular. Present in the triangular and symmetric classes but not in the general class.
- diag:** Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N" for non-unit. The implicit diagonal elements are not explicitly stored when `diag` is "U". Present in the triangular classes only.
- p:** Object of class "integer" of pointers, one for each column (row), to the initial (zero-based) index of elements in the column. Present in compressed column-oriented and compressed row-oriented forms only.
- i:** Object of class "integer" of length `nnzero` (number of non-zero elements). These are the row numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed column-oriented forms only.
- j:** Object of class "integer" of length `nnzero` (number of non-zero elements). These are the column numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed column-oriented forms only.
- Dim:** Object of class "integer" - the dimensions of the matrix.

## Methods

**coerce** signature(from = "dgCMatrix", to = "lgCMatrix")  
**t** signature(x = "lgCMatrix"): returns the transpose of x

## See Also

the class [dgCMatrix](#)

## Examples

```
(m <- Matrix(c(0,0,2:0), 3,5, dimnames=list(LETTERS[1:3],NULL)))
(lm <- (m > 1)) # lgC
!lm          # no longer sparse
stopifnot(is(lm,"lsparseMatrix"),
           identical(!lm, m <= 1))

data(KNex)
str(mmG.1 <- (KNex $ mm) > 0.1) # "lgC..."
table(mmG.1@x) # however with many ``non-structural zeros''
## from logical to nz_pattern -- okay when there are no NA's :
nmG.1 <- as(mmG.1, "nMatrix") # <<< has "TRUE" also where mmG.1 had FALSE
## from logical to "double"
dmG.1 <- as(mmG.1, "dMatrix") # has '0' and back:
```

```

lmG.1 <- as(dmG.1, "lMatrix") # has no extra FALSE, i.e. drop0() included
stopifnot(identical(nmG.1, as((KNex $ mm) != 0, "nMatrix")),
  validObject(lmG.1), all(lmG.1@x),
  # same "logical" but lmG.1 has no 'FALSE' in x slot:
  all(lmG.1 == mmG.1))

class(xnx <- crossprod(nmG.1))# "nsC.."
class(xlx <- crossprod(mmG.1))# "dsC.." : numeric
is0 <- (xlx == 0)
mean(as.vector(is0))# 99.3% zeros: quite sparse, but
table(xlx@x == 0)# more than half of the entries are (non-structural!) 0
stopifnot(isSymmetric(xlx), isSymmetric(xnx),
  ## compare xnx and xlx : have the *same* non-structural 0s :
  sapply(slotNames(xnx),
    function(n) identical(slot(xnx, n), slot(xlx, n))))

```

---

lsyMatrix-class      *Symmetric Dense Logical Matrices*

---

## Description

The "lsyMatrix" class is the class of symmetric, dense logical matrices in non-packed storage and "lspMatrix" is the class of these in packed storage. In the packed form, only the upper triangle or the lower triangle is stored.

## Objects from the Class

Objects can be created by calls of the form `new("lsyMatrix", ...)`.

## Slots

**uplo:** Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

**x:** Object of class "logical". The logical values that constitute the matrix, stored in column-major order.

**Dim,Dimnames:** The dimension (a length-2 "integer") and corresponding names (or NULL), see the [Matrix](#) class.

**factors:** Object of class "list". A named list of factorizations that have been computed for the matrix.

## Extends

Both extend classes "[ldenseMatrix](#)" and "[symmetricMatrix](#)", directly; further, class "[Matrix](#)" and others, *indirectly*. Use `showClass("lsyMatrix")`, e.g., for details.

## Methods

Currently, mainly `t()` and coercion methods (for `as(.)`; use, e.g., `showMethods(class="dsyMatrix")` for details.

## See Also

[lgeMatrix](#), [Matrix](#), [t](#)

**Examples**

```
(M2 <- Matrix(c(TRUE, NA, FALSE, FALSE), 2, 2)) # logical dense (ltr)
str(M2)
# can
(sM <- M2 | t(M2)) # "lge"
as(sM, "lsyMatrix")
str(sM <- as(sM, "lspMatrix")) # packed symmetric
```

---

ltrMatrix-class      *Triangular Dense Logical Matrices*

---

**Description**

The "ltrMatrix" class is the class of triangular, dense, logical matrices in nonpacked storage. The "ltpMatrix" class is the same except in packed storage.

**Slots**

**x:** Object of class "logical". The logical values that constitute the matrix, stored in column-major order.

**uplo:** Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

**diag:** Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see [triangularMatrix](#).

**Dim,Dimnames:** The dimension (a length-2 "integer") and corresponding names (or NULL), see the [Matrix](#) class.

**factors:** Object of class "list". A named list of factorizations that have been computed for the matrix.

**Extends**

Both extend classes "[ldenseMatrix](#)" and "[triangularMatrix](#)", directly; further, class "[Matrix](#)", "[lMatrix](#)" and others, *indirectly*. Use `showClass("ltrMatrix")`, e.g., for details.

**Methods**

Currently, mainly `t()` and coercion methods (for `as(.)`; use, e.g., `showMethods(class="ltpMatrix")` for details.

**See Also**

Classes [lgeMatrix](#), [Matrix](#); function `t`



**Examples**

```
showClass("ltrMatrix")

str(new("ltpMatrix"))
(lutr <- as(upper.tri(matrix(,4,4)), "ltrMatrix"))
str(lutp <- as(lutr, "ltpMatrix"))# packed matrix: only 10 = (4+1)*4/2 entries
!lutp ## the logical negation (is *not* logical triangular !)
## but this one is:
stopifnot(all.equal(lutp, as(!lutp, "ltpMatrix")))
```

lu

*Triangular Decomposition of a Square Matrix***Description**

Computes triangular decompositions of square matrices.

**Usage**

```
lu(x, ...)
## S4 method for signature 'matrix':
lu(x, warnSing = TRUE, ...)
## S4 method for signature 'dgeMatrix':
lu(x, warnSing = TRUE, ...)
## S4 method for signature 'dgCMatrix':
lu(x, errSing = TRUE, ...)
```

**Arguments**

x	a matrix of square dimension. No missing values or IEEE special values are allowed.
warnSing	(when x is a " <a href="#">denseMatrix</a> ") logical specifying if a <a href="#">warning</a> should be signalled when x is singular.
errSing	(when x is a " <a href="#">sparseMatrix</a> ") logical specifying if an error (see <a href="#">stop</a> ) should be signalled when x is singular. When x is singular, <code>lu(x, errSing=FALSE)</code> returns <a href="#">NA</a> instead of an LU decomposition. No warning is signalled and the user should be careful in that case.
...	further arguments passed to or from other methods.

**Details**

`lu()` is a generic function with special methods for different types of matrices. Use `showMethods("lu")` to list all the methods for the `lu` generic.

The method for class `dgeMatrix` (and all dense matrices) is based on LAPACK's "dgetrf" subroutine. It returns a decomposition also for singular matrices.

The method for class `dgCMatrix` (and all sparse matrices) is based on functions from the CSparse library. It signals an error (or returns `NA`, when `errSing = FALSE`, see above) when the decomposition algorithm fails, as when x is (too close to) singular.

**Value**

An object of class "LU", i.e., "denseLU" or "sparseLU", see [sparseLU](#); this is a representation of a triangular decomposition of  $x$ .

**References**

Golub, G., and Van Loan, C. F. (1989). *Matrix Computations*, 2nd edition, Johns Hopkins, Baltimore.

Tim Davis (2005) <http://www.cise.ufl.edu/research/sparse/CSparse/>

Timothy A. Davis (2006) *Direct Methods for Sparse Linear Systems*, SIAM Series "Fundamentals of Algorithms".

**See Also**

Class definitions [LU](#) and [sparseLU](#) and function [expand](#); [qr](#), [chol](#).

**Examples**

```
##--- Dense -----
x <- Matrix(rnorm(9), 3, 3)
lu(x)

##--- Sparse (see more in ?"sparseLU-class")----- % ./sparseLU-class.Rd

pm <- as(readMM(system.file("external/pores_1.mtx",
                           package = "Matrix")),
         "CsparseMatrix")
str(pmLU <- lu(pm)) # p is a 0-based permutation of the rows
                   # q is a 0-based permutation of the columns
## permute rows and columns of original matrix
ppm <- pm[pmLU@p + 1L, pmLU@q + 1L]
pLU <- drop0(pmLU@L %*% pmLU@U) # L %*% U -- dropping extra zeros
## equal up to "rounding"
ppm[1:14, 1:5]
pLU[1:14, 1:5]
```

---

LU-class

*LU (dense) Matrix Decompositions*


---

**Description**

The "LU" class is the *virtual* class of LU decompositions of real matrices. "denseLU" the class of LU decompositions of dense real matrices.

**Objects from the Class**

Objects can be created by calls of the form `new("denseLU", ...)`. More commonly the objects are created explicitly from calls of the form `lu(mm)` where `mm` is an object that inherits from the "dgeMatrix" class or as a side-effect of other functions applied to "dgeMatrix" objects.

**Extends**

"LU" directly extends the virtual class `"MatrixFactorization"`.

"denseLU" directly extends "LU".

**Slots**

**x**: object of class `"numeric"`. The "L" (unit lower triangular) and "U" (upper triangular) factors of the original matrix. These are stored in a packed format described in the Lapack manual.

**perm**: Object of class `"integer"` - a vector of length `min(Dim)` that describes the permutation applied to the rows of the original matrix. The contents of this vector are described in the Lapack manual.

**Dim**: the dimension of the original matrix; inherited from class `MatrixFactorization`.

**Methods**

**expand** signature(`x = "denseLU"`): Produce the "L" and "U" (and "P") factors as a named list of matrices, see also the example below.

**solve** signature(`a = "denseLU"`, `b = "missing"`): Compute the inverse of  $A$ ,  $A^{-1}$ , `solve(A)` using the LU decomposition.

**Note**

The decomposition is of the form

$$A = PLU$$

where all matrices are of size  $n \times n$ , and the matrix  $P$  is a permutation matrix,  $L$  is lower triangular and  $U$  is upper triangular (both of class `dsyMatrix`).

**See Also**

class `sparseLU` for LU decompositions of *sparse* matrices; further, class `dgeMatrix` and functions `lu`, `expand`.

**Examples**

```
set.seed(1)
mm <- Matrix(round(rnorm(9),2), nrow = 3)
mm
str(lum <- lu(mm))
elu <- expand(lum)
elu # three components: "L", "U", and "P", the permutation
elu$L %*% elu$U
(m2 <- with(elu, P %*% L %*% U)) # the same as 'mm'
stopifnot(all.equal(as(mm, "matrix"),
                    as(m2, "matrix")))
```

Matrix

Construct a Classed Matrix

**Description**

Construct a Matrix of a class that inherits from `Matrix`.

**Usage**

```
Matrix(data=NA, nrow=1, ncol=1, byrow=FALSE, dimnames=NULL,
       sparse = NULL, forceCheck = FALSE)
```

**Arguments**

<code>data</code>	an optional numeric data vector or matrix.
<code>nrow</code>	when <code>data</code> is not a matrix, the desired number of rows
<code>ncol</code>	when <code>data</code> is not a matrix, the desired number of columns
<code>byrow</code>	logical. If <code>FALSE</code> (the default) the matrix is filled by columns, otherwise the matrix is filled by rows.
<code>dimnames</code>	a <code>dimnames</code> attribute for the matrix: a list of two character components. They are set if not <code>NULL</code> (as per default).
<code>sparse</code>	logical or <code>NULL</code> , specifying if the result should be sparse or not. By default, it is made sparse when more than half of the entries are 0.
<code>forceCheck</code>	logical indicating if the checks for structure should even happen when <code>data</code> is already a "Matrix" object.

**Details**

If either of `nrow` or `ncol` is not given, an attempt is made to infer it from the length of `data` and the other parameter. Further, `Matrix()` makes efforts to keep `logical` matrices logical, i.e., inheriting from class `lMatrix`, and to determine specially structured matrices such as symmetric, triangular or diagonal ones. Note that a *symmetric* matrix also needs symmetric `dimnames`, e.g., by specifying `dimnames = list(NULL, NULL)`, see the examples.

Most of the time, the function works via a traditional (*full*) `matrix`. However, `Matrix(0, nrow, ncol)` directly constructs an "empty" `sparseMatrix`, as does `Matrix(FALSE, *)`.

Although it is sometime possible to mix unclassed matrices (created with `matrix`) with ones of class "Matrix", it is much safer to always use carefully constructed ones of class "Matrix".

**Value**

Returns matrix of a class that inherits from "Matrix". Only if `data` is not a `matrix` and does not already inherit from class `Matrix` are the arguments `nrow`, `ncol` and `byrow` made use of.

**See Also**

The classes `Matrix`, `symmetricMatrix`, `triangularMatrix`, and `diagonalMatrix`; further, `matrix`.

Special matrices can be constructed, e.g., via `sparseMatrix` (sparse), `bdiag` (block-diagonal), `bandSparse` (banded sparse), or `Diagonal`.

**Examples**

```

Matrix(0, 3, 2) # 3 by 2 matrix of zeros -> sparse
Matrix(0, 3, 2, sparse=FALSE)# forced 'dense'
Matrix(1:6, 3, 2) # a 3 by 2 matrix (+ integer warning)
Matrix(1:6 + 1, nrow=3)

## logical ones:
Matrix(diag(4) > 0)# -> "ldiMatrix" with diag = "U"
Matrix(diag(4) > 0, sparse=TRUE)# -> sparse...
Matrix(diag(4) >= 0)# -> "lsyMatrix" (of all 'TRUE')
## triangular
l3 <- upper.tri(matrix(,3,3))
(M <- Matrix(l3)) # -> "ltCMatrix"
Matrix(! l3)# -> "ltrMatrix"
as(l3, "CsparseMatrix")

Matrix(1:9, nrow=3,
      dimnames = list(c("a", "b", "c"), c("A", "B", "C")))
(I3 <- Matrix(diag(3)))# identity, i.e., unit "diagonalMatrix"
str(I3) # note the empty 'x' slot

(A <- cbind(a=c(2,1), b=1:2))# symmetric *apart* from dimnames
Matrix(A) # hence 'dgeMatrix'
(As <- Matrix(A, dimnames = list(NULL,NULL)))# -> symmetric
stopifnot(is(As, "symmetricMatrix"),
          is(Matrix(0, 3,3), "sparseMatrix"),
          is(Matrix(FALSE, 1,1), "sparseMatrix"))

```

Matrix-class

*Virtual Class "Matrix" Class of Matrices***Description**

The `Matrix` class is a class contained by all actual classes in the **Matrix** package. It is a “virtual” class.

**Slots**

Common to *all* matrix objects in the package:

**Dim:** Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

**Dimnames:** list of length two; each component containing NULL or a [character](#) vector length equal the corresponding `Dim` element.

**Methods**

**determinant** signature(x = "Matrix", logarithm = "missing"): and

**determinant** signature(x = "Matrix", logarithm = "logical"): compute the (log) determinant of x. The method chosen depends on the actual `Matrix` class of x. Note that `det` also works for all our matrices, calling the appropriate `determinant()` method. The `Matrix::det` is an exact copy of `base::det`, but in the correct namespace, and hence calling the S4-aware version of `determinant()`.

**diff** signature(x = "Matrix"): As `diff()` for traditional matrices, i.e., applying `diff()` to each column.

**dim** signature(x = "Matrix"): extract matrix dimensions `dim`.

**dim<-** signature(x = "Matrix", value = "ANY"): where value is integer of length 2. Allows to *reshape* Matrix objects, but only when `prod(value) == prod(dim(x))`.

**dimnames** signature(x = "Matrix"): extract `dimnames`.

**dimnames<-** signature(x = "Matrix", value = "list"): set the `dimnames` to a `list` of length 2, see `dimnames<-`.

**length** signature(x = "Matrix"): simply defined as `prod(dim(x))` (and hence of mode "double").

**show** signature(object = "Matrix"): `show` method for `printing`.

**image** signature(object = "Matrix"): draws an `image` of the matrix entries, using `levelplot()` from package `lattice`.

**head** signature(object = "Matrix"): return only the "head", i.e., the first few rows.

**tail** signature(object = "Matrix"): return only the "tail", i.e., the last few rows of the respective matrix.

**as.matrix, as.array** signature(x = "Matrix"): the same as `as(x, "matrix")`; see also the note below.

**as.vector** signature(x = "Matrix", mode = "missing"): `as.vector(m)` should be identical to `as.vector(as(m, "matrix"))`, implemented more efficiently for some subclasses.

**as(x, "vector"), as(x, "numeric")** etc, similarly.

There are many more methods that (conceptually should) work for all "Matrix" objects, e.g., `colSums`, `rowMeans`. Even **base** functions may work automatically (if they first call `as.matrix()` on their principal argument), e.g., `apply`, `eigen`, `svd` or `kappa` all do work via coercion to a "traditional" (dense) `matrix`.

## Note

Loading the `Matrix` namespace "overloads" `as.matrix` and `as.array` in the **base** namespace by the equivalent of `function(x) as(x, "matrix")`. Consequently, `as.matrix(m)` or `as.array(m)` will properly work when `m` inherits from the "Matrix" class — *also* for functions in package **base** and other packages. E.g., `apply` or `outer` can therefore be applied to "Matrix" matrices.

## Author(s)

Douglas Bates <bates@stat.wisc.edu> and Martin Maechler

## See Also

the classes `dgeMatrix`, `dgCMatrix`, and function `Matrix` for construction (and examples).

Methods, e.g., for `kronecker`.

**Examples**

```

slotNames("Matrix")

cl <- getClass("Matrix")
names(cl@subclasses) # more than 40 ..

showClass("Matrix")#> output with slots and all subclasses

(M <- Matrix(c(0,1,0,0), 6, 4))
dim(M)
diag(M)
cm <- M[1:4,] + 10*Diagonal(4)
diff(M)
## can reshape it even :
dim(M) <- c(2, 12)
M
stopifnot(identical(M, Matrix(c(0,1,0,0), 2,12)),
           all.equal(det(cm),
                     determinant(as(cm,"matrix"), log=FALSE)$modulus,
                     check.attr=FALSE))

```

---

MatrixFactorization-class

*Class "MatrixFactorization" of Matrix Factorizations*

---

**Description**

The class "MatrixFactorization" is the virtual (super) class of (potentially) all matrix factorizations of matrices from package **Matrix**.

**Objects from the Class**

A virtual Class: No objects may be created from it.

**Slots**

**Dim:** Object of class "integer" - the dimensions of the original matrix - must be an integer vector with exactly two non-negative values.

**Methods**

**dim** (x) simply returns x@Dim, see above.

**expand** signature(x = "MatrixFactorization"): this has not been implemented yet for all matrix factorizations. It should return a list whose components are matrices which when multiplied return the original **Matrix** object.

**show** signature(object = "MatrixFactorization"): simple printing, see [show](#).

**solve** signature(a = "MatrixFactorization", b= .): solve  $Ax = b$  for  $x$ ; has not been implemented for all factorizations, but e.g., for [CHMfactor](#), see there.

**See Also**

classes inheriting from "MatrixFactorization", such as [CHMfactor](#), [LU](#), and [sparseQR](#).

**Examples**

```
showClass("MatrixFactorization")
```

---

ndenseMatrix-class *Virtual Class "ndenseMatrix" of Dense Logical Matrices*

---

**Description**

ndenseMatrix is the virtual class of all dense logical (S4) matrices. It extends both [denseMatrix](#) and [lMatrix](#) directly.

**Slots**

**x**: logical vector containing the entries of the matrix.

**Dim, Dimnames**: see [Matrix](#).

**Extends**

Class "lMatrix", directly. Class "denseMatrix", directly. Class "Matrix", by class "lMatrix". Class "Matrix", by class "denseMatrix".

**Methods**

```
%% signature(x = "nsparseMatrix", y = "ndenseMatrix"):...
```

```
%% signature(x = "ndenseMatrix", y = "nsparseMatrix"):...
```

```
coerce signature(from = "matrix", to = "ndenseMatrix"):...
```

```
coerce signature(from = "ndenseMatrix", to = "matrix"):...
```

```
crossprod signature(x = "nsparseMatrix", y = "ndenseMatrix"):...
```

```
crossprod signature(x = "ndenseMatrix", y = "nsparseMatrix"):...
```

```
as.vector signature(x = "ndenseMatrix", mode = "missing"):...
```

```
diag signature(x = "ndenseMatrix"): extracts the diagonal as for all matrices, see the generic diag\(\).
```

**See Also**

Class [ngeMatrix](#) and the other subclasses.

**Examples**

```
showClass("ndenseMatrix")
```

```
as(diag(3) > 0, "ndenseMatrix")# -> "nge"
```



nearPD

*Nearest Positive Definite Matrix***Description**

Compute the nearest positive definite matrix to an approximate one, typically a correlation or variance-covariance matrix.

**Usage**

```
nearPD(x, corr = FALSE, keepDiag = FALSE, do2eigen = TRUE,
       only.values = FALSE,
       eig.tol = 1e-06, conv.tol = 1e-07, posd.tol = 1e-08,
       maxit = 100, trace = FALSE)
```

**Arguments**

<code>x</code>	numeric $n \times n$ approximately positive definite matrix, typically an approximation to a correlation or covariance matrix. If <code>x</code> is not symmetric, <code>symmpart(x)</code> is used.
<code>corr</code>	logical indicating if the matrix should be a <i>correlation</i> matrix.
<code>keepDiag</code>	logical, generalizing <code>corr</code> : if TRUE, the resulting matrix should have the same diagonal ( <code>diag(x)</code> ) as the input matrix.
<code>do2eigen</code>	logical indicating if a <code>posdefify()</code> eigen step should be applied to the result of the Higham algorithm.
<code>only.values</code>	logical; if TRUE, the result is just the vector of eigen values of the approximating matrix.
<code>eig.tol</code>	defines relative positiveness of eigenvalues compared to largest one, $\lambda_1$ . Eigen values $\lambda_k$ are treated as if zero when $\lambda_k/\lambda_1 \leq \text{eig.tol}$ .
<code>conv.tol</code>	convergence tolerance for Higham algorithm.
<code>posd.tol</code>	tolerance for enforcing positive definiteness (in the final <code>posdefify</code> step when <code>do2eigen</code> is TRUE).
<code>maxit</code>	maximum number of iterations allowed.
<code>trace</code>	logical or integer specifying if convergence monitoring should be traced.

**Details**

This implements the algorithm of Higham (2002), and then forces positive definiteness using code from `posdefify`. The algorithm of Knol DL and ten Berge (1989) (not implemented here) is more general in (1) that it allows constraints to fix some rows (and columns) of the matrix and (2) to force the smallest eigenvalue to have a certain value.

Note that setting `corr = TRUE` just sets `diag(.) <- 1` within the algorithm.

**Value**

If `only.values = TRUE`, a numeric vector of eigen values of the approximating matrix; Otherwise, as by default, an S3 object of class `"nearPD"`, basically a list with components

<code>mat</code>	a matrix of class <code>dpoMatrix</code> , the computed positive-definite matrix.
<code>eigenvalues</code>	numeric vector of eigen values of <code>mat</code> .
<code>corr</code>	logical, just the argument <code>corr</code> .
<code>normF</code>	the Frobenius norm ( <code>norm(x-X, "F")</code> ) of the difference between the original and the resulting matrix.
<code>iterations</code>	number of iterations needed.
<code>converged</code>	logical indicating if iterations converged.

**Author(s)**

Jens Oehlschlaegel donated a first version. Subsequent changes by the Matrix package authors.

**References**

Cheng, Sheung Hun and Higham, Nick (1998) A Modified Cholesky Algorithm Based on a Symmetric Indefinite Factorization; *SIAM J. Matrix Anal. Appl.*, **19**, 1097–1110.

Knol DL, ten Berge JMF (1989) Least-squares approximation of an improper correlation matrix by a proper one. *Psychometrika* **54**, 53–61.

Higham, Nick (2002) Computing the nearest correlation matrix - a problem from finance; *IMA Journal of Numerical Analysis* **22**, 329–343.

**See Also**

A first version of this (with non-optional `corr=TRUE`) has been available as `nearcor()`; and more simple versions with a similar purpose `posdefify()`, both from package `sfsmisc`.

**Examples**

```
set.seed(27)
m <- matrix(round(rnorm(25),2), 5, 5)
m <- m + t(m)
diag(m) <- pmax(0, diag(m)) + 1
(m <- round(cov2cor(m), 2))

str(near.m <- nearPD(m, trace = TRUE))
round(near.m$mat, 2)
norm(m - near.m$mat) # 1.102

if(require("sfsmisc")) {
  m2 <- posdefify(m) # a simpler approach
  norm(m - m2) # 1.185, i.e., slightly "less near"
}

round(nearPD(m, only.values=TRUE), 9)

## A longer example, extended from Jens' original,
## showing the effects of some of the options:

pr <- Matrix(c(1,      0.477, 0.644, 0.478, 0.651, 0.826,
```

```

0.477, 1,      0.516, 0.233, 0.682, 0.75,
0.644, 0.516, 1,      0.599, 0.581, 0.742,
0.478, 0.233, 0.599, 1,      0.741, 0.8,
0.651, 0.682, 0.581, 0.741, 1,      0.798,
0.826, 0.75,  0.742, 0.8,   0.798, 1),
nrow = 6, ncol = 6)

nc. <- nearPD(pr, conv.tol = 1e-7) # default
nc.$iterations # 2
nc.1 <- nearPD(pr, conv.tol = 1e-7, corr = TRUE)
nc.1$iterations # 11 (!)
ncr <- nearPD(pr, conv.tol = 1e-15)
str(ncr)# 3 iterations
ncr.1 <- nearPD(pr, conv.tol = 1e-15, corr = TRUE)
ncr.1 $ iterations # 27 !

## But indeed, the 'corr = TRUE' constraint did ensure a better solution;
## cov2cor() does not just fix it up equivalently :
norm(pr - cov2cor(ncr$mat)) # = 0.09994
norm(pr -      ncr.1$mat) # = 0.08746

```

---

ngeMatrix-class      *Class "ngeMatrix" of General Dense Nonzero-pattern Matrices*

---

## Description

This is the class of general dense nonzero-pattern matrices, see [nMatrix](#).

## Slots

- x:** Object of class "logical". The logical values that constitute the matrix, stored in column-major order.
- Dim,Dimnames:** The dimension (a length-2 "integer") and corresponding names (or NULL), see the [Matrix](#) class.
- factors:** Object of class "list". A named list of factorizations that have been computed for the matrix.

## Extends

Class "ndenseMatrix", directly. Class "lMatrix", by class "ndenseMatrix".  
 Class "denseMatrix", by class "ndenseMatrix". Class "Matrix", by class  
 "ndenseMatrix". Class "Matrix", by class "ndenseMatrix".

## Methods

Currently, mainly `t()` and coercion methods (for `as(.)`); use, e.g., `showMethods(class="ngeMatrix")` for details.

## See Also

Non-general logical dense matrix classes such as [ntrMatrix](#), or [nsyMatrix](#); *sparse* logical classes such as [ngCMatrix](#).

**Examples**

```
showClass("ngeMatrix")
## "lgeMatrix" is really more relevant
```

---

nMatrix-class	<i>Class "nMatrix" of Non-zero Pattern Matrices</i>
---------------	---

---

**Description**

The `nMatrix` class is the virtual “mother” class of all *non-zero pattern* (or simply *pattern*) matrices in the **Matrix** package.

**Slots**

Common to *all* matrix object in the package:

**Dim:** Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

**Dimnames:** list of length two; each component containing NULL or a `character` vector length equal the corresponding `Dim` element.

**Methods**

There is a bunch of coercion methods (for `as(.)`), e.g.,

**coerce** signature(from = "nMatrix", to = "matrix"):...

**coerce** signature(from = "nMatrix", to = "dMatrix"):...

**coerce** signature(from = "nMatrix", to = "lMatrix"):...

**coerce** signature(from = "matrix", to = "nMatrix"): Note that these coercions (must) coerce **NAs** to non-zero, hence conceptually **TRUE**. This is particularly important when `sparseMatrix` objects are coerced to "nMatrix" and hence to `nsparseMatrix`.

**coerce** signature(from = "dMatrix", to = "nMatrix"):...

**coerce** signature(from = "lMatrix", to = "nMatrix"):...

. Additional methods contain,

**which** signature(x = "nMatrix"), semantically equivalent to **base** function `which(x, arr.ind)`; for details, see the `lMatrix` class documentation.

**See Also**

The classes `lMatrix`, `nsparseMatrix`, and the mother class, `Matrix`.

**Examples**

```
getClass("nMatrix")

L3 <- Matrix(upper.tri(diag(3)))
L3 # an "ltMatrix"
as(L3, "nMatrix") # -> ntC*

## similar, not using Matrix()
as(upper.tri(diag(3)), "nMatrix") # currently "ngTMatrix"
```

---

 nnzero

*The Number of Non-Zero Values of a Matrix*


---

### Description

Returns the number of non-zero values of a numeric-like R object, and in particular an object `x` inheriting from class `Matrix`.

### Usage

```
nnzero(x, na.counted = NA)
```

### Arguments

`x` an R object, typically inheriting from class `Matrix` or `numeric`.

`na.counted` a `logical` describing how NAs should be counted. There are three possible settings for `na.counted`:

- TRUE** NAs are counted as non-zero (since “they are not zero”).
- NA** (default) the result will be NA if there are NA’s in `x` (since “NA’s are not known, i.e., *may be zero*”).
- FALSE** NAs are *omitted* from `x` before the non-zero entries are counted.

For sparse matrices, you may often want to use `na.counted = TRUE`.

### Value

the number of non zero entries in `x` (typically `integer`).

Note that for a *symmetric* sparse matrix `S` (i.e., inheriting from class `symmetricMatrix`), `nnzero(S)` is typically *twice* the `length(S@x)`.

### Methods

`signature(x = "ANY")` the default method for non-`Matrix` class objects, simply counts the number 0s in `x`, counting NA’s depending on the `na.counted` argument, see above.

`signature(x = "denseMatrix")` conceptually the same as for traditional `matrix` objects, care has to be taken for `"symmetricMatrix"` objects.

`signature(x = "diagonalMatrix")`, **and** `signature(x = "pMatrix")` fast simple methods for these special `"sparseMatrix"` classes.

`signature(x = "sparseMatrix")` typically, the most interesting method, also carefully taking `"symmetricMatrix"` objects into account.

### See Also

The `Matrix` class also has a `length` method; typically, `length(M)` is much larger than `nnzero(M)` for a sparse matrix `M`, and the latter is a better indication of the *size* of `M`.

**Examples**

```

m <- Matrix(0+1:28, nrow = 4)
m[-3,c(2,4:5,7)] <- m[ 3, 1:4] <- m[1:3, 6] <- 0
(mT <- as(m, "dgTMatrix"))
nnzero(mT)
(S <- crossprod(mT))
nnzero(S)
str(S) # slots are smaller than nnzero()
stopifnot(nnzero(S) == sum(as.matrix(S) != 0)) # failed earlier

data(KNex)
M <- KNex$mm
class(M)
dim(M)
length(M); stopifnot(length(M) == prod(dim(M)))
nnzero(M) # more relevant than length
## the above are also visible from
str(M)

```

norm

*Matrix Norms***Description**

Computes a matrix norm of  $x$ , using Lapack for dense matrices. The norm can be the one norm, the infinity norm, the Frobenius norm, or the maximum modulus among elements of a matrix, as determined by the value of `type`.

**Usage**

```
norm(x, type, ...)
```

**Arguments**

<code>x</code>	a real or complex matrix.
<code>type</code>	A character indicating the type of norm desired. " <code>O</code> ", " <code>o</code> " or " <code>1</code> " specifies the one norm, (maximum absolute column sum); " <code>I</code> " or " <code>i</code> " specifies the infinity norm (maximum absolute row sum); " <code>F</code> " or " <code>f</code> " specifies the Frobenius norm (the Euclidean norm of $x$ treated as if it were a vector); and " <code>M</code> " or " <code>m</code> " specifies the maximum modulus of all the elements in $x$ . The default is " <code>O</code> ". Only the first character of <code>type[1]</code> is used.
<code>...</code>	further arguments passed to or from other methods.

**Details**

For dense matrices, the methods eventually call the Lapack functions `dlange`, `dlansy`, `dlantr`, `zlange`, `zlansy`, and `zlantr`.

**Value**

A numeric value of class "`norm`", representing the quantity chosen according to `type`.

## References

Anderson, E., et al. (1994). *LAPACK User's Guide*, 2nd edition, SIAM, Philadelphia.

## Examples

```
x <- Hilbert(9)
norm(x, "1")
norm(x, "I")
norm(x, "F")
norm(x, "M")
```

---

nsparseMatrix-classes

*Sparse "pattern" Matrices*

---

## Description

The `nsparseMatrix` class is a virtual class of sparse “*pattern*” matrices, i.e., binary matrices conceptually with TRUE/FALSE entries. Only the positions of the elements that are TRUE are stored. These can be stored in the “triplet” form (classes `ngTMatrix`, `nsTMatrix`, and `ntTMatrix` which really contain pairs, not triplets) or in compressed column-oriented form (classes `ngCMatrix`, `nsCMatrix`, and `ntCMatrix`) or in compressed row-oriented form (classes `ngRMatrix`, `nsRMatrix`, and `ntRMatrix`). The second letter in the name of these non-virtual classes indicates general, symmetric, or triangular.

## Objects from the Class

Objects can be created by calls of the form `new("ngCMatrix", ...)` and so on. More frequently objects are created by coercion of a numeric sparse matrix to the pattern form for use in the symbolic analysis phase of an algorithm involving sparse matrices. Such algorithms often involve two phases: a symbolic phase wherein the positions of the non-zeros in the result are determined and a numeric phase wherein the actual results are calculated. During the symbolic phase only the positions of the non-zero elements in any operands are of interest, hence numeric sparse matrices can be treated as sparse pattern matrices.

## Slots

- `uplo`: Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular. Present in the triangular and symmetric classes but not in the general class.
- `diag`: Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N" for non-unit. The implicit diagonal elements are not explicitly stored when `diag` is "U". Present in the triangular classes only.
- `p`: Object of class "integer" of pointers, one for each column (row), to the initial (zero-based) index of elements in the column. Present in compressed column-oriented and compressed row-oriented forms only.
- `i`: Object of class "integer" of length `nnzero` (number of non-zero elements). These are the row numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed column-oriented forms only.
- `j`: Object of class "integer" of length `nnzero` (number of non-zero elements). These are the column numbers for each TRUE element in the matrix. All other elements are FALSE. Present in triplet and compressed column-oriented forms only.
- `Dim`: Object of class "integer" - the dimensions of the matrix.

**Methods**

**coerce** signature(`from = "dgCMatrix"`, `to = "ngCMatrix"`), and many similar ones; typically you should coerce to `"nsparseMatrix"` (or `"nMatrix"`). Note that coercion to a sparse pattern matrix records all the potential non-zero entries, i.e., explicit (“non-structural”) zeroes are coerced to `TRUE`, not `FALSE`, see the example.

**t** signature(`x = "ngCMatrix"`): returns the transpose of `x`

**See Also**

the class `dgCMatrix`

**Examples**

```
(m <- Matrix(c(0,0,2:0), 3,5, dimnames=list(LETTERS[1:3],NULL)))
## ``extract the nonzero-pattern of (m) into an nMatrix'':
nm <- as(m, "nsparseMatrix") ## -> will be a "ngCMatrix"
str(nm) # no 'x' slot
nnm <- !nm      # no longer sparse
(nnm <- as(nnm, "sparseMatrix"))# "lgCMatrix"
## consistency check:
stopifnot(xor(as( nm, "matrix"),
              as(nnm, "matrix")))

## low-level way of adding "non-structural zeros" :
nnm@x[2:4] <- c(FALSE,NA,NA)
nnm
as(nnm, "nMatrix") # NAs *and* non-structural 0 |---> 'TRUE'

data(KNex)
nnm <- as(KNex $ mm, "ngCMatrix")
str(xlx <- crossprod(nnm))# "nsCMatrix"
stopifnot(isSymmetric(xlx))
image(xlx, main=paste("crossprod(nnm) : Sparse", class(xlx)))
```

---

nsyMatrix-class      *Symmetric Dense Nonzero-Pattern Matrices*

---

**Description**

The `"nsyMatrix"` class is the class of symmetric, dense nonzero-pattern matrices in non-packed storage and `"nspMatrix"` is the class of these in packed storage. Only the upper triangle or the lower triangle is stored.

**Objects from the Class**

Objects can be created by calls of the form `new("nsyMatrix", ...)`.

**Slots**

**uplo:** Object of class `"character"`. Must be either `"U"`, for upper triangular, and `"L"`, for lower triangular.



**x:** Object of class "logical". The logical values that constitute the matrix, stored in column-major order.

**Dim,Dimnames:** The dimension (a length-2 "integer") and corresponding names (or NULL), see the [Matrix](#) class.

**factors:** Object of class "list". A named list of factorizations that have been computed for the matrix.

### Extends

"nsyMatrix" extends class "ngeMatrix", directly, whereas

"nspMatrix" extends class "ndenseMatrix", directly.

Both extend class "symmetricMatrix", directly, and class "Matrix" and others, *indirectly*, use `showClass("nsyMatrix")`, e.g., for details.

### Methods

Currently, mainly `t()` and coercion methods (for `as(.)`; use, e.g., `showMethods(class="dsyMatrix")` for details.

### See Also

[ngeMatrix](#), [Matrix](#), [t](#)

### Examples

```
(s0 <- new("nsyMatrix"))

(M2 <- Matrix(c(TRUE, NA, FALSE, FALSE), 2, 2)) # logical dense (ltr)
(sM <- M2 & t(M2)) # "lge"
class(sM <- as(sM, "nMatrix")) # -> "nge"
(sM <- as(sM, "nsyMatrix")) # -> "nsy"
str ( sM <- as(sM, "nspMatrix")) # -> "nsp": packed symmetric
```

---

ntrMatrix-class      *Triangular Dense Logical Matrices*

---

### Description

The "ntrMatrix" class is the class of triangular, dense, logical matrices in nonpacked storage. The "ntpMatrix" class is the same except in packed storage.

### Slots

**x:** Object of class "logical". The logical values that constitute the matrix, stored in column-major order.

**uplo:** Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

**diag:** Object of class "character". Must be either "U", for unit triangular (diagonal is all ones), or "N"; see [triangularMatrix](#).

**Dim,Dimnames:** The dimension (a length-2 "integer") and corresponding names (or NULL), see the [Matrix](#) class.

**factors:** Object of class "list". A named list of factorizations that have been computed for the matrix.

**Extends**

"ntrMatrix" extends class "ngeMatrix", directly, whereas  
 "ntpMatrix" extends class "ndenseMatrix", directly.

Both extend Class "triangularMatrix", directly, and class "denseMatrix", "lMatrix"  
 and others, *indirectly*, use [showClass](#) ("nsyMatrix"), e.g., for details.

**Methods**

Currently, mainly [t\(\)](#) and coercion methods (for [as\(.\)](#); use, e.g.,  
[showMethods](#)(class="nsyMatrix") for details.

**See Also**

Classes [ngeMatrix](#), [Matrix](#); function [t](#)

**Examples**

```
showClass("ntrMatrix")

str(new("ntpMatrix"))
(nutr <- as(upper.tri(matrix(,4,4)), "ntrMatrix"))
str(nutp <- as(nutr, "ntpMatrix"))# packed matrix: only 10 = (4+1)*4/2 entries
!nutp ## the logical negation (is *not* logical triangular !)
## but this one is:
stopifnot(all.equal(nutp, as(!nutp, "ntpMatrix")))
```

---

number-class

*Class "number" of Possibly Complex Numbers*

---

**Description**

The class "number" is a virtual class, currently used for vectors of eigen values which can be  
 "numeric" or "complex".

It is a simple class union ([setClassUnion](#)) of "numeric" and "complex".

**Objects from the Class**

Since it is a virtual Class, no objects may be created from it.

**Examples**

```
showClass("number")
stopifnot( is(1i, "number"), is(pi, "number"), is(1:3, "number") )
```

---

pMatrix-class      *Permutation matrices*

---

### Description

The "pMatrix" class is the class of permutation matrices, stored as 1-based integer permutation vectors.

### Objects from the Class

Objects can be created by calls of the form `new("pMatrix", ...)` or by coercion from an integer permutation vector, see below.

### Slots

**perm:** An integer, 1-based permutation vector, i.e. an integer vector of length `Dim[1]` whose elements form a permutation of `1:Dim[1]`.

**Dim:** Object of class "integer". The dimensions of the matrix which must be a two-element vector of equal, non-negative integers.

**Dimnames:** list of length two; each component containing NULL or a `character` vector length equal the corresponding `Dim` element.

### Extends

Class "`sparseMatrix`" and "`generalMatrix`", directly.

### Methods

`%%` signature(`x = "matrix"`, `y = "pMatrix"`) and other signatures (use `showMethods("%*%", class="pMatrix")`): ...

**coerce** signature(`from = "integer"`, `to = "pMatrix"`): This enables typical "pMatrix" construction, given a permutation vector of `1:n`, see the first example.

**coerce** signature(`from = "numeric"`, `to = "pMatrix"`): a user convenience, to allow `as(perm, "pMatrix")` for numeric `perm` with integer values.

**coerce** signature(`from = "pMatrix"`, `to = "matrix"`): coercion to a traditional FALSE/TRUE `matrix` of `mode` logical. (in earlier version of **Matrix**, it resulted in a 0/1-integer matrix; `logical` makes slightly more sense, corresponding better to the "natural" `sparseMatrix` counterpart, "`ngTMatrix`".)

**coerce** signature(`from = "pMatrix"`, `to = "ngTMatrix"`): coercion to sparse logical matrix of class `ngTMatrix`.

**determinant** signature(`x = "pMatrix"`, `logarithm="logical"`): Since permutation matrices are orthogonal, the determinant must be +1 or -1. In fact, it is exactly the *sign of the permutation*.

**solve** signature(`a = "pMatrix"`, `b = "missing"`): return the inverse permutation matrix.

**t** signature(`x = "pMatrix"`): return the transpose of the permutation matrix (which is also the inverse of the permutation matrix).

**Note**

The inverse of the typical "pMatrix" constructor, `P <- as(ip, "pMatrix")` is simply `ip <- P@perm`.

Subsetting ("indexing", including, `diag`) "pMatrix" objects treats them as nonzero-pattern matrices, i.e., as "ngTMatrix" such that non-matrix subsetting result in `logical` vectors. Sub-assignment (`M[i, j] <- v`) is not sensible and hence an error for these permutation matrices.

**Examples**

```
(pm1 <- as(as.integer(c(2,3,1)), "pMatrix"))
t(pm1) # is the same as
solve(pm1)
pm1 %*% t(pm1) # check that the transpose is the inverse
stopifnot(all(diag(3) == as(pm1 %*% t(pm1), "matrix")),
           is.logical(as(pm1, "matrix")))

set.seed(11)
## random permutation matrix :
(p10 <- as(sample(10), "pMatrix"))

## Permute rows / columns of a numeric matrix :
(mm <- round(array(rnorm(3 * 3), c(3, 3)), 2))
mm %*% pm1
pm1 %*% mm
try(as(as.integer(c(3,3,1)), "pMatrix"))# Error: not a permutation

as(pm1, "ngTMatrix")
p10[1:7, 1:4] # gives an "ngTMatrix" (most economic!)
```

---

printSpMatrix

*Print Sparse Matrices Flexibly*


---

**Description**

Print sparse matrices flexibly. These are the "workhorses" used by the `show` and `print` methods for sparse matrices. If `x` is large, `printSpMatrix2(x)` calls `printSpMatrix()` twice, namely, for the first and the last few rows, suppressing those in between, and also suppresses columns when `x` is too wide.

**Usage**

```
printSpMatrix(x, digits = getOption("digits"), maxp = getOption("max.print"),
             cld = getClassDef(class(x)),
             zero.print = ".", col.names, note.dropping.colnames = TRUE,
             col.trailer = "",
             align = c("fancy", "right"))

printSpMatrix2(x, digits = getOption("digits"), maxp = getOption("max.print"),
              zero.print = ".", col.names, note.dropping.colnames = TRUE,
              suppRows = NULL, suppCols = NULL,
              col.trailer = if(suppCols) "....." else "",
              align = c("fancy", "right"))
```

**Arguments**

<code>x</code>	an R object inheriting from class <code>sparseMatrix</code> .
<code>digits</code>	significant digits to use for printing, see <code>print.default</code> .
<code>maxp</code>	integer, default from <code>options(max.print)</code> , influences how many entries of large matrices are printed at all.
<code>cld</code>	the class definition of <code>x</code> ; must be equivalent to <code>getClassDef(class(x))</code> and exists mainly for possible speedup.
<code>zero.print</code>	character which should be printed for <i>structural</i> zeroes. The default "." may occasionally be replaced by " " (blank); using "0" would look almost like <code>print()</code> of non-sparse matrices.
<code>col.names</code>	logical or string specifying if and how column names of <code>x</code> should be printed, possibly abbreviated. The default is taken from <code>options("sparse.colnames")</code> if that is set, otherwise FALSE unless there are less than ten columns. When TRUE the full column names are printed. When <code>col.names</code> is a string beginning with "abb" or "sub" and ending with an integer <code>n</code> (i.e., of the form "abb... <n>"), the column names are <code>abbreviate()</code> d or <code>substring()</code> ed to (target) length <code>n</code> , see the examples.
<code>note.dropping.colnames</code>	logical specifying, when <code>col.names</code> is FALSE if the dropping of the column names should be noted, TRUE by default.
<code>col.trailer</code>	a string to be appended to the right of each column; this is typically made use of by <code>show(&lt;sparseMatrix&gt;)</code> only, when suppressing columns.
<code>suppRows, suppCols</code>	logicals or NULL, for <code>printSpMatrix2()</code> specifying if rows or columns should be suppressed in printing. If NULL, sensible defaults are determined from <code>dim(x)</code> and <code>options(c("width", "max.print"))</code> . Setting both to FALSE may be a very bad idea.
<code>align</code>	a string specifying how the <code>zero.print</code> codes should be aligned, i.e., padded as strings. The default, "fancy", takes some effort to align the typical <code>zero.print = "."</code> with the decimal points of the numbers printed, whereas <code>align = "right"</code> just makes use of <code>print(*, right = TRUE)</code> .

**Value**

returns `x` *invisibly*, see `invisible`.

**Author(s)**

Martin Maechler

**See Also**

the virtual class `sparseMatrix` and the classes extending it; maybe `spMatrix` as a simple constructor of such matrices.

**Examples**

```
f1 <- gl(5, 3, labels = LETTERS[1:5])
X <- as(f1, "sparseMatrix")
```

```

X ## <==> show(X) <==> print(X)
t(X) ## shows column names, since only 5 columns

X2 <- as(g1(12, 3, labels = paste(LETTERS[1:12], "c", sep=".")),
        "sparseMatrix")
X2
## less nice, but possible:
print(X2, col.names = TRUE) # use [,1] [,2] .. => does not fit

t(X2) # suppressing column names
print(t(X2), col.names=TRUE)
print(t(X2), zero.print = "", col.names="abbr. 1")
print(t(X2), zero.print = "-", col.names="substring 2")

```

---

qr-methods

*QR Decomposition – S4 Methods and Generic*


---

### Description

The "Matrix" package provides methods for the QR decomposition of special classes of matrices. There is a generic function which uses `qr` as default, but methods defined in this package can take extra arguments. In particular there is an option for determining a fill-reducing permutation of the columns of a sparse, rectangular matrix.

### Methods

**x = "dgCMatrix"** QR decomposition of a general sparse double-precision matrix with `nrow(x)`  $\times$  `ncol(x)`. Returns an object of class "sparseQR".

**x = "sparseMatrix"** works via "dgCMatrix".

### See Also

`qr`; documentation for classes `sparseQR` and `dgCMatrix`.

---

rankMatrix

*Rank of a Matrix*


---

### Description

Compute the rank of matrix, a well-defined functional in theory, somewhat ambiguous in practice. We provide several methods, the default corresponding to Matlab's definition.

### Usage

```

rankMatrix(x, tol = NULL,
           method = c("tolNorm2", "qrLINPACK", "useGrad", "maybeGrad"),
           sval = svd(x, 0, 0)$d)

```

**Arguments**

<code>x</code>	numeric matrix, of dimension $n \times m$ , say.
<code>tol</code>	nonnegative number specifying a tolerance for “practically zero” with specific meaning depending on method; by default, $\max(\dim(x)) * .Machine\$double.eps * \max(sval)$ is according to Matlab’s default (for its only method “tolNorm2”).
<code>method</code>	a character string specifying the computational method, can be abbreviated: <b>tolNorm2</b> the number of singular values $\geq tol$ ; <b>qrLINPACK</b> = <code>qr(x, tol, LAPACK=FALSE)\$rank</code> ; this used to be <i>the</i> recommended way to compute a matrix rank for a while in the past. For this method, <code>sval</code> are not used (nor computed). <b>useGrad</b> considering the “gradient” of the (decreasing) singular values, the index of the <i>smallest</i> gap. <b>maybeGrad</b> choosing method “useGrad” only when that seems <i>reasonable</i> ; otherwise using “tolNorm2”.
<code>sval</code>	numeric vector of non-increasing singular values of <code>x</code> ; typically unspecified and computed from <code>x</code> .

**Value**

positive integer in  $1:\min(\dim(x))$ , with attributes detailing the method used.

**Author(s)**

Martin Maechler; for the “\*Grad” methods, building on suggestions by Ravi Varadhan.

**See Also**

[qr](#), [svd](#).

**Examples**

```
rankMatrix(cbind(1, 0, 1:3)) # 2

(meths <- eval(formals(rankMatrix)$method))

## a "border" case:
H12 <- Hilbert(12)
rankMatrix(H12, tol = 1e-20) # 12; but 11 with default method & tol.
sapply(meths, function(.m.) rankMatrix(H12, method = .m.))
## tolNorm2 qrLINPACK useGrad maybeGrad
##      11      12      11      11
```

---

rcond

*Estimate the Reciprocal Condition Number*

---

**Description**

Estimate the reciprocal of the condition number of a matrix.

This is a generic function with several methods, as seen by `showMethods(rcond)`.

**Usage**

```
rcond(x, norm, ...)
```

**Arguments**

`x` an R object that inherits from the `Matrix` class.

`norm` Character indicating the type of norm to be used in the estimate. The default is "O" for the 1-norm ("O" is equivalent to "1"). The other possible value is "I" for the infinity norm, see also `norm`.

`...` further arguments passed to or from other methods.

**Value**

An estimate of the reciprocal condition number of `x`.

**BACKGROUND**

The condition number of a regular (square) matrix is the product of the `norm` of the matrix and the norm of its inverse (or pseudo-inverse).

More generally, the condition number is defined (also for non-square matrices  $A$ ) as

$$\kappa(A) = \frac{\max_{\|v\|=1} \|Av\|}{\min_{\|v\|=1} \|Av\|}.$$

Whenever `x` is *not* a square matrix, in our method definitions, this is typically computed via `rcond(qr.R(qr(X)), ...)` where  $X$  is `x` or `t(x)`.

The condition number takes on values between 1 and infinity, inclusive, and can be viewed as a factor by which errors in solving linear systems with this matrix as coefficient matrix could be magnified.

`rcond()` computes the *reciprocal* condition number  $1/\kappa$  with values in  $[0, 1]$  and can be viewed as a scaled measure of how close a matrix is to being rank deficient (aka "singular").

Condition numbers are usually estimated, since exact computation is costly in terms of floating-point operations. An (over) estimate of reciprocal condition number is given, since by doing so overflow is avoided. Matrices are well-conditioned if the reciprocal condition number is near 1 and ill-conditioned if it is near zero.

**References**

Golub, G., and Van Loan, C. F. (1989). *Matrix Computations*, 2nd edition, Johns Hopkins, Baltimore.

**See Also**

`norm`, `kappa()` from package `base` computes an *approximate* condition number of a "traditional" matrix, even non-square ones, with respect to the  $p = 2$  (Euclidean) `norm.solve`.



**Examples**

```
x <- Matrix(rnorm(9), 3, 3)
rcond(x)
## typically "the same" (with more computational effort):
1 / (norm(x) * norm(solve(x)))
rcond(Hilbert(9)) # should be about 9.1e-13

## For non-square matrices:
rcond(x1 <- cbind(1,1:10))# 0.05278
rcond(x2 <- cbind(x1, 2:11))# practically 0, since x2 does not have full rank

## sparse
(S1 <- Matrix(rbind(0:1,0, diag(3:-2))))
rcond(S1)
m1 <- as(S1, "denseMatrix")
all.equal(rcond(S1), rcond(m1))

## wide and sparse
rcond(Matrix(cbind(0, diag(2:-1))))
```

---

rep2abI

*Replicate Vectors into 'abIndex' Result*


---

**Description**

rep2abI(x, times) conceptually computes `rep.int(x, times)` but with an `abIndex` class result.

**Usage**

```
rep2abI(x, times)
```

**Arguments**

x	numeric vector
times	integer (valued) scalar: the number of repetitions

**Value**

a vector of `class abIndex`

**See Also**

`rep.int()`, the base function; `abIseq`, `abIndex`.

**Examples**

```
(ab <- rep2abI(2:7, 4))
stopifnot(identical(as(ab, "numeric"),
  rep(2:7, 4)))
```

---

```
replValue-class
```

*Virtual Class "replValue" - Simple Class for subassignment Values*

---

### Description

The class "replValue" is a virtual class used for values in signatures for sub-assignment of "Matrix" matrices.

In fact, it is a simple class union ([setClassUnion](#)) of "numeric" and "logical" (and maybe "complex" in the future).

### Objects from the Class

Since it is a virtual Class, no objects may be created from it.

### See Also

[Subassign-methods](#), also for examples.

### Examples

```
showClass("replValue")
```

---

```
rleDiff-class
```

*Class "rleDiff" of rle(diff(.)) Stored Vectors*

---

### Description

Class "rleDiff" is for compactly storing long vectors which mainly consist of *linear* stretches. For such a vector  $x$ , `diff(x)` consists of *constant* stretches and is hence well compressable via `rle()`.

### Objects from the Class

Objects can be created by calls of the form `new("rleDiff", ...)`.

Currently experimental, see below.

### Slots

**first:** A single number (of class "numLike", a class union of "numeric" and "logical").

**rle:** Object of class "rle", basically a `list` with components "lengths" and "values", see `rle()`. As this is used to encode potentially huge index vectors, lengths may be of type `double` here.

### Methods

There is a simple `show` method only.

### Note

This is currently an *experimental* auxiliary class for the class `abIndex`, see there.

**See Also**

[rle](#), [abIndex](#).

**Examples**

```
showClass("rleDiff")

ab <- c(abIseq(2, 100), abIseq(20, -2))
ab@rleD # is "rleDiff"
```

---

RsparseMatrix-class

*Class "RsparseMatrix" of Sparse Matrices in Column-compressed Form*

---

**Description**

The "RsparseMatrix" class is the virtual class of all sparse matrices coded in sorted compressed row-oriented form. Since it is a virtual class, no objects may be created from it. See `showClass("RsparseMatrix")` for its subclasses.

**Slots**

**j**: Object of class "integer" of length `nnzero` (number of non-zero elements). These are the row numbers for each non-zero element in the matrix.

**p**: Object of class "integer" of pointers, one for each row, to the initial (zero-based) index of elements in the row.

**Dim, Dimnames**: inherited from the superclass, see [sparseMatrix](#).

**Extends**

Class "sparseMatrix", directly. Class "Matrix", by class "sparseMatrix".

**Methods**

Only **few** methods are defined currently on purpose, since we rather use the [CsparseMatrix](#) in **Matrix**. Recently, more methods were added but *beware* that these typically do *not* return "RsparseMatrix" results, but rather `Csparse*` or `Tsparse*` ones.

```
t signature(x = "RsparseMatrix"):...
coerce signature(from = "RsparseMatrix", to = "CsparseMatrix"):...
coerce signature(from = "RsparseMatrix", to = "TsparseMatrix"):...
```

**See Also**

its superclass, [sparseMatrix](#), and, e.g., class [dgRMatrix](#) for the links to other classes.

**Examples**

```
showClass("RsparseMatrix")
```

Schur

*Schur Decomposition of a Matrix***Description**

Computes the Schur decomposition and eigenvalues of a square matrix; see the BACKGROUND information below.

**Usage**

```
Schur(x, vectors, ...)
```

**Arguments**

<code>x</code>	numeric (or complex, in future) square Matrix (inheriting from class "Matrix"). Missing values (NAs) are not allowed.
<code>vectors</code>	logical. When TRUE (the default), the Schur vectors are computed, and the result is a proper <a href="#">MatrixFactorization</a> of class <a href="#">Schur</a> .
<code>...</code>	further arguments passed to or from other methods.

**Details**

Based on the Lapack subroutine dgees.

**Value**

If `vectors` are TRUE, as per default, an object of class [Schur](#).

If `vectors` are FALSE, a list with components

<code>T</code>	the upper quasi-triangular (square) matrix of the Schur decomposition.
<code>EValues</code>	the vector of <a href="#">numeric</a> or <a href="#">complex</a> eigen values of $T$ or $A$ .

**BACKGROUND**

If  $A$  is a square matrix, then  $A = Q T \iota(Q)$ , where  $Q$  is orthogonal, and  $T$  is upper block-triangular (nearly triangular with either 1 by 1 or 2 by 2 blocks on the diagonal) where the 2 by 2 blocks correspond to (non-real) complex eigenvalues. The eigenvalues of  $A$  are the same as those of  $T$ , which are easy to compute. The Schur form is used most often for computing non-symmetric eigenvalue decompositions, and for computing functions of matrices such as matrix exponentials.

**References**

Anderson, E., et al. (1994). *LAPACK User's Guide*, 2nd edition, SIAM, Philadelphia.

**Examples**

```

Schur(Hilbert(9))           # Schur factorization (real eigenvalues)

(A <- Matrix(round(rnorm(5*5, sd = 100)), nrow = 5))
(Sch.A <- Schur(A))

eTA <- eigen(Sch.A@T)
str(SchA <- Schur(A, vectors=FALSE)) # no 'T' ==> simple list
stopifnot(all.equal(eTA$values, eigen(A)$values, tol = 1e-13),
           all.equal(eTA$values,
                     local({z <- Sch.A@EValues
                             z[order(Mod(z), decreasing=TRUE)]}), tol = 1e-13),
           identical(SchA$T, Sch.A@T),
           identical(SchA$EValues, Sch.A@EValues))

```

Schur-class

*Class "Schur" of Schur Matrix Factorizations***Description**

Class "Schur" is the class of Schur matrix factorizations. These are a generalization of eigen value (or "spectral") decompositions for general (possibly asymmetric) square matrices, see the [Schur\(\)](#) function.

**Objects from the Class**

Objects of class "Schur" are typically created by [Schur\(\)](#).

**Slots**

"Schur" has slots

**T:** Upper Block-triangular [Matrix](#) object.

**Q:** Square *orthogonal* "Matrix".

**EValues:** numeric or complex vector of eigenvalues of T.

**Dim:** the matrix dimension: equal to `c(n, n)` of class "integer".

**Extends**

Class "[MatrixFactorization](#)", directly.

**See Also**

[Schur\(\)](#) for object creation; [MatrixFactorization](#).

**Examples**

```

showClass("Schur")
Schur(M <- Matrix(c(1:7, 10:2), 4, 4))
## Trivial, of course:
str(Schur(Diagonal(5)))

## for more examples, see Schur()

```

---

 sparse.model.matrix

*Construct Sparse Design / Model Matrices*


---

## Description

Construct a Model or “Design” Matrix

## Usage

```
sparse.model.matrix(object, data = environment(object),
                    contrasts.arg = NULL, xlev = NULL, transpose = FALSE, ...)
```

## Arguments

object	an object of an appropriate class. For the default method, a model formula or terms object.
data	a data frame created with <code>model.frame</code> . If another sort of object, <code>model.frame</code> is called first.
contrasts.arg	A list, whose entries are contrasts suitable for input to the <code>contrasts</code> replacement function and whose names are the names of columns of data containing factors.
xlev	to be used as argument of <code>model.frame</code> if data has no "terms" attribute.
transpose	logical indicating if the <i>transpose</i> should be returned; if the transposed is used anyway, setting <code>transpose = TRUE</code> is more efficient.
...	further arguments passed to or from other methods.

## Value

a sparse matrix, inheriting from `CsparseMatrix`, typically of class `dgCMatrix`.

## Author(s)

Doug Bates and Martin Maechler, with initial suggestions from Tim Hesterberg.

## See Also

`model.matrix` in standard R’s package `stats`.

`as(f, "sparseMatrix")` (see `coerce(from = "factor", ..)` in the class doc `sparseMatrix`) produces the *transposed* sparse model matrix for a single factor `f` (and *no* contrasts).

## Examples

```
dd <- data.frame(a = gl(3,4), b = gl(4,1,12)) # balanced 2-way
options("contrasts") # the default: "contr.treatment"
sparse.model.matrix(~ a + b, dd)
sparse.model.matrix(~ -1+ a + b, dd) # no intercept --> even sparser
sparse.model.matrix(~ a + b, dd, contrasts = list(a="contr.sum"))
sparse.model.matrix(~ a + b, dd, contrasts = list(b="contr.SAS"))
```

```
## Sparse method is equivalent to the traditional one :
stopifnot(all(sparse.model.matrix(~ a + b, dd) ==
  Matrix(model.matrix(~ a + b, dd), sparse=TRUE)),
  all(sparse.model.matrix(~ 0+ a + b, dd) ==
  Matrix(model.matrix(~ 0+ a + b, dd), sparse=TRUE)))
```

---

sparseLU-class      *Sparse LU decomposition of a square sparse matrix*

---

### Description

Objects of this class contain the components of the LU decomposition of a sparse square matrix.

### Objects from the Class

Objects can be created by calls of the form `new("sparseLU", ...)` but are more commonly created by function `lu()` applied to a sparse matrix, such as a matrix of class `dgCMatrix`.

### Slots

**L:** Object of class `"dtCMatrix"`, the lower triangular factor from the left.  
**U:** Object of class `"dtCMatrix"`, the upper triangular factor from the right.  
**p:** Object of class `"integer"`, permutation applied from the left.  
**q:** Object of class `"integer"`, permutation applied from the right.  
**Dim:** the dimension of the original matrix; inherited from class `MatrixFactorization`.

### Extends

Class `"LU"`, directly. Class `"MatrixFactorization"`, by class `"LU"`.

### Methods

**expand signature** (`x = "sparseLU"`) Returns a list with components `P`, `L`, `U`, and `Q`, where `P` and `Q` represent fill-reducing permutations, and `L`, and `U` the lower and upper triangular matrices of the decomposition. The original matrix corresponds to the product `PLUQ`.

### Note

The decomposition is of the form

$$A = P'LUQ$$

where all matrices are sparse and of size  $n \times n$ . The matrices `P`, its transpose `P'`, and `Q` are permutation matrices, `L` is lower triangular and `U` is upper triangular.

### See Also

`lu`, `solve`, `dgCMatrix`

**Examples**

```
## Extending the one in examples(lu), calling the matrix A,
## and confirming the factorization identities :
A <- as(readMM(system.file("external/pores_1.mtx",
                           package = "Matrix")),
        "CsparseMatrix")
str(luA <- lu(A)) # p is a 0-based permutation of the rows
                  # q is a 0-based permutation of the columns

xA <- expand(luA)
## which is simply doing
stopifnot(identical(xA$L, luA@L),
          identical(xA$U, luA@U),
          identical(xA$P, as(luA@p + 1L, "pMatrix")),
          identical(xA$Q, as(luA@q + 1L, "pMatrix")))

P.LUQ <- with(xA, t(P) %*% L %*% U %*% Q)
stopifnot(all.equal(A, P.LUQ, tol = 1e-12))
## permute rows and columns of original matrix
pA <- A[luA@p + 1L, luA@q + 1L]
stopifnot(identical(pA, with(xA, P %*% A %*% t(Q))))

pLU <- drop0(luA@L %*% luA@U) # L %*% U -- dropping extra zeros
stopifnot(all.equal(pA, pLU))
```

---

SparseM-conversions

*Sparse Matrix Coercion from and to those from package "SparseM"*

---

**Description**

Methods for coercion from and to sparse matrices from package **SparseM** are provided here, for ease of porting functionality to the **Matrix** package, and comparing functionality of the two packages.

**Methods**

```
from = "matrix.csr", to = "dgRMatrix" ...
from = "matrix.csc", to = "dgCMatrix" ...
from = "matrix.coo", to = "dgTMatrix" ...
from = "dgRMatrix", to = "matrix.csr" ...
from = "dgCMatrix", to = "matrix.csc" ...
from = "dgTMatrix", to = "matrix.coo" ...
from = "sparseMatrix", to = "matrix.csr" ...
from = "matrix.csr", to = "dgCMatrix" ...
from = "matrix.coo", to = "dgCMatrix" ...
from = "matrix.csr", to = "Matrix" ...
from = "matrix.csc", to = "Matrix" ...
from = "matrix.coo", to = "Matrix" ...
```



**See Also**

The documentation in package **SparseM**, such as [SparseM.ontology](#), and one important class, [matrix.csr](#).

---

 sparseMatrix

*General Sparse Matrix Construction from Nonzero Entries*


---

**Description**

User friendly construction of a compressed, column-oriented, sparse matrix, inheriting from [class CsparseMatrix](#), from locations (and values) of its nonzero entries.

This is the recommended user interface rather than direct `new("***Matrix", ...)` calls.

**Usage**

```
sparseMatrix(i = ep, j = ep, p, x, dims, dimnames, index1 = TRUE)
```

**Arguments**

<code>i, j</code>	integer vectors of the same length specifying the locations (row and column indices) of the non-zero (or non-TRUE) entries of the matrix.
<code>p</code>	numeric (integer valued) vector of pointers, one for each column (or row), to the initial (zero-based) index of elements in the column (or row). Exactly one of <code>i</code> , <code>j</code> or <code>p</code> must be missing.
<code>x</code>	optional values of the matrix entries. If specified, must be of the same length as <code>i</code> / <code>j</code> , or of length one where it will be recycled to full length. If missing, the resulting matrix will be a 0/1 pattern matrix, i.e., extending class <a href="#">nsparseMatrix</a> .
<code>dims</code>	optional, non-negative, integer, dimensions vector of length 2. Defaults to <code>c(max(i), max(j))</code> .
<code>dimnames</code>	optional list of <a href="#">dimnames</a> ; if not specified, none, i.e., <code>NULL</code> ones, are used.
<code>index1</code>	logical scalar. If <code>TRUE</code> , the default, the index vectors <code>i</code> and/or <code>j</code> are 1-based, as is the convention in <b>R</b> . That is, counting of rows and columns starts at 1. If <code>FALSE</code> the index vectors are 0-based so counting of rows and columns starts at 0; this corresponds to the internal representation.

**Details**

Exactly one of the arguments `i`, `j` and `p` must be missing.

In typical usage, `p` is missing, `i` and `j` are vectors of positive integers and `x` is a numeric vector. These three vectors, which must have the same length, form the triplet representation of the sparse matrix.

If `i` or `j` is missing then `p` must be a non-decreasing integer vector whose first element is zero. It provides the compressed, or “pointer” representation of the row or column indices, whichever is missing. The expanded form of `p`, `rep(seq_along(dp), dp)` where `dp <- diff(p)`, is used as the (1-based) row or column indices.

The values of `i`, `j`, `p` and `index1` are used to create 1-based index vectors `i` and `j` from which a [TsparseMatrix](#) is constructed, with numerical values given by `x`, if non-missing. The [CsparseMatrix](#) derived from this triplet form is returned.

The reason for returning a `CsparseMatrix` object instead of the triplet format is that the compressed column form is easier to work with when performing matrix operations. In particular, if there are no zeros in `x` then a `CsparseMatrix` is a unique representation of the sparse matrix.

### Value

A sparse matrix in compressed, column-oriented form, as an R object inheriting from both `CsparseMatrix` and `generalMatrix`.

### See Also

`Matrix(*, sparse=TRUE)` for the more usual constructor of such matrices; further `bdiag` and `Diagonal` for (block-)diagonal and `bandSparse` for banded sparse matrix constructors.

Consider `CsparseMatrix` and similar class definition help files.

### Examples

```
## simple example
i <- c(1,3:8); j <- c(2,9,6:10); x <- 7 * (1:7)
(A <- sparseMatrix(i, j, x = x))
summary(A)
str(A) # note that *internally* 0-based row indices are used

## dims can be larger than the maximum row or column indices
(AA <- sparseMatrix(c(1,3:8), c(2,9,6:10), x = 7 * (1:7), dims = c(10,20)))
summary(AA)

## i, j and x can be in an arbitrary order, as long as they are consistent
set.seed(1); (perm <- sample(1:7))
(A1 <- sparseMatrix(i[perm], j[perm], x = x[perm]))
stopifnot(identical(A, A1))

## the (i,j) pairs can be repeated, in which case the x's are summed
(args <- data.frame(i = c(i, 1), j = c(j, 2), x = c(x, 2)))
(Aa <- do.call(sparseMatrix, args))

## pointer vectors can be used, and the (i,x) slots are sorted if necessary:
m <- sparseMatrix(i = c(3, 1, 3:2, 2:1), p = c(0:2, 4,4,6), x = 1:6)
m
str(m)

sparseMatrix(x = 2.72, i=1:3, j=2:4) # recycling x
sparseMatrix(x = TRUE, i=1:3, j=2:4) # recycling x, |--> "lgCMatrix"

## no 'x' --> patter*n* matrix:
(n <- sparseMatrix(i=1:6, j=rev(2:7)))# -> ngCMatrix

## an empty sparse matrix:
(e <- sparseMatrix(dims = c(4,6), i={}, j={}))

## pointers example in converting from other sparse matrix representations.
if(require(SparseM)) {
  X <- model.matrix(read.matrix.hb(system.file("data", "rua_32_ax.rua",
    package = "SparseM")))
  XX <- sparseMatrix(j = X@ja, p = X@ia - 1L, x = X@ra, dims = X@dimension)
  validObject(XX)
}
```

```

## Alternatively, and even more user friendly :
X. <- as(X, "Matrix") # or also
X2 <- as(X, "sparseMatrix")
stopifnot(identical(XX, X.), identical(X., X2))
}

```

---

sparseMatrix-class *Virtual Class "sparseMatrix" — Mother of Sparse Matrices*

---

## Description

Virtual Mother Class of All Sparse Matrices

## Slots

**Dim:** Object of class "integer" - the dimensions of the matrix - must be an integer vector with exactly two non-negative values.

**Dimnames:** a list of length two - inherited from class `Matrix`, see [Matrix](#).

## Extends

Class "Matrix", directly.

## Methods

**show** (object = "sparseMatrix"): The `show` method for sparse matrices prints “*structural*” zeroes as "." using `printSpMatrix()` which allows further customization.

**print** signature(x = "sparseMatrix"),...

The `print` method for sparse matrices by default is the same as `show()` but can be called with extra optional arguments, see `printSpMatrix()`.

**summary** (object = "sparseMatrix"): Returns an object of S3 class "sparseSummary" which is basically a `data.frame` with columns (i, j, x) (or just (i, j) for `nsparseMatrix` class objects) with the stored (typically non-zero) entries. The `print` method resembles Matlab’s way of printing sparse matrices, and also the MatrixMarket format, see `writeMM`.

**determinant** (x = "sparseMatrix", logarithm=TRUE): `determinant()` methods for sparse matrices typically work via `Cholesky` or `lu` decompositions.

**diag** (x = "sparseMatrix"): extracts the diagonal of a sparse matrix.

**dim<-** signature(x = "sparseMatrix", value = "ANY"): allows to *reshape* a sparse matrix to a sparse matrix with the same entries but different dimensions. value must be of length two and fulfill `prod(value) == prod(dim(x))`.

**coerce** signature(from = "factor", to = "sparseMatrix"): Coercion of a factor to "sparseMatrix" produces the matrix of indicator **rows** stored as an object of class "dgCMatrix". To obtain columns representing the interaction of the factor and a numeric covariate, replace the "x" slot of the result by the numeric covariate then take the transpose. Missing values (NA) from the factor are translated to columns of all 0s.

See also `colSums`, `norm`, ... for methods with separate help pages.

**Note**

In method selection for multiplication operations (i.e. `%*%` and the two-argument form of `crossprod`) the `sparseMatrix` class takes precedence in the sense that if one operand is a sparse matrix and the other is any type of dense matrix then the dense matrix is coerced to a `dgeMatrix` and the appropriate sparse matrix method is used.

**Examples**

```
showClass("sparseMatrix") ## and look at the help() of its subclasses
M <- Matrix(0, 10000, 100)
M[1,1] <- M[2,3] <- 3.14
M ## show(.) method suppresses printing of the majority of rows

data(CAex); dim(CAex) # 72 x 72 matrix
determinant(CAex) # works via sparse lu(.)

## factor -> t( <sparse design matrix> ) :
(fact <- gl(5, 3, 30, labels = LETTERS[1:5]))
(Xt <- as(fact, "sparseMatrix")) # indicator rows

## missing values --> all-0 columns:
f.mis <- fact
i.mis <- c(3:5, 17)
is.na(f.mis) <- i.mis
Xt != (X. <- as(f.mis, "sparseMatrix")) # differ only in columns 3:5,17
stopifnot(all(X.[,i.mis] == 0), all(Xt[, -i.mis] == X.[, -i.mis]))
```

---

 sparseQR-class

*Sparse QR decomposition of a sparse matrix*


---

**Description**

Objects of this class represent a QR decomposition of a sparse rectangular matrix.

**Details**

The decomposition is of the form  $A[p+1,] == Q \%*\% R$ , if the `q` slot is of length 0 or  $A[p+1, q+1] == Q \%*\% R$  where  $A$  is a sparse  $m \times n$  matrix ( $m \geq n$ ),  $R$  is an  $m \times n$  matrix that is zero below the main diagonal. The `p` slot is a 0-based permutation of  $1:m$  applied to the rows of the original matrix. If the `q` slot has length  $n$  it is a 0-based permutation of  $1:n$  applied to the columns of the original matrix to reduce the amount of "fill-in" in the matrix  $R$ .

The matrix  $Q$  is a "virtual matrix". It is the product of  $n$  Householder transformations. The information to generate these Householder transformations is stored in the `V` and `beta` slots.

The "sparseQR" methods for the `qr.*` functions return objects of class "dgeMatrix" (see `dgeMatrix`). Results from `qr.coef`, `qr.resid` and `qr.fitted` (when `k == ncol(R)`) are well-defined and should match those from the corresponding dense matrix calculations. However, because the matrix  $Q$  is not uniquely defined, the results of `qr.qy` and `qr.qty` do not necessarily match those from the corresponding dense matrix calculations.

Also, the results of `qr.qy` and `qr.qty` apply to the permuted column order when the `q` slot has length  $n$ .

### Objects from the Class

Objects can be created by calls of the form `new("sparseQR", ...)` but are more commonly created by function `qr` applied to a sparse matrix such as a matrix of class `dgCMatrix`.

### Slots

**V:** Object of class "dgCMatrix". The columns of  $V$  are the vectors that generate the Householder transformations of which the matrix  $Q$  is composed.

**beta:** Object of class "numeric", the normalizing factors for the Householder transformations.

**p:** Object of class "integer": Permutation (of  $0:(n-1)$ ) applied to the rows of the original matrix.

**R:** Object of class "dgCMatrix" An upper triangular matrix of dimension  $\backslash$

**q:** Object of class "integer": Permutation applied from the right. Can be of length 0 which implies no permutation.

### Methods

```
qr.R signature(qr = "sparseQR"):...
qr.coef signature(qr = "sparseQR", y = "dgeMatrix"):...
qr.coef signature(qr = "sparseQR", y = "matrix"):...
qr.coef signature(qr = "sparseQR", y = "numeric"):...
qr.fitted signature(qr = "sparseQR", y = "dgeMatrix"):...
qr.fitted signature(qr = "sparseQR", y = "matrix"):...
qr.fitted signature(qr = "sparseQR", y = "numeric"):...
qr.qty signature(qr = "sparseQR", y = "dgeMatrix"):...
qr.qty signature(qr = "sparseQR", y = "matrix"):...
qr.qty signature(qr = "sparseQR", y = "numeric"):...
qr.qy signature(qr = "sparseQR", y = "dgeMatrix"):...
qr.qy signature(qr = "sparseQR", y = "matrix"):...
qr.qy signature(qr = "sparseQR", y = "numeric"):...
qr.resid signature(qr = "sparseQR", y = "dgeMatrix"):...
qr.resid signature(qr = "sparseQR", y = "matrix"):...
qr.resid signature(qr = "sparseQR", y = "numeric"):...
solve signature(a = "sparseQR", b = "ANY"): simply uses qr.coef(a,b).
```

### See Also

`qr`, `qr.Q`, `qr.R`, `qr.fitted`, `qr.resid`, `qr.coef`, `qr.qty`, `qr.qy`, `dgCMatrix`, `dgeMatrix`.

### Examples

```
data(KNex); mm <- KNex$mm
str(mmQR <- qr(mm))
```

---

sparseVector-class *Sparse Vector Classes*

---

## Description

**Sparse Vector Classes:** The virtual mother class "sparseVector" has the five actual daughter classes "dsparseVector", "isparseVector", "lsparseVector", "nsparseVector", and "zsparseVector", where we've mainly implemented methods for the  $d^*$ ,  $l^*$  and  $n^*$  ones.

## Slots

**length:** class "numeric" - the `length` of the sparse vector. Note that "numeric" can be considerably larger than the maximal "integer", `.Machine$integer.max`, on purpose.

**i:** class "integer" - the (1-based) indices of the non-zero entries. Must *not* be NA.

**x:** (for all but "nsparseVector"): the non-zero entries. This is of class "numeric" for class "dsparseVector", "logical" for class "lsparseVector", etc.

Note that "nsparseVector"s have no `x` slot. Further, mainly for ease of method definitions, we've defined the class union (see `setClassUnion`) of all sparse vector classes which *have* an `x` slot, as class "xsparseVector".

## Methods

**length** signature (`x = "sparseVector"`): simply extracts the `length` slot.

**show** signature (`object = "sparseVector"`): The `show` method for sparse vectors prints "structural" zeroes as "." using the non-exported `prSpVector` function which allows further customization such as replacing "." by " " (blank).

Note that `options(max.print)` will influence how many entries of large sparse vectors are printed at all.

**as.vector** signature (`x = "sparseVector", mode = "character"`) coerces sparse vectors to "regular", i.e., atomic vectors. This is the same as `as(x, "vector")`.

**dim<-** signature (`x = "sparseVector", value = "integer"`) coerces a sparse vector to a sparse Matrix, i.e., an object inheriting from `sparseMatrix`, of the appropriate dimension.

**rep** signature (`x = "sparseVector"`) repeat `x`, with the same argument list (`x`, `times`, `length.out`, `each`, ...) as the default method for `rep()`.

**Ops** signature (`e1 = "sparseVector", e2 = "*"`): define arithmetic, compare and logic operations, (see `Ops`).

**Summary** signature (`x = "sparseVector"`): define all the `Summary` methods.

## Examples

```
getClass("sparseVector")
getClass("dsparseVector")
getClass("xsparseVector") # those with an 'x' slot

sx <- c(0,0,3, 3.2, 0,0,0,-3:1,0,0,2,0,0,5,0,0)
```

```

(ss <- as(sx, "sparseVector"))

ix <- as.integer(round(sx))
(is <- as(ix, "sparseVector"))
## an "isparsedVector" (!)

## rep() works too:
(ri <- rep(is, length.out= 25))

## Using `dim<-` as in base R :
r <- ss
dim(r) <- c(4,5) # becomes a sparse Matrix:
r

## currently has "non-structural" FALSE -- printing as ":"
(lis <- is & FALSE)
(nn <- is[is == 0]) # all "structural" FALSE

## NA-case
sN <- sx; sN[4] <- NA
(svN <- as(sN, "sparseVector"))

stopifnot(identical(is | FALSE, is != 0),
  validObject(svN), validObject(lis), as.logical(is.na(svN[4])),
  identical(is^2 > 0, is & TRUE),
  all(!lis), !any(lis), length(nn@i) == 0, !any(nn), all(!nn),
  sum(lis) == 0, !prod(lis), range(lis) == c(0,0))

```

---

spMatrix

*Sparse Matrix Constructor From Triplet*


---

## Description

User friendly construction of a sparse matrix (inheriting from class `TsparseMatrix`) from the triplet representation.

## Usage

```
spMatrix(nrow, ncol, i = integer(), j = integer(), x = numeric())
```

## Arguments

nrow, ncol	integers specifying the desired number of rows and columns.
i, j	integer vectors of the same length specifying the locations of the non-zero (or non-TRUE) entries of the matrix.
x	atomic vector of the same length as i and j, specifying the values of the non-zero entries.

**Value**

A sparse matrix in triplet form, as an R object inheriting from both `TsparseMatrix` and `generalMatrix`.

The matrix  $M$  will have  $M[i[k], j[k]] == x[k]$ , for  $k = 1, 2, \dots, n$ , where  $n = \text{length}(i)$  and  $M[i', j'] == 0$  for all other pairs  $(i', j')$ .

**See Also**

`Matrix(*, sparse=TRUE)` for the more usual constructor of such matrices; similarly, `sparseMatrix` which is a bit more general than `spMatrix()` and returns a `CsparseMatrix` which is often slightly more desirable. Further, `bdiag` and `Diagonal` for (block-)diagonal matrix constructors.

Consider `TsparseMatrix` and similar class definition help files.

**Examples**

```
## simple example
A <- spMatrix(10,20, i = c(1,3:8),
              j = c(2,9,6:10),
              x = 7 * (1:7))

A # a "dgTMatrix"
summary(A)
str(A) # note that *internally* 0-based indices (i,j) are used

L <- spMatrix(9, 30, i = rep(1:9, 3), 1:27,
             (1:27) %% 4 != 1)
L # an "lgTMatrix"

### This is a useful utility, to be used for experiments :

rSpMatrix <- function(nrow, ncol, nnz,
                     rand.x = function(n) round(rnorm(nnz), 2))
{
  ## Purpose: random sparse matrix
  ## -----
  ## Arguments: (nrow,ncol): dimension
  ##           nnz : number of non-zero entries
  ##           rand.x: random number generator for 'x' slot
  ## -----
  ## Author: Martin Maechler, Date: 14.-16. May 2007
  stopifnot((nnz <- as.integer(nnz)) >= 0,
            nrow >= 0, ncol >= 0,
            nnz <= nrow * ncol)
  spMatrix(nrow, ncol,
           i = sample(nrow, nnz, replace = TRUE),
           j = sample(ncol, nnz, replace = TRUE),
           x = rand.x(nnz))
}

M1 <- rSpMatrix(100000, 20, nnz = 200)
summary(M1)
```



---

 symmetricMatrix-class

*Virtual Class of Symmetric Matrices in package:Matrix*


---

## Description

The virtual class of symmetric matrices, "symmetricMatrix", from the package **Matrix** contains numeric and logical, dense and sparse matrices, e.g., see the examples.

The main use is in methods (and C functions) that can deal with all symmetric matrices.

## Slots

**uplo:** Object of class "character". Must be either "U", for upper triangular, and "L", for lower triangular.

**Dim, Dimnames:** The dimension (a length-2 "integer") and corresponding names (or NULL), inherited from the [Matrix](#), see there.

**factors:** a list of matrix factorizations, also from the [Matrix](#) class.

## Extends

Class "Matrix", directly.

## Methods

There's a C function `symmetricMatrix_validity()` called by the internal validity checking functions.

## See Also

Classes [triangularMatrix](#), and, e.g., [dsyMatrix](#) for numeric *dense* matrices, or [lsCMatrix](#) for a logical *sparse* matrix class.

## Examples

```
showClass("symmetricMatrix")

## The names of direct subclasses:
scl <- getClass("symmetricMatrix")@subclasses
directly <- sapply(lapply(scl, slot, "by"), length) == 0
names(scl)[directly]
```

---

 symmpart

*Symmetric Part and Skew(symmetric) Part of a Matrix*


---

**Description**

symmpart(x) computes the symmetric part  $(x + t(x))/2$  and the skew symmetric part  $(x - t(x))/2$  of a square matrix x. Note that  $x == \text{symmpart}(x) + \text{skewpart}(x)$  for all square matrices – apart from extraneous NA values in the RHS.

**Usage**

```
symmpart(x)
skewpart(x)
```

**Arguments**

x a *square* matrix; either “traditional” of class "matrix", or typically, inheriting from the [Matrix](#) class.

**Value**

symmpart() returns a symmetric matrix, inheriting from [symmetricMatrix](#) iff x inherited from [Matrix](#).

skewpart() returns a skew-symmetric matrix, typically of the same class as x (or the closest “general” one, see [generalMatrix](#)).

**Examples**

```
m <- Matrix(1:4, 2, 2)
symmpart(m)
skewpart(m)

stopifnot(all(m == symmpart(m) + skewpart(m)))
```

---

 tcrossprod

*Cross-product of transpose*


---

**Description**

Take the cross-product of the transpose of a matrix. tcrossprod(x) is formally equivalent to, but faster than, the call  $x \%*\% t(x)$ , and so is tcrossprod(x, y) instead of  $x \%*\% t(y)$ .

**Usage**

```
tcrossprod(x, y = NULL)
```

**Arguments**

x a matrix-like object  
 y a matrix-like object or NULL (by default); the latter case is formally equivalent to  $y = x$ .

**Details**

For some classes in the `Matrix` package, such as `dgCMatrix`, it is much faster to calculate the cross-product of the transpose directly instead of calculating the transpose first and then its cross-product.

**Value**

An object of an appropriate symmetric matrix class.

**Methods**

`x = "dgCMatrix"` method for compressed, sparse, column-oriented matrices.

**See Also**

[crossprod](#)

**Examples**

```
## A random sparse "incidence" matrix :
m <- matrix(0, 400, 500)
set.seed(12)
m[runif(314, 0, length(m))] <- 1
mm <- as(m, "dgCMatrix")
object.size(m) / object.size(mm) # smaller by a factor of > 200

## tcrossprod() is very fast:
system.time(tCmm <- tcrossprod(mm)) # 0 (PIII, 933 MHz)
system.time(cm <- crossprod(t(m))) # 0.16
system.time(cm. <- tcrossprod(m)) # 0.02

stopifnot(cm == as(tCmm, "matrix"))

## show sparse sub matrix
tCmm[1:16, 1:30]
```

---

triangularMatrix-class

*Virtual Class of Triangular Matrices in package:Matrix*

---

**Description**

The virtual class of triangular matrices, "`triangularMatrix`", from the package **Matrix** contains numeric and logical, dense and sparse matrices, e.g., see the examples.

The main use will be in methods (and C functions) that can deal with all triangular matrices.

**Slots**

**uplo:** String (of class "character"). Must be either "U", for upper triangular, and "L", for lower triangular.

**diag:** String (of class "character"). Must be either "U", for unit triangular (diagonal is all ones), or "N" for non-unit. The diagonal elements are not accessed internally when **diag** is "U". For `denseMatrix` classes, they need to be allocated though, i.e., the length of the **x** slot does not depend on **diag**.

**Dim, Dimnames:** The dimension (a length-2 "integer") and corresponding names (or NULL), inherited from the `Matrix`, see there.

**Extends**

Class "Matrix", directly.

**Methods**

There's a C function `triangularMatrix_validity()` called by the internal validity checking functions.

Currently, `Schur`, `isSymmetric` and `as()` (i.e. `coerce`) have methods with `triangularMatrix` in their signature.

**See Also**

Classes `symmetricMatrix`, and, e.g., `dtrMatrix` for numeric *dense* matrices, or `ltcMatrix` for a logical *sparse* matrix subclass of "triangularMatrix".

**Examples**

```
showClass("triangularMatrix")

## The names of direct subclasses:
scl <- getClass("triangularMatrix")@subclasses
directly <- sapply(lapply(scl, slot, "by"), length) == 0
names(scl)[directly]
```

---

TsparseMatrix-class

*Class "TsparseMatrix" of Sparse Matrices in Triplet Form*

---

**Description**

The "TsparseMatrix" class is the virtual class of all sparse matrices coded in triplet form. Since it is a virtual class, no objects may be created from it. See `showClass("TsparseMatrix")` for its subclasses.

**Slots**

- `Dim, Dimnames:` from the `"Matrix"` class,
- `i:` Object of class `"integer"` - the row indices of non-zero entries *in 0-base*, i.e., must be in `0:(nrow(.)-1)`.
  - `j:` Object of class `"integer"` - the column indices of non-zero entries. Must be the same length as slot `i` and *0-based* as well, i.e., in `0:(ncol(.)-1)`. For numeric `Tsparse` matrices, `(i, j)` pairs can occur more than once, see `dgTMatrix`.

**Extends**

Class `"sparseMatrix"`, directly. Class `"Matrix"`, by class `"sparseMatrix"`.

**Methods**

Extraction (`"["`) methods, see `[-methods`.

**Note**

Most operations with sparse matrices are performed using the compressed, column-oriented or `CsparseMatrix` representation. The triplet representation is convenient for creating a sparse matrix or for reading and writing such matrices. Once it is created, however, the matrix is generally coerced to a `CsparseMatrix` for further operations.

For convenience, methods for some operations such as `%*%` and `crossprod` are defined for `TsparseMatrix` objects. These methods simply coerce the `TsparseMatrix` object to a `CsparseMatrix` object then perform the operation.

**See Also**

its superclass, `sparseMatrix`, and the `dgTMatrix` class, for the links to other classes.

**Examples**

```
showClass("TsparseMatrix")
## or just the subclasses' names
names(getClass("TsparseMatrix")@subclasses)
```

---

 unpack

---

*Full Storage Representation of Packed Matrices*


---

**Description**

Expands decompositions stored in compact form into matrix factors.

**Usage**

```
unpack(x, ...)
```

**Arguments**

- `x` a matrix stored in packed form, e.g., of class `"d?pMatrix"` where `"?"` is `"t"` for triangular or `"s"` for symmetric.
- `...` further arguments passed to or from other methods.

**Details**

This is a generic function with special methods for different types of packed matrices. Use `showMethods("unpack")` to list the methods for `unpack()`.

**Value**

A `Matrix` object containing the full-storage representation of `x`.

**Examples**

```
showMethods("unpack")
(cp4 <- chol(Hilbert(4))) # is triangular
tp4 <- as(cp4, "dtpMatrix") # [t]riangular [p]acked
str(tp4)
(unpack(tp4))

## Not run:
## once we have Diagonal() :
unpack(Diagonal( 1:3))

## End(Not run)
```

---

 Unused-classes

*Virtual Classes Not Yet Really Implemented and Used*


---

**Description**

`iMatrix` is the virtual class of all integer (S4) matrices. It extends the `Matrix` class directly.

`zMatrix` is the virtual class of all `complex` (S4) matrices. It extends the `Matrix` class directly.

**Examples**

```
showClass("iMatrix")
showClass("zMatrix")
```

---

 USCounties

*USCounties Contiguity Matrix*


---

**Description**

This matrix represents the contiguities of 3111 US counties using the Queen criterion of at least a single shared boundary point. The representation is as a row standardised spatial weights matrix transformed to a symmetric matrix (see Ord (1975), p. 125).

**Usage**

```
data(USCounties)
```

**Format**

A  $3111^2$  symmetric sparse matrix of class `dsCMatrix` with 9101 non-zero entries.

## Details

The data were read into R using `read.gal`, and row-standardised and transformed to symmetry using `nb2listw` and `similar.listw`. This spatial weights object was converted to class `dsCMatrix` using `as_dsTMatrix_listw` and coercion.

## Source

The data were retrieved from <http://sal.uiuc.edu/weights/zips/usc.zip>, files “usc.txt” and “usc\\_q.GAL”, with permission for use and distribution from Luc Anselin.

## References

Ord, J. K. (1975) Estimation methods for models of spatial interaction; *Journal of the American Statistical Association* **70**, 120–126.

## Examples

```
data(USCounties)
(n <- ncol(USCounties))
IM <- .symDiagonal(n)
nn <- 50
set.seed(1)
rho <- runif(nn, 0, 1)
system.time(MJ <- sapply(rho, function(x) determinant(IM - x * USCounties, logarithm = TRUE)))

nWC <- -USCounties
C1 <- Cholesky(nWC, Imult = 2)
system.time(MJ1 <- n * log(rho) +
             sapply(rho, function(x) c(determinant(update(C1, nWC, 1/x))$modulus)))
all.equal(MJ, MJ1)

C2 <- Cholesky(nWC, super = TRUE, Imult = 2)
system.time(MJ2 <- n * log(rho) +
             sapply(rho, function(x) c(determinant(update(C2, nWC, 1/x))$modulus)))
all.equal(MJ, MJ2)
system.time(MJ3 <- n * log(rho) + Matrix::ldetL2up(C1, nWC, 1/rho))
all.equal(MJ, MJ3)
system.time(MJ4 <- n * log(rho) + Matrix::ldetL2up(C2, nWC, 1/rho))
all.equal(MJ, MJ4)
```

## Description

Create a contingency table from cross-classifying factors, usually contained in a data frame, using a formula interface.

This is a fully compatible extension of the standard `stats` package `xtabs()` function with the added option to produce a *sparse* matrix result via `sparse = TRUE`.

**Usage**

```
xtabs(formula = ~., data = parent.frame(), subset, sparse = FALSE, na.action,
      exclude = c(NA, NaN), drop.unused.levels = FALSE)
```

**Arguments**

<code>formula</code>	a <a href="#">formula</a> object with the cross-classifying variables (separated by +) on the right hand side (or an object which can be coerced to a formula). Interactions are not allowed. On the left hand side, one may optionally give a vector or a matrix of counts; in the latter case, the columns are interpreted as corresponding to the levels of a variable. This is useful if the data have already been tabulated, see the examples below.
<code>data</code>	an optional matrix or data frame (or similar: see <a href="#">model.frame</a> ) containing the variables in the formula <code>formula</code> . By default the variables are taken from <code>environment(formula)</code> .
<code>subset</code>	an optional vector specifying a subset of observations to be used.
<code>sparse</code>	logical specifying if the result should be a <i>sparse</i> matrix, i.e., inheriting from <a href="#">sparseMatrix</a> . Only works for two factors (since there are no higher-order sparse array classes yet).
<code>na.action</code>	a function which indicates what should happen when the data contain NAs.
<code>exclude</code>	a vector of values to be excluded when forming the set of levels of the classifying factors.
<code>drop.unused.levels</code>	a logical indicating whether to drop unused levels in the classifying factors. If this is <code>FALSE</code> and there are unused levels, the table will contain zero marginals, and a subsequent chi-squared test for independence of the factors will not work.

**Details**

For (non-sparse) `xtabs` results, there is a `summary` method for contingency table objects created by `table` or `xtabs`, which gives basic information and performs a chi-squared test for independence of factors (note that the function `chisq.test` currently only handles 2-d tables).

If a left hand side is given in `formula`, its entries are simply summed over the cells corresponding to the right hand side; this also works if the lhs does not give counts.

**Value**

By default, when `sparse=FALSE`, a contingency table in array representation of S3 class `c("xtabs", "table")`, with a `"call"` attribute storing the matched call.

When `sparse=TRUE`, a sparse numeric matrix, specifically an object of S4 class [dgTMatrix](#).

**See Also**

The `stats` package version [xtabs](#) and its references.

**Examples**

```
## See for non-sparse examples:
example(xtabs, package = "stats")

## similar to "nlme"s 'ergoStool' :
```



```
d.ergo <- data.frame(Type = paste("T", rep(1:4, 9*4), sep=""),
                    Subj = gl(9,4, 36*4))
xtabs(~ Type + Subj, data=d.ergo) # 4 replicates each
set.seed(15) # a subset of cases:
xtabs(~ Type + Subj, data=d.ergo[sample(36, 10),], sparse=TRUE)

## Hypothetical two level setup:
inner <- factor(sample(letters[1:25], 100, replace = TRUE))
inout <- factor(sample(LETTERS[1:5], 25, replace = TRUE))
fr <- data.frame(inner = inner, outer = inout[as.integer(inner)])
xtabs(~ inner + outer, fr, sparse = TRUE)
```

[-methods

*Methods for "[": Extraction or Subsetting in Package 'Matrix'*

## Description

Methods for "[" , i.e., extraction or subsetting mostly of matrices, in package **Matrix**.

## Methods

There are more than these:

```
x = "Matrix", i = "missing", j = "missing", drop= "ANY" ...
x = "Matrix", i = "numeric", j = "missing", drop= "missing" ...
x = "Matrix", i = "missing", j = "numeric", drop= "missing" ...
x = "dsparseMatrix", i = "missing", j = "numeric", drop= "logical" ...
x = "dsparseMatrix", i = "numeric", j = "missing", drop= "logical" ...
x = "dsparseMatrix", i = "numeric", j = "numeric", drop= "logical" ...
```

## See Also

[\[<--methods](#) for subassignment to "Matrix" objects. [Extract](#) about the standard extraction.

## Examples

```
str(m <- Matrix(round(rnorm(7*4),2), nrow = 7))
stopifnot(identical(m, m[]))
m[2, 3] # simple number
m[2, 3:4] # simple numeric of length 2
m[2, 3:4, drop=FALSE] # sub matrix of class 'dgeMatrix'
## rows or columns only:
m[1,] # first row, as simple numeric vector
m[,1:2] # sub matrix of first two columns

showMethods("[", inherited = FALSE)
```

**Description**

Methods for "[<-", i.e., extraction or subsetting mostly of matrices, in package **Matrix**.

**Methods**

There are more than these:

`x = "Matrix", i = "missing", j = "missing", value = "ANY"` is currently a simple fallback method implementation which ensures “readable” error messages.

`x = "Matrix", i = "ANY", j = "ANY", value = "ANY"` currently gives an error

`x = "denseMatrix", i = "index", j = "missing", value = "numeric" ...`

`x = "denseMatrix", i = "index", j = "index", value = "numeric" ...`

`x = "denseMatrix", i = "missing", j = "index", value = "numeric" ...`

**See Also**

[\[-methods](#) for subsetting "Matrix" objects; the [index](#) class; [Extract](#) about the standard subset assignment (and extraction).

**Examples**

```
set.seed(101)
(a <- m <- Matrix(round(rnorm(7*4),2), nrow = 7))

a[] <- 2.2 # <<- replaces every entry
a
## as do these:
a[,] <- 3 ; a[TRUE,] <- 4

m[2, 3] <- 3.14 # simple number
m[3, 3:4] <- 3:4 # simple numeric of length 2

## sub matrix assignment:
m[-(4:7), 3:4] <- cbind(1,2:4) #-> upper right corner of 'm'
m[3:5, 2:3] <- 0
m[6:7, 1:2] <- Diagonal(2)
m

## rows or columns only:
m[1,] <- 10
m[,2] <- 1:7
m[-(1:6), ] <- 3:0 # not the first 6 rows, i.e. only the 7th
as(m, "sparseMatrix")
```



## Chapter 13

# The `boot` package

---

`abc.ci`

*Nonparametric ABC Confidence Intervals*

---

### Description

Calculate equi-tailed two-sided nonparametric approximate bootstrap confidence intervals for a parameter, given a set of data and an estimator of the parameter, using numerical differentiation.

### Usage

```
abc.ci(data, statistic, index=1, strata=rep(1, n), conf=0.95,  
       eps=0.001/n, ...)
```

### Arguments

<code>data</code>	A data set expressed as a vector, matrix or data frame.
<code>statistic</code>	A function which returns the statistic of interest. The function must take at least 2 arguments; the first argument should be the data and the second a vector of weights. The weights passed to <code>statistic</code> will be normalized to sum to 1 within each stratum. Any other arguments should be passed to <code>abc.ci</code> as part of the <code>...{}</code> argument.
<code>index</code>	If <code>statistic</code> returns a vector of length greater than 1, then this indicates the position of the variable of interest within that vector.
<code>strata</code>	A factor or numerical vector indicating to which sample each observation belongs in multiple sample problems. The default is the one-sample case.
<code>conf</code>	A scalar or vector containing the confidence level(s) of the required interval(s).
<code>eps</code>	The value of epsilon to be used for the numerical differentiation.
<code>...</code>	Any other arguments for <code>statistic</code> . These will be passed unchanged to <code>statistic</code> each time it is called within <code>abc.ci</code> .

## Details

This function is based on the function `abcnon` written by R. Tibshirani. A listing of the original function is available in DiCiccio and Efron (1996). The function uses numerical differentiation for the first and second derivatives of the statistic and then uses these values to approximate the bootstrap BCa intervals. The total number of evaluations of the statistic is  $2 \cdot n + 2 + 2 \cdot \text{length}(\text{conf})$  where  $n$  is the number of data points (plus calculation of the original value of the statistic). The function works for the multiple sample case without the need to rewrite the statistic in an artificial form since the stratified normalization is done internally by the function.

## Value

A `length(conf)` by 3 matrix where each row contains the confidence level followed by the lower and upper end-points of the ABC interval at that level.

## References

- Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*, Chapter 5. Cambridge University Press.
- DiCiccio, T. J. and Efron B. (1992) More accurate confidence intervals in exponential families. *Biometrika*, **79**, 231–245.
- DiCiccio, T. J. and Efron B. (1996) Bootstrap confidence intervals (with Discussion). *Statistical Science*, **11**, 189–228.

## See Also

[boot.ci](#)

## Examples

```
# 90% and 95% confidence intervals for the correlation
# coefficient between the columns of the bigcity data

abc.ci(bigcity, corr, conf=c(0.90,0.95))

# A 95% confidence interval for the difference between the means of
# the last two samples in gravity
mean.diff <- function(y, w)
{   gp1 <- 1:table(as.numeric(y$series))[1]
    sum(y[gp1,1] * w[gp1]) - sum(y[-gp1,1] * w[-gp1])
}
grav1 <- gravity[as.numeric(gravity[,2])>=7,]
abc.ci(grav1, mean.diff, strata=grav1$series)
```

---

acme

*Monthly Excess Returns*

---

## Description

The `acme` data frame has 60 rows and 3 columns.

The excess return for the Acme Cleveland Corporation are recorded along with those for all stocks listed on the New York and American Stock Exchanges were recorded over a five year period. These excess returns are relative to the return on a risk-less investment such a U.S. Treasury bills.

**Usage**

acme

**Format**

This data frame contains the following columns:

month A character string representing the month of the observation.

market The excess return of the market as a whole.

acme The excess return for the Acme Cleveland Corporation.

**Source**

The data were obtained from

Simonoff, J.S. and Tsai, C.-L. (1994) Use of modified profile likelihood for improved tests of constancy of variance in regression. *Applied Statistics*, **43**, 353–370.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

aids

*Delay in AIDS Reporting in England and Wales*

---

**Description**

The `aids` data frame has 570 rows and 6 columns.

Although all cases of AIDS in England and Wales must be reported to the Communicable Disease Surveillance Centre, there is often a considerable delay between the time of diagnosis and the time that it is reported. In estimating the prevalence of AIDS, account must be taken of the unknown number of cases which have been diagnosed but not reported. The data set here records the reported cases of AIDS diagnosed from July 1983 and until the end of 1992. The data are cross-classified by the date of diagnosis and the time delay in the reporting of the cases.

**Usage**

aids

**Format**

This data frame contains the following columns:

year The year of the diagnosis.

quarter The quarter of the year in which diagnosis was made.

delay The time delay (in months) between diagnosis and reporting. 0 means that the case was reported within one month. Longer delays are grouped in 3 month intervals and the value of `delay` is the midpoint of the interval (therefore a value of 2 indicates that reporting was delayed for between 1 and 3 months).

`dud` An indicator of censoring. These are categories for which full information is not yet available and the number recorded is a lower bound only.

`time` The time interval of the diagnosis. That is the number of quarters from July 1983 until the end of the quarter in which these cases were diagnosed.

`y` The number of AIDS cases reported.

### Source

The data were obtained from

De Angelis, D. and Gilks, W.R. (1994) Estimating acquired immune deficiency syndrome accounting for reporting delay. *Journal of the Royal Statistical Society, A*, **157**, 31–40.

### References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

aircondit

*Failures of Air-conditioning Equipment*

---

### Description

Proschan (1963) reported on the times between failures of the air-conditioning equipment in 10 Boeing 720 aircraft. The `aircondit` data frame contains the intervals for the ninth aircraft while `aircondit7` contains those for the seventh aircraft.

Both data frames have just one column. Note that the data have been sorted into increasing order.

### Usage

```
aircondit
```

### Format

The data frames contain the following column:

`hours` The time interval in hours between successive failures of the air-conditioning equipment

### Source

The data were taken from

Cox, D.R. and Snell, E.J. (1981) *Applied Statistics: Principles and Examples*. Chapman and Hall.

### References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Proschan, F. (1963) Theoretical explanation of observed decreasing failure rate. *Technometrics*, **5**, 375-383.

---

`amis`*Car Speeding and Warning Signs*

---

**Description**

The `amis` data frame has 8437 rows and 4 columns.

In a study into the effect that warning signs have on speeding patterns, Cambridgeshire County Council considered 14 pairs of locations. The locations were paired to account for factors such as traffic volume and type of road. One site in each pair had a sign erected warning of the dangers of speeding and asking drivers to slow down. No action was taken at the second site. Three sets of measurements were taken at each site. Each set of measurements was nominally of the speeds of 100 cars but not all sites have exactly 100 measurements. These speed measurements were taken before the erection of the sign, shortly after the erection of the sign, and again after the sign had been in place for some time.

**Usage**

```
amis
```

**Format**

This data frame contains the following columns:

`speed` Speeds of cars (in miles per hour).

`period` A numeric column indicating the time that the reading was taken. A value of 1 indicates a reading taken before the sign was erected, a 2 indicates a reading taken shortly after erection of the sign and a 3 indicates a reading taken after the sign had been in place for some time.

`warning` A numeric column indicating whether the location of the reading was chosen to have a warning sign erected. A value of 1 indicates presence of a sign and a value of 2 indicates that no sign was erected.

`pair` A numeric column giving the pair number at which the reading was taken. Pairs were numbered from 1 to 14.

**Source**

The data were kindly made available by Mr. Graham Amis, Cambridgeshire County Council, U.K.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.



aml

---

*Remission Times for Acute Myelogenous Leukaemia*

---

**Description**

The `aml` data frame has 23 rows and 3 columns.

A clinical trial to evaluate the efficacy of maintenance chemotherapy for acute myelogenous leukaemia was conducted by Embury et al. (1977) at Stanford University. After reaching a stage of remission through treatment by chemotherapy, patients were randomized into two groups. The first group received maintenance chemotherapy and the second group did not. The aim of the study was to see if maintenance chemotherapy increased the length of the remission. The data here formed a preliminary analysis which was conducted in October 1974.

**Usage**

`aml`

**Format**

This data frame contains the following columns:

`time` The length of the complete remission (in weeks).

`cens` An indicator of right censoring. 1 indicates that the patient had a relapse and so `time` is the length of the remission. 0 indicates that the patient had left the study or was still in remission in October 1974, that is the length of remission is right-censored.

`group` The group into which the patient was randomized. Group 1 received maintenance chemotherapy, group 2 did not.

**Note**

Package **survival** also has a dataset `aml`. It is the same data with different names and with `group` replaced by a factor `x`.

**Source**

The data were obtained from

Miller, R.G. (1981) *Survival Analysis*. John Wiley.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Embury, S.H, Elias, L., Heller, P.H., Hood, C.E., Greenberg, P.L. and Schrier, S.L. (1977) Remission maintenance therapy in acute myelogenous leukaemia. *Western Journal of Medicine*, **126**, 267-272.

---

`beaver`*Beaver Body Temperature Data*

---

### Description

The `beaver` data frame has 100 rows and 4 columns. It is a multivariate time series of class `"ts"` and also inherits from class `"data.frame"`.

This data set is part of a long study into body temperature regulation in beavers. Four adult female beavers were live-trapped and had a temperature-sensitive radio transmitter surgically implanted. Readings were taken every 10 minutes. The location of the beaver was also recorded and her activity level was dichotomized by whether she was in the retreat or outside of it since high-intensity activities only occur outside of the retreat.

The data in this data frame are those readings for one of the beavers on a day in autumn.

### Usage

```
beaver
```

### Format

This data frame contains the following columns:

`day` The day number. The data includes only data from day 307 and early 308.

`time` The time of day formatted as hour-minute.

`temp` The body temperature in degrees Celsius.

`activ` The dichotomized activity indicator. 1 indicates that the beaver is outside of the retreat and therefore engaged in high-intensity activity.

### Source

The data were obtained from

Reynolds, P.S. (1994) Time-series analyses of beaver body temperatures. In *Case Studies in Biometry*. N. Lange, L. Ryan, L. Billard, D. Brillinger, L. Conquest and J. Greenhouse (editors), 211–228. John Wiley.

### References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

 bigcity

*Population of U.S. Cities*


---

### Description

The `bigcity` data frame has 49 rows and 2 columns.

The `city` data frame has 10 rows and 2 columns.

The measurements are the population (in 1000's) of 49 U.S. cities in 1920 and 1930. The 49 cities are a random sample taken from the 196 largest cities in 1920. The `city` data frame consists of the first 10 observations in `bigcity`.

### Usage

```
bigcity
```

### Format

This data frame contains the following columns:

- u The 1920 population.
- x The 1930 population.

### Source

The data were obtained from

Cochran, W.G. (1977) *Sampling Techniques*. Third edition. John Wiley

### References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

 boot

*Bootstrap Resampling*


---

### Description

Generate R bootstrap replicates of a statistic applied to data. Both parametric and nonparametric resampling are possible. For the nonparametric bootstrap, possible resampling methods are the ordinary bootstrap, the balanced bootstrap, antithetic resampling, and permutation. For nonparametric multi-sample problems stratified resampling is used. This is specified by including a vector of strata in the call to `boot`. Importance resampling weights may be specified.

### Usage

```
boot(data, statistic, R, sim="ordinary", stype="i",
      strata=rep(1,n), L=NULL, m=0, weights=NULL,
      ran.gen=function(d, p) d, mle=NULL, simple=FALSE, ...)
```

**Arguments**

<code>data</code>	The data as a vector, matrix or data frame. If it is a matrix or data frame then each row is considered as one multivariate observation.
<code>statistic</code>	A function which when applied to data returns a vector containing the statistic(s) of interest. When <code>sim="parametric"</code> , the first argument to <code>statistic</code> must be the data. For each replicate a simulated dataset returned by <code>ran.gen</code> will be passed. In all other cases <code>statistic</code> must take at least two arguments. The first argument passed will always be the original data. The second will be a vector of indices, frequencies or weights which define the bootstrap sample. Further, if predictions are required, then a third argument is required which would be a vector of the random indices used to generate the bootstrap predictions. Any further arguments can be passed to <code>statistic</code> through the <code>...{}</code> argument.
<code>R</code>	The number of bootstrap replicates. Usually this will be a single positive integer. For importance resampling, some resamples may use one set of weights and others use a different set of weights. In this case <code>R</code> would be a vector of integers where each component gives the number of resamples from each of the rows of weights.
<code>sim</code>	A character string indicating the type of simulation required. Possible values are "ordinary" (the default), "parametric", "balanced", "permutation", or "antithetic". Importance resampling is specified by including importance weights; the type of importance resampling must still be specified but may only be "ordinary" or "balanced" in this case.
<code>stype</code>	A character string indicating what the second argument of <code>statistic</code> represents. Possible values of <code>stype</code> are "i" (indices - the default), "f" (frequencies), or "w" (weights).
<code>strata</code>	An integer vector or factor specifying the strata for multi-sample problems. This may be specified for any simulation, but is ignored when <code>sim</code> is "parametric". When <code>strata</code> is supplied for a nonparametric bootstrap, the simulations are done within the specified strata.
<code>L</code>	Vector of influence values evaluated at the observations. This is used only when <code>sim</code> is "antithetic". If not supplied, they are calculated through a call to <code>empinf</code> . This will use the infinitesimal jackknife provided that <code>stype</code> is "w", otherwise the usual jackknife is used.
<code>m</code>	The number of predictions which are to be made at each bootstrap replicate. This is most useful for (generalized) linear models. This can only be used when <code>sim</code> is "ordinary". <code>m</code> will usually be a single integer but, if there are strata, it may be a vector with length equal to the number of strata, specifying how many of the errors for prediction should come from each strata. The actual predictions should be returned as the final part of the output of <code>statistic</code> , which should also take a vector of indices of the errors to be used for the predictions.
<code>weights</code>	Vector or matrix of importance weights. If a vector then it should have as many elements as there are observations in <code>data</code> . When simulation from more than one set of weights is required, <code>weights</code> should be a matrix where each row of the matrix is one set of importance weights. If <code>weights</code> is a matrix then <code>R</code> must be a vector of length <code>nrow(weights)</code> . This parameter is ignored if <code>sim</code> is not "ordinary" or "balanced".
<code>ran.gen</code>	This function is used only when <code>sim</code> is "parametric" when it describes how random values are to be generated. It should be a function of two arguments.

The first argument should be the observed data and the second argument consists of any other information needed (e.g. parameter estimates). The second argument may be a list, allowing any number of items to be passed to `ran.gen`. The returned value should be a simulated data set of the same form as the observed data which will be passed to `statistic` to get a bootstrap replicate. It is important that the returned value be of the same shape and type as the original dataset. If `ran.gen` is not specified, the default is a function which returns the original data in which case all simulation should be included as part of `statistic`. Use of `sim="parametric"` with a suitable `ran.gen` allows the user to implement any types of nonparametric resampling which are not supported directly.

<code>mle</code>	The second argument to be passed to <code>ran.gen</code> . Typically these will be maximum likelihood estimates of the parameters. For efficiency <code>mle</code> is often a list containing all of the objects needed by <code>ran.gen</code> which can be calculated using the original data set only.
<code>simple</code>	logical, only allowed to be TRUE for <code>sim="ordinary"</code> , <code>stype="i"</code> , <code>n=0</code> (otherwise ignored with a warning). By default a <code>n*R</code> index array is created: this can be large and if <code>simple = TRUE</code> this is avoided by sampling separately for each replication, which is slower but uses less memory.
<code>...</code>	Any other arguments for <code>statistic</code> which are passed unchanged each time it is called. Any such arguments to <code>statistic</code> must follow the arguments which <code>statistic</code> is required to have for the simulation.

## Details

The statistic to be bootstrapped can be as simple or complicated as desired as long as its arguments correspond to the dataset and (for a nonparametric bootstrap) a vector of indices, frequencies or weights. `statistic` is treated as a black box by the `boot` function and is not checked to ensure that these conditions are met.

The first order balanced bootstrap is described in Davison, Hinkley and Schechtman (1986). The antithetic bootstrap is described by Hall (1989) and is experimental, particularly when used with strata. The other non-parametric simulation types are the ordinary bootstrap (possibly with unequal probabilities), and permutation which returns random permutations of cases. All of these methods work independently within strata if that argument is supplied.

For the parametric bootstrap it is necessary for the user to specify how the resampling is to be conducted. The best way of accomplishing this is to specify the function `ran.gen` which will return a simulated data set from the observed data set and a set of parameter estimates specified in `mle`.

## Value

The returned value is an object of class "boot", containing the following components :

<code>t0</code>	The observed value of <code>statistic</code> applied to <code>data</code> .
<code>t</code>	A matrix with <code>R</code> rows each of which is a bootstrap replicate of <code>statistic</code> .
<code>R</code>	The value of <code>R</code> as passed to <code>boot</code> .
<code>data</code>	The data as passed to <code>boot</code> .
<code>seed</code>	The value of <code>.Random.seed</code> when <code>boot</code> was called.
<code>statistic</code>	The function <code>statistic</code> as passed to <code>boot</code> .
<code>sim</code>	Simulation type used.

stype	Statistic type as passed to <code>boot</code> .
call	The original call to <code>boot</code> .
strata	The strata used. This is the vector passed to <code>boot</code> , if it was supplied or a vector of ones if there were no strata. It is not returned if <code>sim</code> is "parametric".
weights	The importance sampling weights as passed to <code>boot</code> or the empirical distribution function weights if no importance sampling weights were specified. It is omitted if <code>sim</code> is not one of "ordinary" or "balanced".
pred.i	If predictions are required ( <code>m</code> >0) this is the matrix of indices at which predictions were calculated as they were passed to <code>statistic</code> . Omitted if <code>m</code> is 0 or <code>sim</code> is not "ordinary".
L	The influence values used when <code>sim</code> is "antithetic". If no such values were specified and <code>stype</code> is not "w" then L is returned as consecutive integers corresponding to the assumption that data is ordered by influence values. This component is omitted when <code>sim</code> is not "antithetic".
ran.gen	The random generator function used if <code>sim</code> is "parametric". This component is omitted for any other value of <code>sim</code> .
mle	The parameter estimates passed to <code>boot</code> when <code>sim</code> is "parametric". It is omitted for all other values of <code>sim</code> .

## References

- There are many references explaining the bootstrap and its variations. Among them are :
- Booth, J.G., Hall, P. and Wood, A.T.A. (1993) Balanced importance resampling for the bootstrap. *Annals of Statistics*, **21**, 286–298.
- Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.
- Davison, A.C., Hinkley, D.V. and Schechtman, E. (1986) Efficient bootstrap simulation. *Biometrika*, **73**, 555–566.
- Efron, B. and Tibshirani, R. (1993) *An Introduction to the Bootstrap*. Chapman & Hall.
- Gleason, J.R. (1988) Algorithms for balanced bootstrap simulations. *American Statistician*, **42**, 263–266.
- Hall, P. (1989) Antithetic resampling for the bootstrap. *Biometrika*, **73**, 713–724.
- Hinkley, D.V. (1988) Bootstrap methods (with Discussion). *Journal of the Royal Statistical Society, B*, **50**, 312–337, 355–370.
- Hinkley, D.V. and Shi, S. (1989) Importance sampling and the nested bootstrap. *Biometrika*, **76**, 435–446.
- Johns M.V. (1988) Importance sampling for bootstrap confidence intervals. *Journal of the American Statistical Association*, **83**, 709–714.
- Noreen, E.W. (1989) *Computer Intensive Methods for Testing Hypotheses*. John Wiley & Sons.

## See Also

[boot.array](#), [boot.ci](#), [censboot](#), [empinf](#), [jack.after.boot](#), [tilt.boot](#), [tsboot](#)

**Examples**

```

# usual bootstrap of the ratio of means using the city data
ratio <- function(d, w)
  sum(d$x * w)/sum(d$u * w)
boot(city, ratio, R=999, stype="w")

# Stratified resampling for the difference of means. In this
# example we will look at the difference of means between the final
# two series in the gravity data.
diff.means <- function(d, f)
{
  n <- nrow(d)
  gp1 <- 1:table(as.numeric(d$series))[1]
  m1 <- sum(d[gp1,1] * f[gp1])/sum(f[gp1])
  m2 <- sum(d[-gp1,1] * f[-gp1])/sum(f[-gp1])
  ss1 <- sum(d[gp1,1]^2 * f[gp1]) -
    (m1 * m1 * sum(f[gp1]))
  ss2 <- sum(d[-gp1,1]^2 * f[-gp1]) -
    (m2 * m2 * sum(f[-gp1]))
  c(m1-m2, (ss1+ss2)/(sum(f)-2))
}
grav1 <- gravity[as.numeric(gravity[,2])>=7,]
boot(grav1, diff.means, R=999, stype="f", strata=grav1[,2])

# In this example we show the use of boot in a prediction from
# regression based on the nuclear data. This example is taken
# from Example 6.8 of Davison and Hinkley (1997). Notice also
# that two extra arguments to statistic are passed through boot.
nuke <- nuclear[,c(1,2,5,7,8,10,11)]
nuke.lm <- glm(log(cost)~date+log(cap)+ne+ ct+log(cum.n)+pt, data=nuke)
nuke.diag <- glm.diag(nuke.lm)
nuke.res <- nuke.diag$res+nuke.diag$sd
nuke.res <- nuke.res-mean(nuke.res)

# We set up a new data frame with the data, the standardized
# residuals and the fitted values for use in the bootstrap.
nuke.data <- data.frame(nuke,resid=nuke.res,fit=fitted(nuke.lm))

# Now we want a prediction of plant number 32 but at date 73.00
new.data <- data.frame(cost=1, date=73.00, cap=886, ne=0,
  ct=0, cum.n=11, pt=1)
new.fit <- predict(nuke.lm, new.data)

nuke.fun <- function(dat, inds, i.pred, fit.pred, x.pred)
{
  assign(".inds", inds, envir=.GlobalEnv)
  lm.b <- glm(fit+resid[.inds] ~date+log(cap)+ne+ct+
    log(cum.n)+pt, data=dat)
  pred.b <- predict(lm.b,x.pred)
  remove(".inds", envir=.GlobalEnv)
  c(coef(lm.b), pred.b-(fit.pred+dat$resid[i.pred]))
}

```

```

nuke.boot <- boot(nuke.data, nuke.fun, R=999, m=1,
  fit.pred=new.fit, x.pred=new.data)
# The bootstrap prediction error would then be found by
mean(nuke.boot$t[,8]^2)
# Basic bootstrap prediction limits would be
new.fit-sort(nuke.boot$t[,8])[c(975,25)]

# Finally a parametric bootstrap. For this example we shall look
# at the air-conditioning data. In this example our aim is to test
# the hypothesis that the true value of the index is 1 (i.e. that
# the data come from an exponential distribution) against the
# alternative that the data come from a gamma distribution with
# index not equal to 1.
air.fun <- function(data)
{
  ybar <- mean(data$hours)
  para <- c(log(ybar),mean(log(data$hours)))
  ll <- function(k) {
    if (k <= 0) out <- 1e200 # not NA
    else out <- lgamma(k)-k*(log(k)-1-para[1]+para[2])
    out
  }
  khat <- nlm(ll,ybar^2/var(data$hours))$estimate
  c(ybar, khat)
}

air.rg <- function(data, mle)
# Function to generate random exponential variates. mle will contain
# the mean of the original data
{
  out <- data
  out$hours <- rexp(nrow(out), 1/mle)
  out
}

air.boot <- boot(aircondit, air.fun, R=999, sim="parametric",
  ran.gen=air.rg, mle=mean(aircondit$hours))

# The bootstrap p-value can then be approximated by
sum(abs(air.boot$t[,2]-1) > abs(air.boot$t0[2]-1))/(1+air.boot$R)

```

---

boot.array

*Bootstrap Resampling Arrays*


---

## Description

This function takes a bootstrap object calculated by one of the functions `boot`, `censboot`, or `tilt.boot` and returns the frequency (or index) array for the bootstrap resamples.



**Usage**

```
boot.array(boot.out, indices=)
```

**Arguments**

<code>boot.out</code>	An object of class "boot" returned by one of the generation functions for such an object.
<code>indices</code>	A logical argument which specifies whether to return the frequency array or the raw index array. The default is <code>indices=FALSE</code> unless <code>boot.out</code> was created by <code>tsboot</code> in which case the default is <code>indices=TRUE</code> .

**Details**

The process by which the original index array was generated is repeated with the same value of `.Random.seed`. If the frequency array is required then `freq.array` is called to convert the index array to a frequency array.

A resampling array can only be returned when such a concept makes sense. In particular it cannot be found for any parametric or model-based resampling schemes. Hence for objects generated by `censboot` the only resampling scheme for which such an array can be found is ordinary case resampling. Similarly if `boot.out$sim` is "parametric" in the case of `boot` or "model" in the case of `tsboot` the array cannot be found. Note also that for post-blackened bootstraps from `tsboot` the indices found will relate to those prior to any post-blackening and so will not be useful.

Frequency arrays are used in many post-bootstrap calculations such as the jackknife-after-bootstrap and finding importance sampling weights. They are also used to find empirical influence values through the regression method.

**Value**

A matrix with `boot.out$R` rows and `n` columns where `n` is the number of observations in `boot.out$data`. If `indices` is `FALSE` then this will give the frequency of each of the original observations in each bootstrap resample. If `indices` is `TRUE` it will give the indices of the bootstrap resamples in the order in which they would have been passed to the statistic.

**Side Effects**

This function temporarily resets `.Random.seed` to the value in `boot.out$seed` and then returns it to its original value at the end of the function.

**See Also**

[boot](#), [censboot](#), [freq.array](#), [tilt.boot](#), [tsboot](#)

**Examples**

```
# A frequency array for a nonparametric bootstrap
city.boot <- boot(city, corr, R=40, stype="w")
boot.array(city.boot)

perm.cor <- function(d,i)
  cor(d$x, d$u[i])
city.perm <- boot(city, perm.cor, R=40, sim="permutation")
boot.array(city.perm, indices=TRUE)
```

## Description

This function generates 5 different types of equi-tailed two-sided nonparametric confidence intervals. These are the first order normal approximation, the basic bootstrap interval, the studentized bootstrap interval, the bootstrap percentile interval, and the adjusted bootstrap percentile (BCa) interval. All or a subset of these intervals can be generated.

## Usage

```
boot.ci(boot.out, conf = 0.95, type = "all",
        index = 1:min(2,length(boot.out$t0)), var.t0 = NULL,
        var.t = NULL, t0 = NULL, t = NULL, L = NULL, h = function(t) t,
        hdot = function(t) rep(1,length(t)), hinvc = function(t) t, ...)
```

## Arguments

boot.out	An object of class "boot" containing the output of a bootstrap calculation.
conf	A scalar or vector containing the confidence level(s) of the required interval(s).
type	A vector of character strings representing the type of intervals required. The value should be any subset of the values c("norm", "basic", "stud", "perc", "bca") or simply "all" which will compute all five types of intervals.
index	This should be a vector of length 1 or 2. The first element of index indicates the position of the variable of interest in boot.out\$t0 and the relevant column in boot.out\$t. The second element indicates the position of the variance of the variable of interest. If both var.t0 and var.t are supplied then the second element of index (if present) is ignored. The default is that the variable of interest is in position 1 and its variance is in position 2 (as long as there are 2 positions in boot.out\$t0).
var.t0	If supplied, a value to be used as an estimate of the variance of the statistic for the normal approximation and studentized intervals. If it is not supplied and length(index) is 2 then var.t0 defaults to boot.out\$t0[index[2]] otherwise var.t0 is undefined. For studentized intervals var.t0 must be defined. For the normal approximation, if var.t0 is undefined it defaults to var(t). If a transformation is supplied through the argument h then var.t0 should be the variance of the untransformed statistic.
var.t	This is a vector (of length boot.out\$R) of variances of the bootstrap replicates of the variable of interest. It is used only for studentized intervals. If it is not supplied and length(index) is 2 then var.t defaults to boot.out\$t[,index[2]], otherwise its value is undefined which will cause an error for studentized intervals. If a transformation is supplied through the argument h then var.t should be the variance of the untransformed bootstrap statistics.

<code>t0</code>	The observed value of the statistic of interest. The default value is <code>boot.out\$t0[index[1]]</code> . Specification of <code>t0</code> and <code>t</code> allows the user to get intervals for a transformed statistic which may not be in the bootstrap output object. See the second example below. An alternative way of achieving this would be to supply the functions <code>h</code> , <code>hdot</code> , and <code>hinv</code> below.
<code>t</code>	The bootstrap replicates of the statistic of interest. It must be a vector of length <code>boot.out\$R</code> . It is an error to supply one of <code>t0</code> or <code>t</code> but not the other. Also if studentized intervals are required and <code>t0</code> and <code>t</code> are supplied then so should be <code>var.t0</code> and <code>var.t</code> . The default value is <code>boot.out\$t[,index]</code> .
<code>L</code>	The empirical influence values of the statistic of interest for the observed data. These are used only for BCa intervals. If a transformation is supplied through the parameter <code>h</code> then <code>L</code> should be the influence values for <code>t</code> ; the values for <code>h(t)</code> are derived from these and <code>hdot</code> within the function. If <code>L</code> is not supplied then the values are calculated using <code>empinf</code> if they are needed.
<code>h</code>	A function defining a transformation. The intervals are calculated on the scale of <code>h(t)</code> and the inverse function <code>hinv</code> applied to the resulting intervals. It must be a function of one variable only and for a vector argument, it must return a vector of the same length, i.e. <code>h(c(t1,t2,t3))</code> should return <code>c(h(t1),h(t2),h(t3))</code> . The default is the identity function.
<code>hdot</code>	A function of one argument returning the derivative of <code>h</code> . It is a required argument if <code>h</code> is supplied and normal, studentized or BCa intervals are required. The function is used for approximating the variances of <code>h(t0)</code> and <code>h(t)</code> using the delta method, and also for finding the empirical influence values for BCa intervals. Like <code>h</code> it should be able to take a vector argument and return a vector of the same length. The default is the constant function 1.
<code>hinv</code>	A function, like <code>h</code> , which returns the inverse of <code>h</code> . It is used to transform the intervals calculated on the scale of <code>h(t)</code> back to the original scale. The default is the identity function. If <code>h</code> is supplied but <code>hinv</code> is not, then the intervals returned will be on the transformed scale.
<code>...</code>	Any extra arguments that <code>boot.out\$statistic</code> is expecting. These arguments are needed only if BCa intervals are required and <code>L</code> is not supplied since in that case <code>L</code> is calculated through a call to <code>empinf</code> which calls <code>boot.out\$statistic</code> .

### Details

The formulae on which the calculations are based can be found in Chapter 5 of Davison and Hinkley (1997). Function `boot` must be run prior to running this function to create the object to be passed as `boot.out`.

Variance estimates are required for studentized intervals. The variance of the observed statistic is optional for normal theory intervals. If it is not supplied then the bootstrap estimate of variance is used. The normal intervals also use the bootstrap bias correction.

Interpolation on the normal quantile scale is used when a non-integer order statistic is required. If the order statistic used is the smallest or largest of the `R` values in `boot.out` a warning is generated and such intervals should not be considered reliable.

### Value

An object of type "`boot.ci`" which contains the intervals. It has components

`R` The number of bootstrap replicates on which the intervals were based.

t0	The observed value of the statistic on the same scale as the intervals.
call	The call to <code>boot.ci</code> which generated the object. It will also contain one or more of the following components depending on the value of <code>type</code> used in the call to <code>boot.ci</code> .
normal	A matrix of intervals calculated using the normal approximation. It will have 3 columns, the first being the level and the other two being the upper and lower endpoints of the intervals.
basic	The intervals calculated using the basic bootstrap method.
student	The intervals calculated using the studentized bootstrap method.
percent	The intervals calculated using the bootstrap percentile method.
bca	The intervals calculated using the adjusted bootstrap percentile (BCa) method. These latter four components will be matrices with 5 columns, the first column containing the level, the next two containing the indices of the order statistics used in the calculations and the final two the calculated endpoints themselves.

## References

- Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*, Chapter 5. Cambridge University Press.
- DiCiccio, T.J. and Efron B. (1996) Bootstrap confidence intervals (with Discussion). *Statistical Science*, **11**, 189–228.
- Efron, B. (1987) Better bootstrap confidence intervals (with Discussion). *Journal of the American Statistical Association*, **82**, 171–200.

## See Also

[abc.ci](#), [boot](#), [empinf](#), [norm.ci](#)

## Examples

```
# confidence intervals for the city data
ratio <- function(d, w) sum(d$x * w)/sum(d$u * w)
city.boot <- boot(city, ratio, R = 999, stype = "w", sim = "ordinary")
boot.ci(city.boot, conf = c(0.90, 0.95),
        type = c("norm", "basic", "perc", "bca"))

# studentized confidence interval for the two sample
# difference of means problem using the final two series
# of the gravity data.
diff.means <- function(d, f)
{
  n <- nrow(d)
  gp1 <- 1:table(as.numeric(d$series))[1]
  m1 <- sum(d[gp1,1] * f[gp1])/sum(f[gp1])
  m2 <- sum(d[-gp1,1] * f[-gp1])/sum(f[-gp1])
  ss1 <- sum(d[gp1,1]^2 * f[gp1]) - (m1 * m1 * sum(f[gp1]))
  ss2 <- sum(d[-gp1,1]^2 * f[-gp1]) - (m2 * m2 * sum(f[-gp1]))
  c(m1-m2, (ss1+ss2)/(sum(f)-2))
}

grav1 <- gravity[as.numeric(gravity[,2])>=7,]
grav1.boot <- boot(grav1, diff.means, R=999, stype="f", strata=grav1[,2])
boot.ci(grav1.boot, type=c("stud", "norm"))
```

```

# Nonparametric confidence intervals for mean failure time
# of the air-conditioning data as in Example 5.4 of Davison
# and Hinkley (1997)
mean.fun <- function(d, i)
{
  m <- mean(d$hours[i])
  n <- length(i)
  v <- (n-1)*var(d$hours[i])/n^2
  c(m, v)
}
air.boot <- boot(aircondit, mean.fun, R=999)
boot.ci(air.boot, type = c("norm", "basic", "perc", "stud"))

# Now using the log transformation
# There are two ways of doing this and they both give the
# same intervals.

# Method 1
boot.ci(air.boot, type = c("norm", "basic", "perc", "stud"),
        h = log, hdot = function(x) 1/x)

# Method 2
vt0 <- air.boot$t0[2]/air.boot$t0[1]^2
vt <- air.boot$t[,2]/air.boot$t[,1]^2
boot.ci(air.boot, type = c("norm", "basic", "perc", "stud"),
        t0 = log(air.boot$t0[1]), t = log(air.boot$t[,1]),
        var.t0 = vt0, var.t = vt)

```

brambles

*Spatial Location of Bramble Canes***Description**

The brambles data frame has 823 rows and 3 columns.

The location of living bramble canes in a 9m square plot was recorded. We take 9m to be the unit of distance so that the plot can be thought of as a unit square. The bramble canes were also classified by their age.

**Usage**

```
brambles
```

**Format**

This data frame contains the following columns:

- x The x coordinate of the position of the cane in the plot.
- y The y coordinate of the position of the cane in the plot.
- age The age classification of the canes; 0 indicates a newly emerged cane, 1 indicates a one year old cane and 2 indicates a two year old cane.

**Source**

The data were obtained from

Diggle, P.J. (1983) *Statistical Analysis of Spatial Point Patterns*. Academic Press.

## References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

breslow

*Smoking Deaths Among Doctors*

---

## Description

The `breslow` data frame has 10 rows and 5 columns.

In 1961 Doll and Hill sent out a questionnaire to all men on the British Medical Register enquiring about their smoking habits. Almost 70% of such men replied. Death certificates were obtained for medical practitioners and causes of death were assigned on the basis of these certificates. The `breslow` data set contains the person-years of observations and deaths from coronary artery disease accumulated during the first ten years of the study.

## Usage

```
breslow
```

## Format

This data frame contains the following columns:

`age` The mid-point of the 10 year age-group for the doctors.

`smoke` An indicator of whether the doctors smoked (1) or not (0).

`n` The number of person-years in the category.

`y` The number of deaths attributed to coronary artery disease.

`ns` The number of smoker years in the category (`smoke*n`).

## Source

The data were obtained from

Breslow, N.E. (1985) Cohort Analysis in Epidemiology. In *A Celebration of Statistics* A.C. Atkinson and S.E. Fienberg (editors), 109–143. Springer-Verlag.

## References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Doll, R. and Hill, A.B. (1966) Mortality of British doctors in relation to smoking: Observations on coronary thrombosis. *National Cancer Institute Monograph*, **19**, 205-268.

---

 calcium

*Calcium Uptake Data*


---

**Description**

The calcium data frame has 27 rows and 2 columns.

Howard Grimes from the Botany Department, North Carolina State University, conducted an experiment for biochemical analysis of intracellular storage and transport of calcium across plasma membrane. Cells were suspended in a solution of radioactive calcium for a certain length of time and then the amount of radioactive calcium that was absorbed by the cells was measured. The experiment was repeated independently with 9 different times of suspension each replicated 3 times.

**Usage**

calcium

**Format**

This data frame contains the following columns:

time The time (in minutes) that the cells were suspended in the solution.

cal The amount of calcium uptake (nmoles/mg).

**Source**

The data were obtained from

Rawlings, J.O. (1988) *Applied Regression Analysis*. Wadsworth and Brooks/Cole Statistics/Probability Series.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

 cane

*Sugar-cane Disease Data*


---

**Description**

The cane data frame has 180 rows and 5 columns. The data frame represents a randomized block design with 45 varieties of sugar-cane and 4 blocks.

**Usage**

cane

**Format**

This data frame contains the following columns:

- n The total number of shoots in each plot.
- r The number of diseased shoots.
- x The number of pieces of the stems, out of 50, planted in each plot.
- var A factor indicating the variety of sugar-cane in each plot.
- block A factor for the blocks.

**Details**

The aim of the experiment was to classify the varieties into resistant, intermediate and susceptible to a disease called "coal of sugar-cane" (carvão da cana-de-açúcar). This is a disease that is common in sugar-cane plantations in certain areas of Brazil.

For each plot, fifty pieces of sugar-cane stem were put in a solution containing the disease agent and then some were planted in the plot. After a fixed period of time, the total number of shoots and the number of diseased shoots were recorded.

**Source**

The data were kindly supplied by Dr. C.G.B. Demetrio of Escola Superior de Agricultura, Universidade de São Paulo, Brazil.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

capability

*Simulated Manufacturing Process Data*

---

**Description**

The `capability` data frame has 75 rows and 1 column.

The data are simulated successive observations from a process in equilibrium. The process is assumed to have specification limits (5.49, 5.79).

**Usage**

```
capability
```

**Format**

This data frame contains the following column:

- y The simulated measurements.

**Source**

The data were obtained from

Bissell, A.F. (1990) How reliable is your capability index? *Applied Statistics*, **39**, 331–340.



## References

- Canty, A.J. and Davison, A.C. (1996) Implementation of saddlepoint approximations to resampling distributions. To appear in *Computing Science and Statistics; Proceedings of the 28th Symposium on the Interface*.
- Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

catsM

*Weight Data for Domestic Cats*

---

## Description

The `catsM` data frame has 97 rows and 3 columns.

144 adult (over 2kg in weight) cats used for experiments with the drug digitalis had their heart and body weight recorded. 47 of the cats were female and 97 were male. The `catsM` data frame consists of the data for the male cats. The full data are in dataset `cats` in package `MASS`.

## Usage

```
cats
```

## Format

This data frames contain the following columns:

`Sex` A factor for the sex of the cat (levels are F and M).

`Bwt` Body weight in kg.

`Hwt` Heart weight in g.

## Source

The data were obtained from

Fisher, R.A. (1947) The analysis of covariance method for the relation between a part and the whole. *Biometrics*, **3**, 65–68.

## References

- Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.
- Venables, W.N. and Ripley, B.D. (1994) *Modern Applied Statistics with S-Plus*. Springer-Verlag.

## See Also

`cats`

---

`cav`*Position of Muscle Caveolae*

---

**Description**

The `cav` data frame has 138 rows and 2 columns.

The data gives the positions of the individual caveolae in a square region with sides of length 500 units. This grid was originally on a 2.65µm square of muscle fibre. The data are those points falling in the lower left hand quarter of the region used for the dataset `caveolae.dat` in the **spatial** package by B.D. Ripley (1994) which is part of the recommended **VR** bundle.

**Usage**`cav`**Format**

This data frame contains the following columns:

- `x` The x coordinate of the caveola's position in the region.
- `y` The y coordinate of the caveola's position in the region.

**References**

Appleyard, S.T., Witkowski, J.A., Ripley, B.D., Shotton, D.M. and Dubowicz, V. (1985) A novel procedure for pattern analysis of features present on freeze fractured plasma membranes. *Journal of Cell Science*, **74**, 105–117.

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

`cd4`*CD4 Counts for HIV-Positive Patients*

---

**Description**

The `cd4` data frame has 20 rows and 2 columns.

CD4 cells are carried in the blood as part of the human immune system. One of the effects of the HIV virus is that these cells die. The count of CD4 cells is used in determining the onset of full-blown AIDS in a patient. In this study of the effectiveness of a new anti-viral drug on HIV, 20 HIV-positive patients had their CD4 counts recorded and then were put on a course of treatment with this drug. After using the drug for one year, their CD4 counts were again recorded. The aim of the experiment was to show that patients taking the drug had increased CD4 counts which is not generally seen in HIV-positive patients.

**Usage**`cd4`

**Format**

This data frame contains the following columns:

`baseline` The CD4 counts (in 100's) on admission to the trial.

`oneyear` The CD4 counts (in 100's) after one year of treatment with the new drug.

**Source**

The data were obtained from

DiCiccio, T.J. and Efron B. (1996) Bootstrap confidence intervals (with Discussion). *Statistical Science*, **11**, 189–228.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

<code>cd4.nested</code>	<i>Nested Bootstrap of cd4 data</i>
-------------------------	-------------------------------------

---

**Description**

This is an example of a nested bootstrap for the correlation coefficient of the `cd4` data frame. It is used in a practical in Chapter 5 of Davison and Hinkley (1997).

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

**See Also**

[cd4](#)

---

<code>censboot</code>	<i>Bootstrap for Censored Data</i>
-----------------------	------------------------------------

---

**Description**

This function applies types of bootstrap resampling which have been suggested to deal with right-censored data. It can also do model-based resampling using a Cox regression model.

**Usage**

```
censboot(data, statistic, R, F.surv, G.surv, strata=matrix(1,n,2),
          sim="ordinary", cox=NULL, index=c(1, 2), ...)
```

**Arguments**

<code>data</code>	The data frame or matrix containing the data. It must have at least two columns, one of which contains the times and the other the censoring indicators. It is allowed to have as many other columns as desired (although efficiency is reduced for large numbers of columns) except for <code>sim="weird"</code> when it should only have two columns - the times and censoring indicators. The columns of <code>data</code> referenced by the components of <code>index</code> are taken to be the times and censoring indicators.
<code>statistic</code>	A function which operates on the data frame and returns the required statistic. Its first argument must be the data. Any other arguments that it requires can be passed using the <code>...{}</code> argument. In the case of <code>sim="weird"</code> , the data passed to <code>statistic</code> only contains the times and censoring indicator regardless of the actual number of columns in <code>data</code> . In all other cases the data passed to <code>statistic</code> will be of the same form as the original data. When <code>sim="weird"</code> , the actual number of observations in the resampled data sets may not be the same as the number in <code>data</code> . For this reason, if <code>sim="weird"</code> and <code>strata</code> is supplied, <code>statistic</code> should also take a numeric vector indicating the strata. This allows the statistic to depend on the strata if required.
<code>R</code>	The number of bootstrap replicates.
<code>F.surv</code>	An object returned from a call to <code>survfit</code> giving the survivor function for the data. This is a required argument unless <code>sim="ordinary"</code> or <code>sim="model"</code> and <code>cox</code> is missing.
<code>G.surv</code>	Another object returned from a call to <code>survfit</code> but with the censoring indicators reversed to give the product-limit estimate of the censoring distribution. Note that for consistency the uncensored times should be reduced by a small amount in the call to <code>survfit</code> . This is a required argument whenever <code>sim="cond"</code> or when <code>sim="model"</code> and <code>cox</code> is supplied.
<code>strata</code>	The strata used in the calls to <code>survfit</code> . It can be a vector or a matrix with 2 columns. If it is a vector then it is assumed to be the strata for the survival distribution, and the censoring distribution is assumed to be the same for all observations. If it is a matrix then the first column is the strata for the survival distribution and the second is the strata for the censoring distribution. When <code>sim="weird"</code> only the strata for the survival distribution are used since the censoring times are considered fixed. When <code>sim="ordinary"</code> , only one set of strata is used to stratify the observations, this is taken to be the first column of <code>strata</code> when it is a matrix.
<code>sim</code>	The simulation type. Possible types are "ordinary" (case resampling), "model" (equivalent to "ordinary" if <code>cox</code> is missing, otherwise it is model based resampling), "weird" (the weird bootstrap - this cannot be used if <code>cox</code> is supplied), and "cond" (the conditional bootstrap, in which censoring times are resampled from the conditional censoring distribution).
<code>cox</code>	An object returned from <code>coxph</code> . If it is supplied, then <code>F.surv</code> should have been generated by a call of the form <code>survfit(cox)</code> .
<code>index</code>	A vector of length two giving the positions of the columns in <code>data</code> which correspond to the times and censoring indicators respectively.
<code>...</code>	Any other arguments which are passed to <code>statistic</code> .

**Details**

The various types of resampling are described in Davison and Hinkley (1997) in sections 3.5 and 7.3. The simplest is case resampling which simply resamples with replacement from the observa-

tions.

The conditional bootstrap simulates failure times from the estimate of the survival distribution. Then, for each observation its simulated censoring time is equal to the observed censoring time if the observation was censored and generated from the estimated censoring distribution conditional on being greater than the observed failure time if the observation was uncensored. If the largest value is censored then it is given a nominal failure time of `Inf` and conversely if it is uncensored it is given a nominal censoring time of `Inf`. This is necessary to allow the largest observation to be in the resamples.

If a Cox regression model is fitted to the data and supplied, then the failure times are generated from the survival distribution using that model. In this case the censoring times can either be simulated from the estimated censoring distribution (`sim="model"`) or from the conditional censoring distribution as in the previous paragraph (`sim="cond"`).

The weird bootstrap holds the censored observations as fixed and also the observed failure times. It then generates the number of events at each failure time using a binomial distribution with mean 1 and denominator the number of failures that could have occurred at that time in the original data set. In our implementation we insist that there is a least one simulated event in each stratum for every bootstrap dataset.

When there are strata involved and `sim` is either `"model"` or `"cond"` the situation becomes more difficult. Since the strata for the survival and censoring distributions are not the same it is possible that for some observations both the simulated failure time and the simulated censoring time are infinite. To see this consider an observation in stratum 1F for the survival distribution and stratum 1G for the censoring distribution. Now if the largest value in stratum 1F is censored it is given a nominal failure time of `Inf`, also if the largest value in stratum 1G is uncensored it is given a nominal censoring time of `Inf` and so both the simulated failure and censoring times could be infinite. When this happens the simulated value is considered to be a failure at the time of the largest observed failure time in the stratum for the survival distribution.

## Value

An object of class `"boot"` containing the following components:

<code>t0</code>	The value of <code>statistic</code> when applied to the original data.
<code>t</code>	A matrix of bootstrap replicates of the values of <code>statistic</code> .
<code>R</code>	The number of bootstrap replicates performed.
<code>sim</code>	The simulation type used. This will usually be the input value of <code>sim</code> unless that was <code>"model"</code> but <code>cox</code> was not supplied, in which case it will be <code>"ordinary"</code> .
<code>data</code>	The data used for the bootstrap. This will generally be the input value of <code>data</code> unless <code>sim="weird"</code> , in which case it will just be the columns containing the times and the censoring indicators.
<code>seed</code>	The value of <code>.Random.seed</code> when <code>censboot</code> was called.
<code>statistic</code>	The input value of <code>statistic</code> .
<code>strata</code>	The strata used in the resampling. When <code>sim="ordinary"</code> this will be a vector which stratifies the observations, when <code>sim="weird"</code> it is the strata for the survival distribution and in all other cases it is a matrix containing the strata for the survival distribution and the censoring distribution.
<code>call</code>	The original call to <code>censboot</code> .

**Author(s)**

Angelo J. Canty

**References**

Andersen, P.K., Borgan, O., Gill, R.D. and Keiding, N. (1993) *Statistical Models Based on Counting Processes*. Springer-Verlag.

Burr, D. (1994) A comparison of certain bootstrap confidence intervals in the Cox model. *Journal of the American Statistical Association*, **89**, 1290–1302.

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Efron, B. (1981) Censored data and the bootstrap. *Journal of the American Statistical Association*, **76**, 312–319.

Hjort, N.L. (1985) Bootstrapping Cox's regression model. Technical report NSF-241, Dept. of Statistics, Stanford University.

**See Also**

[boot](#), [coxph](#), [survfit](#)

**Examples**

```
data(aml, package="boot")
library(survival)
# Example 3.9 of Davison and Hinkley (1997) does a bootstrap on some
# remission times for patients with a type of leukaemia. The patients
# were divided into those who received maintenance chemotherapy and
# those who did not. Here we are interested in the median remission
# time for the two groups.
aml.fun <- function(data) {
  surv <- survfit(Surv(time, cens)~group, data=data)
  out <- NULL
  st <- 1
  for (s in 1:length(surv$strata)) {
    inds <- st:(st+surv$strata[s]-1)
    md <- min(surv$time[inds[1-surv$surv[inds]>=0.5]])
    st <- st+surv$strata[s]
    out <- c(out,md)
  }
  out
}
aml.case <- censboot(aml,aml.fun,R=499,strata=aml$group)

# Now we will look at the same statistic using the conditional
# bootstrap and the weird bootstrap. For the conditional bootstrap
# the survival distribution is stratified but the censoring
# distribution is not.

aml.s1 <- survfit(Surv(time,cens)~group, data=aml)
aml.s2 <- survfit(Surv(time-0.001*cens,1-cens)~1, data=aml)
aml.cond <- censboot(aml,aml.fun,R=499,strata=aml$group,
  F.surv=aml.s1,G.surv=aml.s2,sim="cond")
```

```

# For the weird bootstrap we must redefine our function slightly since
# the data will not contain the group number.
aml.fun1 <- function(data, str) {
  surv <- survfit(Surv(data[,1], data[,2])~str)
  out <- NULL
  st <- 1
  for (s in 1:length(surv$strata)) {
    inds <- st:(st+surv$strata[s]-1)
    md <- min(surv$time[inds[1-surv$surv[inds]>=0.5]])
    st <- st+surv$strata[s]
    out <- c(out, md)
  }
  out
}
aml.wei <- censboot(cbind(aml$time, aml$cens), aml.fun1, R=499,
  strata=aml$group, F.surv=aml.sl, sim="weird")

# Now for an example where a cox regression model has been fitted
# the data we will look at the melanoma data of Example 7.6 from
# Davison and Hinkley (1997). The fitted model assumes that there
# is a different survival distribution for the ulcerated and
# non-ulcerated groups but that the thickness of the tumour has a
# common effect. We will also assume that the censoring distribution
# is different in different age groups. The statistic of interest
# is the linear predictor. This is returned as the values at a
# number of equally spaced points in the range of interest.
data(melanoma, package="boot")
library(splines) # for ns
mel.cox <- coxph(Surv(time, status==1)~ns(thickness, df=4)+strata(ulcer),
  data=melanoma)
mel.surv <- survfit(mel.cox)
agec <- cut(melanoma$age, c(0, 39, 49, 59, 69, 100))
mel.cens <- survfit(Surv(time-0.001*(status==1), status!=1)~
  strata(agec), data=melanoma)
mel.fun <- function(d) {
  t1 <- ns(d$thickness, df=4)
  cox <- coxph(Surv(d$time, d$status==1) ~ t1+strata(d$ulcer))
  ind <- !duplicated(d$thickness)
  u <- d$thickness[!ind]
  eta <- cox$linear.predictors[!ind]
  sp <- smooth.spline(u, eta, df=20)
  th <- seq(from=0.25, to=10, by=0.25)
  predict(sp, th)$y
}
mel.str <- cbind(melanoma$ulcer, agec)
# this is slow!
mel.mod <- censboot(melanoma, mel.fun, R=999, F.surv=mel.surv,
  G.surv=mel.cens, cox=mel.cox, strata=mel.str, sim="model")
# To plot the original predictor and a 95% pointwise envelope for it
mel.env <- envelope(mel.mod)$point
plot(seq(0.25, 10, by=0.25), mel.env[1,], ylim=c(-2, 2),
  xlab="thickness (mm)", ylab="linear predictor", type="n")
lines(seq(0.25, 10, by=0.25), mel.env[1,], lty=2)
lines(seq(0.25, 10, by=0.25), mel.env[2,], lty=2)
lines(seq(0.25, 10, by=0.25), mel.mod$t0, lty=1)

```

---

`channing`*Channing House Data*

---

**Description**

The `channing` data frame has 462 rows and 5 columns.

Channing House is a retirement centre in Palo Alto, California. These data were collected between the opening of the house in 1964 until July 1, 1975. In that time 97 men and 365 women passed through the centre. For each of these, their age on entry and also on leaving or death was recorded. A large number of the observations were censored mainly due to the resident being alive on July 1, 1975 when the data was collected. Over the time of the study 130 women and 46 men died at Channing House. Differences between the survival of the sexes, taking age into account, was one of the primary concerns of this study.

**Usage**`channing`**Format**

This data frame contains the following columns:

`sex` A factor for the sex of each resident ("Male" or "Female").

`entry` The residents age (in months) on entry to the centre

`exit` The age (in months) of the resident on death, leaving the centre or July 1, 1975 whichever event occurred first.

`time` The length of time (in months) that the resident spent at Channing House. (`time=exit-entry`)

`cens` The indicator of right censoring. 1 indicates that the resident died at Channing House, 0 indicates that they left the house prior to July 1, 1975 or that they were still alive and living in the centre at that date.

**Source**

The data were obtained from

Hyde, J. (1980) Testing survival with incomplete observations. *Biostatistics Casebook*. R.G. Miller, B. Efron, B.W. Brown and L.E. Moses (editors), 31–46. John Wiley.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.



---

`claridge`*Genetic Links to Left-handedness*

---

**Description**

The `claridge` data frame has 37 rows and 2 columns.

The data are from an experiment which was designed to look for a relationship between a certain genetic characteristic and handedness. The 37 subjects were women who had a son with mental retardation due to inheriting a defective X-chromosome. For each such mother a genetic measurement of their DNA was made. Larger values of this measurement are known to be linked to the defective gene and it was hypothesized that larger values might also be linked to a progressive shift away from right-handedness. Each woman also filled in a questionnaire regarding which hand they used for various tasks. From these questionnaires a measure of hand preference was found for each mother. The scale of this measure goes from 1, indicating someone who always favours their right hand, to 8, indicating someone who always favours their left hand. Between these two extremes are people who favour one hand for some tasks and the other for other tasks.

**Usage**

```
claridge
```

**Format**

This data frame contains the following columns:

`dnan` The genetic measurement on each woman's DNA.

`hand` The measure of left-handedness on an integer scale from 1 to 8.

**Source**

The data were kindly made available by Dr. Gordon S. Claridge from the Department of Experimental Psychology, University of Oxford.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

`cloth`*Number of Flaws in Cloth*

---

**Description**

The `cloth` data frame has 32 rows and 2 columns.

**Usage**

```
cloth
```

**Format**

This data frame contains the following columns:

- x The length of the roll of cloth.
- y The number of flaws found in the roll.

**Source**

The data were obtained from

Bissell, A.F. (1972) A negative binomial model with varying element size. *Biometrika*, **59**, 435–441.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

co.transfer

*Carbon Monoxide Transfer*

---

**Description**

The `co.transfer` data frame has 7 rows and 2 columns. Seven smokers with chickenpox had their levels of carbon monoxide transfer measured on entry to hospital and then again after 1 week. The main question being whether one week of hospitalization has changed the carbon monoxide transfer factor.

**Usage**

```
co.transfer
```

**Format**

This data frame contains the following columns:

- entry Carbon monoxide transfer factor on entry to hospital.
- week Carbon monoxide transfer one week after admittance to hospital.

**Source**

The data were obtained from

Hand, D.J., Daly, F., Lunn, A.D., McConway, K.J. and Ostrowski, E (1994) *A Handbook of Small Data Sets*. Chapman and Hall.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Ellis, M.E., Neal, K.R. and Webb, A.K. (1987) Is smoking a risk factor for pneumonia in patients with chickenpox? *British Medical Journal*, **294**, 1002.

---

`coal`*Dates of Coal Mining Disasters*

---

**Description**

The `coal` data frame has 191 rows and 1 columns.

This data frame gives the dates of 191 explosions in coal mines which resulted in 10 or more fatalities. The time span of the data is from March 15, 1851 until March 22 1962.

**Usage**

```
coal
```

**Format**

This data frame contains the following column:

`date` The date of the disaster. The integer part of `date` gives the year. The day is represented as the fraction of the year that had elapsed on that day.

**Source**

The data were obtained from

Hand, D.J., Daly, F., Lunn, A.D., McConway, K.J. and Ostrowski, E. (1994) *A Handbook of Small Data Sets*, Chapman and Hall.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Jarrett, R.G. (1979) A note on the intervals between coal-mining disasters. *Biometrika*, **66**, 191-193.

---

`control`*Control Variate Calculations*

---

**Description**

This function will find control variate estimates from a bootstrap output object. It can either find the adjusted bias estimate using post-simulation balancing or it can estimate the bias, variance, third cumulant and quantiles, using the linear approximation as a control variate.

**Usage**

```
control(boot.out, L = NULL, distn = NULL, index = 1, t0 = NULL,  
        t = NULL, bias.adj = FALSE, alpha = NULL, ...)
```

**Arguments**

<code>boot.out</code>	A bootstrap output object returned from <code>boot</code> . The bootstrap replicates must have been generated using the usual nonparametric bootstrap.
<code>L</code>	The empirical influence values for the statistic of interest. If <code>L</code> is not supplied then <code>empinf</code> is called to calculate them from <code>boot.out</code> .
<code>distn</code>	If present this must be the output from <code>smooth.spline</code> giving the distribution function of the linear approximation. This is used only if <code>bias.adj</code> is <code>FALSE</code> . Normally this would be found using a saddlepoint approximation. If it is not supplied in that case then it is calculated by <code>saddle.distn</code> .
<code>index</code>	The index of the variable of interest in the output of <code>boot.out\$statistic</code> .
<code>t0</code>	The observed value of the statistic of interest on the original data set <code>boot.out\$data</code> . This argument is used only if <code>bias.adj</code> is <code>FALSE</code> . The input value is ignored if <code>t</code> is not also supplied. The default value is <code>boot.out\$t0[index]</code> .
<code>t</code>	The bootstrap replicate values of the statistic of interest. This argument is used only if <code>bias.adj</code> is <code>FALSE</code> . The input is ignored if <code>t0</code> is not supplied also. The default value is <code>boot.out\$t[, index]</code> .
<code>bias.adj</code>	A logical variable which if <code>TRUE</code> specifies that the adjusted bias estimate using post-simulation balance is all that is required. If <code>bias.adj</code> is <code>FALSE</code> (default) then the linear approximation to the statistic is calculated and used as a control variate in estimates of the bias, variance and third cumulant as well as quantiles.
<code>alpha</code>	The alpha levels for the required quantiles if <code>bias.adj</code> is <code>FALSE</code> .
<code>...</code>	Any additional arguments that <code>boot.out\$statistic</code> requires. These are passed unchanged every time <code>boot.out\$statistic</code> is called. <code>boot.out\$statistic</code> is called once if <code>bias.adj</code> is <code>TRUE</code> , otherwise it may be called by <code>empinf</code> for empirical influence calculations if <code>L</code> is not supplied.

**Details**

If `bias.adj` is `FALSE` then the linear approximation to the statistic is found and evaluated at each bootstrap replicate. Then using the equation  $T^* = Tl^* + (T^* - Tl^*)$ , moment estimates can be found. For quantile estimation the distribution of the linear approximation to `t` is approximated very accurately by saddlepoint methods, this is then combined with the bootstrap replicates to approximate the bootstrap distribution of `t` and hence to estimate the bootstrap quantiles of `t`.

**Value**

If `bias.adj` is `TRUE` then the returned value is the adjusted bias estimate.

If `bias.adj` is `FALSE` then the returned value is a list with the following components

<code>L</code>	The empirical influence values used. These are the input values if supplied, and otherwise they are the values calculated by <code>empinf</code> .
<code>tL</code>	The linear approximations to the bootstrap replicates <code>t</code> of the statistic of interest.
<code>bias</code>	The control estimate of bias using the linear approximation to <code>t</code> as a control variate.
<code>var</code>	The control estimate of variance using the linear approximation to <code>t</code> as a control variate.

k3	The control estimate of the third cumulant using the linear approximation to $t$ as a control variate.
quantiles	A matrix with two columns; the first column are the alpha levels used for the quantiles and the second column gives the corresponding control estimates of the quantiles using the linear approximation to $t$ as a control variate.
distn	An output object from <code>smooth.spline</code> describing the saddlepoint approximation to the bootstrap distribution of the linear approximation to $t$ . If <code>distn</code> was supplied on input then this is the same as the input otherwise it is calculated by a call to <code>saddle.distn</code> .

## References

- Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.
- Davison, A.C., Hinkley, D.V. and Schechtman, E. (1986) Efficient bootstrap simulation. *Biometrika*, **73**, 555–566.
- Efron, B. (1990) More efficient bootstrap computations. *Journal of the American Statistical Association*, **55**, 79–89.

## See Also

[boot](#), [empinf](#), [k3.linear](#), [linear.approx](#), [saddle.distn](#), [smooth.spline](#), [var.linear](#)

## Examples

```
# Use of control variates for the variance of the air-conditioning data
mean.fun <- function(d, i)
{
  m <- mean(d$hours[i])
  n <- nrow(d)
  v <- (n-1)*var(d$hours[i])/n^2
  c(m, v)
}
air.boot <- boot(aircondit, mean.fun, R = 999)
control(air.boot, index = 2, bias.adj = TRUE)
air.cont <- control(air.boot, index = 2)
# Now let us try the variance on the log scale.
air.cont1 <- control(air.boot, t0=log(air.boot$t0[2]),
  t=log(air.boot$t[,2]))
```

---

corr

*Correlation Coefficient*

---

## Description

Calculates the weighted correlation given a data set and a set of weights.

## Usage

```
corr(d, w=rep(1, nrow(d))/nrow(d))
```

**Arguments**

- d** A matrix with two columns corresponding to the two variables whose correlation we wish to calculate.
- w** A vector of weights to be applied to each pair of observations. The default is equal weights for each pair. Normalization takes place within the function so `sum(w)` need not equal 1.

**Details**

This function finds the correlation coefficient in weighted form. This is often useful in bootstrap methods since it allows for numerical differentiation to get the empirical influence values. It is also necessary to have the statistic in this form to find ABC intervals.

**Value**

The correlation coefficient between `d[, 1]` and `d[, 2]`.

**See Also**

[cor](#)

---

cum3

*Calculate Third Order Cumulants*

---

**Description**

Calculates an estimate of the third cumulant, or skewness, of a vector. Also, if more than one vector is specified, a product-moment of order 3 is estimated.

**Usage**

```
cum3(a, b=a, c=a, unbiased=TRUE)
```

**Arguments**

- a** A vector of observations.
- b** Another vector of observations, if not supplied it is set to the value of `a`. If supplied then it must be the same length as `a`.
- c** Another vector of observations, if not supplied it is set to the value of `a`. If supplied then it must be the same length as `a`.
- unbiased** A logical value indicating whether the unbiased estimator should be used.

**Details**

The unbiased estimator uses a multiplier of  $n / ((n-1) * (n-2))$  where  $n$  is the sample size, if `unbiased` is `FALSE` then a multiplier of  $1/n$  is used. This is multiplied by `sum((a - mean(a)) * (b - mean(b)) * (c - mean(c)))` to give the required estimate.

**Value**

The required estimate.

---

 cv.glm

---

*Cross-validation for Generalized Linear Models*


---

### Description

This function calculates the estimated K-fold cross-validation prediction error for generalized linear models.

### Usage

```
cv.glm(data, glmfit, cost, K)
```

### Arguments

data	A matrix or data frame containing the data. The rows should be cases and the columns correspond to variables, one of which is the response.
glmfit	An object of class "glm" containing the results of a generalized linear model fitted to data.
cost	A function of two vector arguments specifying the cost function for the cross-validation. The first argument to <code>cost</code> should correspond to the observed responses and the second argument should correspond to the predicted or fitted responses from the generalized linear model. <code>cost</code> must return a non-negative scalar value. The default is the average squared error function.
K	The number of groups into which the data should be split to estimate the cross-validation prediction error. The value of <code>K</code> must be such that all groups are of approximately equal size. If the supplied value of <code>K</code> does not satisfy this criterion then it will be set to the closest integer which does and a warning is generated specifying the value of <code>K</code> used. The default is to set <code>K</code> equal to the number of observations in <code>data</code> which gives the usual leave-one-out cross-validation.

### Details

The data is divided randomly into `K` groups. For each group the generalized linear model is fit to `data` omitting that group, then the function `cost` is applied to the observed responses in the group that was omitted from the fit and the prediction made by the fitted models for those observations.

When `K` is the number of observations leave-one-out cross-validation is used and all the possible splits of the data are used. When `K` is less than the number of observations the `K` splits to be used are found by randomly partitioning the data into `K` groups of approximately equal size. In this latter case a certain amount of bias is introduced. This can be reduced by using a simple adjustment (see equation 6.48 in Davison and Hinkley, 1997). The second value returned in `delta` is the estimate adjusted by this method.

### Value

The returned value is a list with the following components.

call	The original call to <code>cv.glm</code> .
K	The value of <code>K</code> used for the K-fold cross validation.

delta	A vector of length two. The first component is the raw cross-validation estimate of prediction error. The second component is the adjusted cross-validation estimate. The adjustment is designed to compensate for the bias introduced by not using leave-one-out cross-validation.
seed	The value of <code>.Random.seed</code> when <code>cv.glm</code> was called.

### Side Effects

The value of `.Random.seed` is updated.

### References

- Breiman, L., Friedman, J.H., Olshen, R.A. and Stone, C.J. (1984) *Classification and Regression Trees*. Wadsworth.
- Burman, P. (1989) A comparative study of ordinary cross-validation,  $v$ -fold cross-validation and repeated learning-testing methods. *Biometrika*, **76**, 503–514
- Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.
- Efron, B. (1986) How biased is the apparent error rate of a prediction rule? *Journal of the American Statistical Association*, **81**, 461–470.
- Stone, M. (1974) Cross-validation choice and assessment of statistical predictions (with Discussion). *Journal of the Royal Statistical Society, B*, **36**, 111–147.

### See Also

[glm](#), [glm.diag](#), [predict](#)

### Examples

```
# leave-one-out and 6-fold cross-validation prediction error for
# the mammals data set.
data(mammals, package="MASS")
mammals.glm <- glm(log(brain)~log(body), data=mammals)
cv.err <- cv.glm(mammals, mammals.glm)
cv.err.6 <- cv.glm(mammals, mammals.glm, K=6)

# As this is a linear model we could calculate the leave-one-out
# cross-validation estimate without any extra model-fitting.
muhat <- mammals.glm$fitted
mammals.diag <- glm.diag(mammals.glm)
cv.err <- mean((mammals.glm$y-muhat)^2/(1-mammals.diag$h)^2)

# leave-one-out and 11-fold cross-validation prediction error for
# the nodal data set. Since the response is a binary variable an
# appropriate cost function is
cost <- function(r, pi=0) mean(abs(r-pi)>0.5)

nodal.glm <- glm(r~stage+xray+acid, binomial, data=nodal)
cv.err <- cv.glm(nodal, nodal.glm, cost, K=nrow(nodal))$delta
cv.11.err <- cv.glm(nodal, nodal.glm, cost, K=11)$delta
```



---

`darwin`*Darwin's Plant Height Differences*

---

**Description**

The `darwin` data frame has 15 rows and 1 columns.

Charles Darwin conducted an experiment to examine the superiority of cross-fertilized plants over self-fertilized plants. 15 pairs of plants were used. Each pair consisted of one cross-fertilized plant and one self-fertilized plant which germinated at the same time and grew in the same pot. The plants were measured at a fixed time after planting and the difference in heights between the cross- and self-fertilized plants are recorded in eighths of an inch.

**Usage**`darwin`**Format**

This data frame contains the following column:

`y` The difference in heights for the pairs of plants (in units of 0.125 inches).

**Source**

The data were obtained from

Fisher, R.A. (1935) *Design of Experiments*. Oliver and Boyd.

**References**

Darwin, C. (1876) *The Effects of Cross- and Self-fertilisation in the Vegetable Kingdom*. John Murray.

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

`dogs`*Cardiac Data for Domestic Dogs*

---

**Description**

The `dogs` data frame has 7 rows and 2 columns.

Data on the cardiac oxygen consumption and left ventricular pressure were gathered on 7 domestic dogs.

**Usage**`dogs`

**Format**

This data frame contains the following columns:

**mvo** Cardiac Oxygen Consumption

**lvp** Left Ventricular Pressure

**References**

Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

downs.bc

*Incidence of Down's Syndrome in British Columbia*

---

**Description**

The `downs.bc` data frame has 30 rows and 3 columns.

Down's syndrome is a genetic disorder caused by an extra chromosome 21 or a part of chromosome 21 being translocated to another chromosome. The incidence of Down's syndrome is highly dependent on the mother's age and rises sharply after age 30. In the 1960's a large scale study of the effect of maternal age on the incidence of Down's syndrome was conducted at the British Columbia Health Surveillance Registry. These are the data which was collected in that study.

Mothers were classified by age. Most groups correspond to the age in years but the first group comprises all mothers with ages in the range 15-17 and the last is those with ages 46-49. No data for mothers over 50 or below 15 were collected.

**Usage**

`downs.bc`

**Format**

This data frame contains the following columns:

**age** The average age of all mothers in the age category.

**m** The total number of live births to mothers in the age category.

**r** The number of cases of Down's syndrome.

**Source**

The data were obtained from

Geyer, C.J. (1991) Constrained maximum likelihood exemplified by isotonic convex logistic regression. *Journal of the American Statistical Association*, **86**, 717-724.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

ducks

*Behavioral and Plumage Characteristics of Hybrid Ducks***Description**

The `ducks` data frame has 11 rows and 2 columns.

Each row of the data frame represents a male duck who is a second generation cross of mallard and pintail ducks. For 11 such ducks a behavioural and plumage index were calculated. These were measured on scales devised for this experiment which was to examine whether there was any link between which species the ducks resembled physically and which they resembled in behaviour. The scale for the physical appearance ranged from 0 (identical in appearance to a mallard) to 20 (identical to a pintail). The behavioural traits of the ducks were on a scale from 0 to 15 with lower numbers indicating closer to mallard-like in behaviour.

**Usage**

```
ducks
```

**Format**

This data frame contains the following columns:

`plumage` The index of physical appearance based on the plumage of individual ducks.

`behaviour` The index of behavioural characteristics of the ducks.

**Source**

The data were obtained from

Larsen, R.J. and Marx, M.L. (1986) *An Introduction to Mathematical Statistics and its Applications* (Second Edition). Prentice-Hall.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Sharpe, R.S., and Johnsgard, P.A. (1966) Inheritance of behavioral characters in  $F_2$  mallard x pintail (*Anas Platyrhynchos L. x Anas Acuta L.*) hybrids. *Behaviour*, **27**, 259-272.

EEF.profile

*Empirical Likelihoods***Description**

Construct the empirical log likelihood or empirical exponential family log likelihood for a mean.

**Usage**

```
EEF.profile(y, tmin=min(y) + 0.1, tmax=max(y) - 0.1, n.t=25,
           u=function(y, t) { y-t})
EL.profile(y, tmin = min(y) + 0.1, tmax = max(y) - 0.1, n.t = 25,
          u = function(y, t) y - t)
```

**Arguments**

<code>y</code>	A vector or matrix of data
<code>tmin</code>	The minimum value of the range over which the likelihood should be computed. This must be larger than <code>min(y)</code> .
<code>tmax</code>	The maximum value of the range over which the likelihood should be computed. This must be smaller than <code>max(y)</code> .
<code>n.t</code>	The number of points between <code>tmin</code> and <code>tmax</code> at which the value of the log-likelihood should be computed.
<code>u</code>	A function of the data and the parameter.

**Details**

These functions calculate the log likelihood for a mean using either an empirical likelihood or an empirical exponential family likelihood. They are supplied as part of the package `boot` for demonstration purposes with the practicals in chapter 10 of Davison and Hinkley (1997). The functions are not intended for general use and are not supported as part of the `boot` package. For more general and more robust code to calculate empirical likelihoods see Professor A. B. Owen's empirical likelihood home page at the URL <http://www-stat.stanford.edu/~owen/empirical/>.

**Value**

A matrix with `n.t` rows. The first column contains the values of the parameter used. The second column of the output of `EL.profile` contains the values of the empirical log likelihood. The second and third columns of the output of `EEF.profile` contain two versions of the empirical exponential family log-likelihood. The final column of the output matrix contains the values of the Lagrange multiplier used in the optimization procedure.

**Author(s)**

Angelo J. Canty

**References**

Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

empinf

*Empirical Influence Values***Description**

This function calculates the empirical influence values for a statistic applied to a data set. It allows four types of calculation, namely the infinitesimal jackknife (using numerical differentiation), the usual jackknife estimates, the ‘positive’ jackknife estimates and a method which estimates the empirical influence values using regression of bootstrap replicates of the statistic. All methods can be used with one or more samples.

**Usage**

```
empinf(boot.out = NULL, data = NULL, statistic = NULL,
       type = NULL, stype = NULL, index = 1, t = NULL,
       strata = rep(1, n), eps = 0.001, ...)
```

**Arguments**

- |                        |  |
|------------------------|--|
| <code>boot.out</code>  | A bootstrap object created by the function <code>boot</code> . If <code>type</code> is "reg" then this argument is required. For any of the other types it is an optional argument. If it is included when optional then the values of <code>data</code> , <code>statistic</code> , <code>stype</code> , and <code>strata</code> are taken from the components of <code>boot.out</code> and any values passed to <code>empinf</code> directly are ignored.   |
| <code>data</code>      | A vector, matrix or data frame containing the data for which empirical influence values are required. It is a required argument if <code>boot.out</code> is not supplied. If <code>boot.out</code> is supplied then <code>data</code> is set to <code>boot.out\$data</code> and any value supplied is ignored.   |
| <code>statistic</code> | The statistic for which empirical influence values are required. It must be a function of at least two arguments, the data set and a vector of weights, frequencies or indices. The nature of the second argument is given by the value of <code>stype</code> . Any other arguments that it takes must be supplied to <code>empinf</code> and will be passed to <code>statistic</code> unchanged. This is a required argument if <code>boot.out</code> is not supplied, otherwise its value is taken from <code>boot.out</code> and any value supplied here will be ignored.   |
| <code>type</code>      | The calculation type to be used for the empirical influence values. Possible values of <code>type</code> are "inf" (infinitesimal jackknife), "jack" (usual jackknife), "pos" (positive jackknife), and "reg" (regression estimation). The default value depends on the other arguments. If <code>t</code> is supplied then the default value of <code>type</code> is "reg" and <code>boot.out</code> should be present so that its frequency array can be found. If <code>t</code> is not supplied then if <code>stype</code> is "w", the default value of <code>type</code> is "inf"; otherwise, if <code>boot.out</code> is present the default is "reg". If none of these conditions apply then the default is "jack". Note that it is an error for <code>type</code> to be "reg" if <code>boot.out</code> is missing or to be "inf" if <code>stype</code> is not "w". |
| <code>stype</code>     | A character variable giving the nature of the second argument to <code>statistic</code> . It can take on three values: "w" (weights), "f" (frequencies), or "i" (indices). If <code>boot.out</code> is supplied the value of <code>stype</code> is set to <code>boot.out\$stype</code> and any value supplied here is ignored. Otherwise it is an optional argument which defaults to "w". If <code>type</code> is "inf" then <code>stype</code> MUST be "w".  |

index	An integer giving the position of the variable of interest in the output of <code>statistic</code> .
t	A vector of length <code>boot.out\$R</code> which gives the bootstrap replicates of the statistic of interest. <code>t</code> is used only when <code>type</code> is <code>reg</code> and it defaults to <code>boot.out\$t[, index]</code> .
strata	An integer vector or a factor specifying the strata for multi-sample problems. If <code>boot.out</code> is supplied the value of <code>strata</code> is set to <code>boot.out\$strata</code> . Otherwise it is an optional argument which has default corresponding to the single sample situation.
eps	This argument is used only if <code>type</code> is <code>"inf"</code> . In that case the value of epsilon to be used for numerical differentiation will be <code>eps</code> divided by the number of observations in <code>data</code> .
...	Any other arguments that <code>statistic</code> takes. They will be passed unchanged to <code>statistic</code> every time that it is called.

### Details

If `type` is `"inf"` then numerical differentiation is used to approximate the empirical influence values. This makes sense only for statistics which are written in weighted form (i.e. `stype` is `"w"`). If `type` is `"jack"` then the usual leave-one-out jackknife estimates of the empirical influence are returned. If `type` is `"pos"` then the positive (include-one-twice) jackknife values are used. If `type` is `"reg"` then a bootstrap object must be supplied. The regression method then works by regressing the bootstrap replicates of `statistic` on the frequency array from which they were derived. The bootstrap frequency array is obtained through a call to `boot.array`. Further details of the methods are given in Section 2.7 of Davison and Hinkley (1997).

Empirical influence values are often used frequently in nonparametric bootstrap applications. For this reason many other functions call `empinf` when they are required. Some examples of their use are for nonparametric delta estimates of variance, BCa intervals and finding linear approximations to statistics for use as control variates. They are also used for antithetic bootstrap resampling.

### Value

A vector of the empirical influence values of `statistic` applied to `data`. The values will be in the same order as the observations in `data`.

### Warning

All arguments to `empinf` must be passed using the `name = value` convention. If this is not followed then unpredictable errors can occur.

### References

- Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.
- Efron, B. (1982) *The Jackknife, the Bootstrap and Other Resampling Plans*. CBMS-NSF Regional Conference Series in Applied Mathematics, **38**, SIAM.
- Fernholtz, L.T. (1983) *von Mises Calculus for Statistical Functionals*. Lecture Notes in Statistics, **19**, Springer-Verlag.

**See Also**

[boot](#), [boot.array](#), [boot.ci](#), [control](#), [jack.after.boot](#), [linear.approx](#), [var.linear](#)

**Examples**

```
# The empirical influence values for the ratio of means in
# the city data.
ratio <- function(d, w) sum(d$x *w)/sum(d$u*w)
empinf(data=city, statistic=ratio)
city.boot <- boot(city, ratio, 499, stype="w")
empinf(boot.out=city.boot, type="reg")

# A statistic that may be of interest in the difference of means
# problem is the t-statistic for testing equality of means. In
# the bootstrap we get replicates of the difference of means and
# the variance of that statistic and then want to use this output
# to get the empirical influence values of the t-statistic.
grav1 <- gravity[as.numeric(gravity[,2])>=7,]
grav.fun <- function(dat, w)
{
  strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
  d <- dat[, 1]
  ns <- tabulate(strata)
  w <- w/tapply(w, strata, sum)[strata]
  mns <- tapply(d * w, strata, sum)
  mn2 <- tapply(d * d * w, strata, sum)
  s2hat <- sum((mn2 - mns^2)/ns)
  c(mns[2]-mns[1], s2hat)
}

grav.boot <- boot(grav1, grav.fun, R=499, stype="w", strata=grav1[,2])

# Since the statistic of interest is a function of the bootstrap
# statistics, we must calculate the bootstrap replicates and pass
# them to empinf using the t argument.
grav.z <- (grav.boot$t[,1]-grav.boot$t0[1])/sqrt(grav.boot$t[,2])
empinf(boot.out=grav.boot, t=grav.z)
```

---

envelope

*Confidence Envelopes for Curves*


---

**Description**

This function calculates overall and pointwise confidence envelopes for a curve based on bootstrap replicates of the curve evaluated at a number of fixed points.

**Usage**

```
envelope(boot.out=NULL, mat=NULL, level=0.95, index=1:ncol(mat))
```

**Arguments**

<code>boot.out</code>	An object of class "boot" for which <code>boot.out\$t</code> contains the replicates of the curve at a number of fixed points.
<code>mat</code>	A matrix of bootstrap replicates of the values of the curve at a number of fixed points. This is a required argument if <code>boot.out</code> is not supplied and is set to <code>boot.out\$t</code> otherwise.
<code>level</code>	The confidence level of the envelopes required. The default is to find 95% confidence envelopes. It can be a scalar or a vector of length 2. If it is scalar then both the pointwise and the overall envelopes are found at that level. If is a vector then the first element gives the level for the pointwise envelope and the second gives the level for the overall envelope.
<code>index</code>	The numbers of the columns of <code>mat</code> which contain the bootstrap replicates. This can be used to ensure that other statistics which may have been calculated in the bootstrap are not considered as values of the function.

**Details**

The pointwise envelope is found by simply looking at the quantiles of the replicates at each point. The overall error for that envelope is then calculated using equation (4.17) of Davison and Hinkley (1997). A sequence of pointwise envelopes is then found until one of them has overall error approximately equal to the level required. If no such envelope can be found then the envelope returned will just contain the extreme values of each column of `mat`.

**Value**

A list with the following components :

<code>point</code>	A matrix with two rows corresponding to the values of the upper and lower pointwise confidence envelope at the same points as the bootstrap replicates were calculated.
<code>overall</code>	A matrix similar to <code>point</code> but containing the envelope which controls the overall error.
<code>k.pt</code>	The quantiles used for the pointwise envelope.
<code>err.pt</code>	A vector with two components, the first gives the pointwise error rate for the pointwise envelope, and the second the overall error rate for that envelope.
<code>k.ov</code>	The quantiles used for the overall envelope.
<code>err.ov</code>	A vector with two components, the first gives the pointwise error rate for the overall envelope, and the second the overall error rate for that envelope.
<code>err.nom</code>	A vector of length 2 giving the nominal error rates for the pointwise and the overall envelopes.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

**See Also**

[boot](#), [boot.ci](#)



**Examples**

```

# Testing whether the final series of measurements of the gravity data
# may come from a normal distribution. This is done in Examples 4.7
# and 4.8 of Davison and Hinkley (1997).
grav1 <- gravity$g[gravity$series==8]
grav.z <- (grav1-mean(grav1))/sqrt(var(grav1))
grav.gen <- function(dat,mle)
  rnorm(length(dat))
grav.qqboot <- boot(grav.z,sort,R=999,sim="parametric",ran.gen=grav.gen)
grav.qq <- qqnorm(grav.z,plot=FALSE)
grav.qq <- lapply(grav.qq,sort)
plot(grav.qq,ylim=c(-3.5,3.5),ylab="Studentized Order Statistics",
      xlab="Normal Quantiles")
grav.env <- envelope(grav.qqboot,level=0.9)
lines(grav.qq$x,grav.env$point[1,],lty=4)
lines(grav.qq$x,grav.env$point[2,],lty=4)
lines(grav.qq$x,grav.env$overall[1,],lty=1)
lines(grav.qq$x,grav.env$overall[2,],lty=1)

```

exp.tilt

*Exponential Tilting***Description**

This function calculates exponentially tilted multinomial distributions such that the resampling distributions of the linear approximation to a statistic have the required means.

**Usage**

```
exp.tilt(L, theta=NULL, t0=0, lambda=NULL,
         strata=rep(1, length(L)))
```

**Arguments**

L	The empirical influence values for the statistic of interest based on the observed data. The length of L should be the same as the size of the original data set. Typically L will be calculated by a call to <code>empinf</code> .
theta	The value at which the tilted distribution is to be centred. This is not required if lambda is supplied but is needed otherwise.
t0	The current value of the statistic. The default is that the statistic equals 0.
lambda	The Lagrange multiplier(s). For each value of lambda a multinomial distribution is found with probabilities proportional to $\exp(\lambda * L)$ . In general lambda is not known and so theta would be supplied, and the corresponding value of lambda found. If both lambda and theta are supplied then lambda is ignored and the multipliers for tilting to theta are found.
strata	A vector or factor of the same length as L giving the strata for the observed data and the empirical influence values L.

## Details

Exponential tilting involves finding a set of weights for a data set to ensure that the bootstrap distribution of the linear approximation to a statistic of interest has mean `theta`. The weights chosen to achieve this are given by `p[j]` proportional to  $\exp(\lambda * L[j] / n)$ , where `n` is the number of data points. `lambda` is then chosen to make the mean of the bootstrap distribution, of the linear approximation to the statistic of interest, equal to the required value `theta`. Thus `lambda` is defined as the solution of a nonlinear equation. The equation is solved by minimizing the Euclidean distance between the left and right hand sides of the equation using the function `nlmin`. If this minimum is not equal to zero then the method fails.

Typically exponential tilting is used to find suitable weights for importance resampling. If a small tail probability or quantile of the distribution of the statistic of interest is required then a more efficient simulation is to centre the resampling distribution close to the point of interest and then use the functions `imp.prob` or `imp.quantile` to estimate the required quantity.

Another method of achieving a similar shifting of the distribution is through the use of `smooth.f`. The function `tilt.boot` uses `exp.tilt` or `smooth.f` to find the weights for a tilted bootstrap.

## Value

A list with the following components :

<code>p</code>	The tilted probabilities. There will be <code>m</code> distributions where <code>m</code> is the length of <code>theta</code> (or <code>lambda</code> if supplied). If <code>m</code> is 1 then <code>p</code> is a vector of length( <code>L</code> ) probabilities. If <code>m</code> is greater than 1 then <code>p</code> is a matrix with <code>m</code> rows, each of which contain length( <code>L</code> ) probabilities. In this case the vector <code>p[i, ]</code> is the distribution tilted to <code>theta[i]</code> . <code>p</code> is in the form required by the argument <code>weights</code> of the function <code>boot</code> for importance resampling.
<code>lambda</code>	The Lagrange multiplier used in the equation to determine the tilted probabilities. <code>lambda</code> is a vector of the same length as <code>theta</code> .
<code>theta</code>	The values of <code>theta</code> to which the distributions have been tilted. In general this will be the input value of <code>theta</code> but if <code>lambda</code> was supplied then this is the vector of the corresponding <code>theta</code> values.

## References

- Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.
- Efron, B. (1981) Nonparametric standard errors and confidence intervals (with Discussion). *Canadian Journal of Statistics*, **9**, 139–172.

## See Also

[empinf](#), [imp.prob](#), [imp.quantile](#), [optim](#), [smooth.f](#), [tilt.boot](#)

## Examples

```
# Example 9.8 of Davison and Hinkley (1997) requires tilting the resampling
# distribution of the studentized statistic to be centred at the observed
# value of the test statistic 1.84. This can be achieved as follows.
grav1 <- gravity[as.numeric(gravity[,2])>=7,]
grav.fun <- function(dat, w, orig)
{   strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
    d <- dat[, 1]
```

```

ns <- tabulate(strata)
w <- w/tapply(w, strata, sum)[strata]
mns <- tapply(d * w, strata, sum)
mn2 <- tapply(d * d * w, strata, sum)
s2hat <- sum((mn2 - mns^2)/ns)
as.vector(c(mns[2]-mns[1],s2hat,(mns[2]-mns[1]-orig)/sqrt(s2hat)))
}
grav.z0 <- grav.fun(grav1,rep(1,26),0)
grav.L <- empinf(data=grav1, statistic=grav.fun, stype="w",
                 strata=grav1[,2], index=3, orig=grav.z0[1])
grav.tilt <- exp.tilt(grav.L, grav.z0[3], strata=grav1[,2])
boot(grav1, grav.fun, R=499, stype="w", weights=grav.tilt$p,
     strata=grav1[,2], orig=grav.z0[1])

```

---

fir

*Counts of Balsam-fir Seedlings*


---

### Description

The `fir` data frame has 50 rows and 3 columns.

The number of balsam-fir seedlings in each quadrant of a grid of 50 five foot square quadrants were counted. The grid consisted of 5 rows of 10 quadrants in each row.

### Usage

```
fir
```

### Format

This data frame contains the following columns:

`count` The number of seedlings in the quadrant.

`row` The row number of the quadrant.

`col` The quadrant number within the row.

### Source

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

`freq.array`*Bootstrap Frequency Arrays*

---

**Description**

Take a matrix of indices for nonparametric bootstrap resamples and return the frequencies of the original observations in each resample.

**Usage**

```
freq.array(i.array)
```

**Arguments**

`i.array` This will be an matrix of integers between 1 and `n`, where `n` is the number of observations in a data set. The matrix will have `n` columns and `R` rows where `R` is the number of bootstrap resamples. Such matrices are found by `boot` when doing nonparametric bootstraps. They can also be found after a bootstrap has been run through the function `boot.array`.

**Value**

A matrix of the same dimensions as the input matrix. Each row of the matrix corresponds to a single bootstrap resample. Each column of the matrix corresponds to one of the original observations and specifies its frequency in each bootstrap resample. Thus the first column tells us how often the first observation appeared in each bootstrap resample. Such frequency arrays are often useful for diagnostic purposes such as the jackknife-after-bootstrap plot. They are also necessary for the regression estimates of empirical influence values and for finding importance sampling weights.

**See Also**

[boot.array](#)

---

`frets`*Head Dimensions in Brothers*

---

**Description**

The `frets` data frame has 25 rows and 4 columns.

The data consist of measurements of the length and breadth of the heads of pairs of adult brothers in 25 randomly sampled families. All measurements are expressed in millimetres.

**Usage**

```
frets
```

**Format**

This data frame contains the following columns:

- l1 The head length of the eldest son.
- b1 The head breadth of the eldest son.
- l2 The head length of the second son.
- b2 The head breadth of the second son.

**Source**

The data were obtained from

Frets, G.P. (1921) Heredity of head form in man. *Genetica*, **3**, 193.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Whittaker, J. (1990) *Graphical Models in Applied Multivariate Statistics*. John Wiley.

---

glm.diag

*Generalized Linear Model Diagnostics*

---

**Description**

Calculates jackknife deviance residuals, standardized deviance residuals, standardized Pearson residuals, approximate Cook statistic, leverage and estimated dispersion.

**Usage**

```
glm.diag(glmfit)
```

**Arguments**

glmfit            glmfit is a glm.object - the result of a call to glm()

**Value**

Returns a list with the following components

- |      |  |
|------|--|
| res  | The vector of jackknife deviance residuals.  |
| rd   | The vector of standardized deviance residuals.   |
| rp   | The vector of standardized Pearson residuals.  |
| cook | The vector of approximate Cook statistics.   |
| h    | The vector of leverages of the observations.   |
| sd   | The value used to standardize the residuals. This is the estimate of residual standard deviation in the Gaussian family and is the square root of the estimated shape parameter in the Gamma family. In all other cases it is 1. |

**Note**

See the help for `glm.diag.plots` for an example of the use of `glm.diag`.

**References**

Davison, A.C. and Snell, E.J. (1991) Residuals and diagnostics. In *Statistical Theory and Modelling: In Honour of Sir David Cox*. D.V. Hinkley, N. Reid and E.J. Snell (editors), 83–106. Chapman and Hall.

**See Also**

`glm`, `glm.diag.plots`, `summary.glm`

---

<code>glm.diag.plots</code>	<i>Diagnostics plots for generalized linear models</i>
-----------------------------	--

---

**Description**

Makes plot of jackknife deviance residuals against linear predictor, normal scores plots of standardized deviance residuals, plot of approximate Cook statistics against leverage/(1-leverage), and case plot of Cook statistic.

**Usage**

```
glm.diag.plots(glmfit, glmdiag=glm.diag(glmfit),
              subset=NULL, iden=FALSE, labels=NULL, ret=FALSE)
```

**Arguments**

<code>glmfit</code>	<code>glm.object</code> : the result of a call to <code>glm()</code>
<code>glmdiag</code>	Diagnostics of <code>glmfit</code> obtained from a call to <code>glm.diag</code> . If it is not supplied then it is calculated.
<code>subset</code>	Subset of data for which <code>glm</code> fitting performed: should be the same as the <code>subset</code> option used in the call to <code>glm()</code> which generated <code>glmfit</code> . Needed only if the <code>subset=</code> option was used in the call to <code>glm</code> .
<code>iden</code>	A logical argument. If <code>TRUE</code> then, after the plots are drawn, the user will be prompted for an integer between 0 and 4. A positive integer will select a plot and invoke <code>identify()</code> on that plot. After exiting <code>identify()</code> , the user is again prompted, this loop continuing until the user responds to the prompt with 0. If <code>iden</code> is <code>FALSE</code> (default) the user cannot interact with the plots.
<code>labels</code>	A vector of labels for use with <code>identify()</code> if <code>iden</code> is <code>TRUE</code> . If it is not supplied then the labels are derived from <code>glmfit</code> .
<code>ret</code>	A logical argument indicating if <code>glmdiag</code> should be returned. The default is <code>FALSE</code> .

## Details

The diagnostics required for the plots are calculated by `glm.diag`. These are then used to produce the four plots on the current graphics device.

The plot on the top left is a plot of the jackknife deviance residuals against the fitted values.

The plot on the top right is a normal QQ plot of the standardized deviance residuals. The dotted line is the expected line if the standardized residuals are normally distributed, i.e. it is the line with intercept 0 and slope 1.

The bottom two panels are plots of the Cook statistics. On the left is a plot of the Cook statistics against the standardized leverages. In general there will be two dotted lines on this plot. The horizontal line is at  $8/(n-2p)$  where  $n$  is the number of observations and  $p$  is the number of parameters estimated. Points above this line may be points with high influence on the model. The vertical line is at  $2p/(n-2p)$  and points to the right of this line have high leverage compared to the variance of the raw residual at that point. If all points are below the horizontal line or to the left of the vertical line then the line is not shown.

The final plot again shows the Cook statistic this time plotted against case number enabling us to find which observations are influential.

Use of `iden=T` is encouraged for proper exploration of these four plots as a guide to how well the model fits the data and whether certain observations have an unduly large effect on parameter estimates.

## Value

If `ret` is TRUE then the value of `glm.diag` is returned otherwise there is no returned value.

## Side Effects

The current device is cleared and four plots are plotted by use of `split.screen(c(2,2))`. If `iden` is TRUE, interactive identification of points is enabled. All screens are closed, but not cleared, on termination of the function.

## References

Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Davison, A.C. and Snell, E.J. (1991) Residuals and diagnostics. In *Statistical Theory and Modelling: In Honour of Sir David Cox* D.V. Hinkley, N. Reid, and E.J. Snell (editors), 83–106. Chapman and Hall.

## See Also

`glm`, `glm.diag`, `identify`

## Examples

```
# In this example we look at the leukaemia data which was looked at in
# Example 7.1 of Davison and Hinkley (1997)
data(leuk, package="MASS")
leuk.mod <- glm(time~ag-1+log10(wbc), family=Gamma(log), data=leuk)
leuk.diag <- glm.diag(leuk.mod)
glm.diag.plots(leuk.mod,leuk.diag)
```

---

`gravity`*Acceleration Due to Gravity*

---

**Description**

The `gravity` data frame has 81 rows and 2 columns.

The `grav` data set has 26 rows and 2 columns.

Between May 1934 and July 1935, the National Bureau of Standards in Washington D.C. conducted a series of experiments to estimate the acceleration due to gravity,  $g$ , at Washington. Each experiment produced a number of replicate estimates of  $g$  using the same methodology. Although the basic method remained the same for all experiments, that of the reversible pendulum, there were changes in configuration.

The `gravity` data frame contains the data from all eight experiments. The `grav` data frame contains the data from the experiments 7 and 8. The data are expressed as deviations from 980.000 in centimetres per second squared.

**Usage**

```
gravity
```

**Format**

This data frame contains the following columns:

`g` The deviation of the estimate from 980.000 centimetres per second squared.

`series` A factor describing from which experiment the estimate was derived.

**Source**

The data were obtained from

Cressie, N. (1982) Playing safe with misweighted means. *Journal of the American Statistical Association*, **77**, 754–759.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

`hirose`*Failure Time of PET Film*

---

**Description**

The `hirose` data frame has 44 rows and 3 columns.

PET film is used in electrical insulation. In this accelerated life test the failure times for 44 samples in gas insulated transformers. 4 different voltage levels were used.



**Usage**

```
hirose
```

**Format**

This data frame contains the following columns:

`volt` The voltage (in kV).

`time` The failure or censoring time in hours.

`cens` The censoring indicator; 1 means right-censored data.

**Source**

The data were obtained from

Hirose, H. (1993) Estimation of threshold stress in accelerated life-testing. *IEEE Transactions on Reliability*, **42**, 650–657.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

Imp.Estimates

*Importance Sampling Estimates*

---

**Description**

Central moment, tail probability, and quantile estimates for a statistic under importance resampling.

**Usage**

```
imp.moments(boot.out=NULL, index=1, t=boot.out$t[, index],
            w=NULL, def=TRUE, q=NULL)
imp.prob(boot.out=NULL, index=1, t0=boot.out$t0[index],
         t=boot.out$t[, index], w=NULL, def=TRUE, q=NULL)
imp.quantile(boot.out=NULL, alpha=NULL, index=1,
            t=boot.out$t[, index], w=NULL, def=TRUE, q=NULL)
```

**Arguments**

<code>boot.out</code>	A object of class "boot" generated by a call to <code>boot</code> or <code>tilt.boot</code> . Use of these functions makes sense only when the bootstrap resampling used unequal weights for the observations. If the importance weights <code>w</code> are not supplied then <code>boot.out</code> is a required argument. It is also required if <code>t</code> is not supplied.
<code>alpha</code>	The alpha levels for the required quantiles. The default is to calculate the 1%, 2.5%, 5%, 10%, 90%, 95%, 97.5% and 99% quantiles.
<code>index</code>	The index of the variable of interest in the output of <code>boot.out\$statistic</code> . This is not used if the argument <code>t</code> is supplied.

<code>t0</code>	The values at which tail probability estimates are required. For each value <code>t0[i]</code> the function will estimate the bootstrap cdf evaluated at <code>t0[i]</code> . If <code>imp.prob</code> is called without the argument <code>t0</code> then the bootstrap cdf evaluated at the observed value of the statistic is found.
<code>t</code>	The bootstrap replicates of a statistic. By default these are taken from the bootstrap output object <code>boot.out</code> but they can be supplied separately if required (e.g. when the statistic of interest is a function of the calculated values in <code>boot.out</code> ). Either <code>boot.out</code> or <code>t</code> must be supplied.
<code>w</code>	The importance resampling weights for the bootstrap replicates. If they are not supplied then <code>boot.out</code> must be supplied, in which case the importance weights are calculated by a call to <code>imp.weights</code> .
<code>def</code>	A logical value indicating whether a defensive mixture is to be used for weight calculation. This is used only if <code>w</code> is missing and it is passed unchanged to <code>imp.weights</code> to calculate <code>w</code> .
<code>q</code>	A vector of probabilities specifying the resampling distribution from which any estimates should be found. In general this would correspond to the usual bootstrap resampling distribution which gives equal weight to each of the original observations. The estimates depend on this distribution only through the importance weights <code>w</code> so this argument is ignored if <code>w</code> is supplied. If <code>w</code> is missing then <code>q</code> is passed as an argument to <code>imp.weights</code> and used to find <code>w</code> .

### Value

A list with the following components :

<code>alpha</code>	The alpha levels used for the quantiles, if <code>imp.quantile</code> is used.
<code>t0</code>	The values at which the tail probabilities are estimated, if <code>imp.prob</code> is used.
<code>raw</code>	The raw importance resampling estimates. For <code>imp.moments</code> this has length 2, the first component being the estimate of the mean and the second being the variance estimate. For <code>imp.prob</code> , <code>raw</code> is of the same length as <code>t0</code> , and for <code>imp.quantile</code> it is of the same length as <code>alpha</code> .
<code>rat</code>	The ratio importance resampling estimates. In this method the weights <code>w</code> are rescaled to have average value one before they are used. The format of this vector is the same as <code>raw</code> .
<code>reg</code>	The regression importance resampling estimates. In this method the weights which are used are derived from a regression of <code>t*w</code> on <code>w</code> . This choice of weights can be shown to minimize the variance of the weights and also the Euclidean distance of the weights from the uniform weights. The format of this vector is the same as <code>raw</code> .

### References

- Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.
- Hesterberg, T. (1995) Weighted average importance sampling and defensive mixture distributions. *Technometrics*, **37**, 185–194.
- Johns, M.V. (1988) Importance sampling for bootstrap confidence intervals. *Journal of the American Statistical Association*, **83**, 709–714.

**See Also**

`boot`, `exp.tilt`, `imp.weights`, `smooth.f`, `tilt.boot`

**Examples**

```
# Example 9.8 of Davison and Hinkley (1997) requires tilting the
# resampling distribution of the studentized statistic to be centred
# at the observed value of the test statistic, 1.84. In this example
# we show how certain estimates can be found using resamples taken from
# the tilted distribution.
grav1 <- gravity[as.numeric(gravity[,2])>=7,]
grav.fun <- function(dat, w, orig)
{   strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
    d <- dat[, 1]
    ns <- tabulate(strata)
    w <- w/tapply(w, strata, sum)[strata]
    mns <- tapply(d * w, strata, sum)
    mn2 <- tapply(d * d * w, strata, sum)
    s2hat <- sum((mn2 - mns^2)/ns)
    as.vector(c(mns[2]-mns[1],s2hat, (mns[2]-mns[1]-orig)/sqrt(s2hat)))
}
grav.z0 <- grav.fun(grav1,rep(1,26),0)
grav.L <- empinf(data=grav1, statistic=grav.fun, stype="w",
                strata=grav1[,2], index=3, orig=grav.z0[1])
grav.tilt <- exp.tilt(grav.L,grav.z0[3],strata=grav1[,2])
grav.tilt.boot <- boot(grav1, grav.fun, R=199, stype="w",
                     strata=grav1[,2], weights=grav.tilt$p,
                     orig=grav.z0[1])
# Since the weights are needed for all calculations, we shall calculate
# them once only.
grav.w <- imp.weights(grav.tilt.boot)
grav.mom <- imp.moments(grav.tilt.boot, w=grav.w, index=3)
grav.p <- imp.prob(grav.tilt.boot, w=grav.w, index=3, t0=grav.z0[3])
grav.q <- imp.quantile(grav.tilt.boot, w=grav.w, index=3,
                     alpha=c(0.9,0.95,0.975,0.99))
```

---

imp.weights

*Importance Sampling Weights*

---

**Description**

This function calculates the importance sampling weight required to correct for simulation from a distribution with probabilities  $p$  when estimates are required assuming that simulation was from an alternative distribution with probabilities  $q$ .

**Usage**

```
imp.weights(boot.out, def=TRUE, q=NULL)
```

**Arguments**

<code>boot.out</code>	A object of class "boot" generated by <code>boot</code> or <code>tilt.boot</code> . Typically the bootstrap simulations would have been done using importance resampling and we wish to do our calculations under the assumption of sampling with equal probabilities.
<code>def</code>	A logical variable indicating whether the defensive mixture distribution weights should be calculated. This makes sense only in the case where the replicates in <code>boot.out</code> were simulated under a number of different distributions. If this is the case then the defensive mixture weights use a mixture of the distributions used in the bootstrap. The alternative is to calculate the weights for each replicate using knowledge of the distribution from which the bootstrap resample was generated.
<code>q</code>	A vector of probabilities specifying the resampling distribution from which we require inferences to be made. In general this would correspond to the usual bootstrap resampling distribution which gives equal weight to each of the original observations and this is the default. <code>q</code> must have length equal to the number of observations in the <code>boot.out\$data</code> and all elements of <code>q</code> must be positive.

**Details**

The importance sampling weight for a bootstrap replicate with frequency vector  $\mathbf{f}$  is given by  $\text{prod}((q/p)^{\mathbf{f}})$ . This reweights the replicates so that estimates can be found as if the bootstrap resamples were generated according to the probabilities  $q$  even though, in fact, they came from the distribution  $p$ .

**Value**

A vector of importance weights of the same length as `boot.out$t`. These weights can then be used to reweight `boot.out$t` so that estimates can be found as if the simulations were from a distribution with probabilities  $q$ .

**Note**

See the example in the help for `imp.moments` for an example of using `imp.weights`.

**References**

- Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.
- Hesterberg, T. (1995) Weighted average importance sampling and defensive mixture distributions. *Technometrics*, **37**, 185–194.
- Johns, M.V. (1988) Importance sampling for bootstrap confidence intervals. *Journal of the American Statistical Association*, **83**, 709–714.

**See Also**

[boot](#), [exp.tilt](#), [imp.moments](#), [smooth.f](#), [tilt.boot](#)

---

`inv.logit`*Inverse Logit Function*

---

**Description**

Given a numeric object return the inverse logit of the values.

**Usage**

```
inv.logit(x)
```

**Arguments**

`x` A numeric object. Missing values (NAs) are allowed.

**Details**

The inverse logit is defined by  $\exp(x) / (1 + \exp(x))$ . Values in `x` of `-Inf` or `Inf` return logits of 0 or 1 respectively. Any NAs in the input will also be NAs in the output.

**Value**

An object of the same type as `x` containing the inverse logits of the input values.

**See Also**

`logit`, `plogis` which is the underlying function.

---

`islay`*Jura Quartzite Azimuths on Islay*

---

**Description**

The `islay` data frame has 18 rows and 1 columns.

Measurements were taken of paleocurrent azimuths from the Jura Quartzite on the Scottish island of Islay.

**Usage**

```
islay
```

**Format**

This data frame contains the following column:

`theta` The angle of the azimuth in degrees East of North.

**Source**

The data were obtained from

Hand, D.J., Daly, F., Lunn, A.D., McConway, K.J. and Ostrowski, E. (1994) *A Handbook of Small Data Sets*, Chapman and Hall.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Till, R. (1974) *Statistical Methods for the Earth Scientist*. Macmillan.

---

jack.after.boot      *Jackknife-after-Bootstrap Plots*

---

**Description**

This function calculates the jackknife influence values from a bootstrap output object and plots the corresponding jackknife-after-bootstrap plot.

**Usage**

```
jack.after.boot(boot.out, index=1, t=NULL, L=NULL, useJ=TRUE,
               stinf=TRUE, alpha=NULL, main="", ylab=NULL, ...)
```

**Arguments**

boot.out	An object of class "boot" which would normally be created by a call to <code>boot</code> . It should represent a nonparametric bootstrap. For reliable results <code>boot.out\$R</code> should be reasonably large.
index	The index of the statistic of interest in the output of <code>boot.out\$statistic</code> .
t	A vector of length <code>boot.out\$R</code> giving the bootstrap replicates of the statistic of interest. This is useful if the statistic of interest is a function of the calculated bootstrap output. If it is not supplied then the default is <code>boot.out\$t[, index]</code> .
L	The empirical influence values for the statistic of interest. These are used only if <code>useJ</code> is <code>FALSE</code> . If they are not supplied and are needed, they are calculated by a call to <code>empinf</code> . If <code>L</code> is supplied then it is assumed that they are the infinitesimal jackknife values.
useJ	A logical variable indicating if the jackknife influence values calculated from the bootstrap replicates should be used. If <code>FALSE</code> the empirical influence values are used. The default is <code>TRUE</code> .
stinf	A logical variable indicating whether to standardize the jackknife values before plotting them. If <code>TRUE</code> then the jackknife values used are divided by their standard error.
alpha	The quantiles at which the plots are required. The default is <code>c(0.05, 0.1, 0.16, 0.5, 0.84, 0.9, 0.95)</code> .
main	A character string giving the main title for the plot.

ylab	The label for the Y axis. If the default values of alpha are used and ylab is not supplied then a label indicating which percentiles are plotted is used. If alpha is supplied then the default label will not say which percentiles were used.
...	Any extra arguments required by <code>boot.out\$statistic</code> . These are required only if <code>useJ</code> is <code>FALSE</code> and <code>L</code> is not supplied, in which case they are passed to <code>empinf</code> for use in calculation of the empirical influence values.

### Details

The centred jackknife quantiles for each observation are estimated from those bootstrap samples in which the particular observation did not appear. These are then plotted against the influence values. If `useJ` is `TRUE` then the influence values are found in the same way as the difference between the mean of the statistic in the samples excluding the observations and the mean in all samples. If `useJ` is `FALSE` then empirical influence values are calculated by calling `empinf`.

The resulting plots are useful diagnostic tools for looking at the way individual observations affect the bootstrap output.

The plot will consist of a number of horizontal dotted lines which correspond to the quantiles of the centred bootstrap distribution. For each data point the quantiles of the bootstrap distribution calculated by omitting that point are plotted against the (possibly standardized) jackknife values. The observation number is printed below the plots. To make it easier to see the effect of omitting points on quantiles, the plotted quantiles are joined by line segments. These plots provide a useful diagnostic tool in establishing the effect of individual observations on the bootstrap distribution. See the references below for some guidelines on the interpretation of the plots.

### Value

There is no returned value but a plot is generated on the current graphics display.

### Side Effects

A plot is created on the current graphics device.

### References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Efron, B. (1992) Jackknife-after-bootstrap standard errors and influence functions (with Discussion). *Journal of the Royal Statistical Society, B*, **54**, 83–127.

### See Also

[boot](#), [empinf](#)

### Examples

```
# To draw the jackknife-after-bootstrap plot for the head size data as in
# Example 3.24 of Davison and Hinkley (1997)
pcorr <- function( x )
{
# function to find the correlations and partial correlations between
# the four measurements.
  v <- cor(x)
```

```

v.d <- diag(var(x))
iv <- solve(v)
iv.d <- sqrt(diag(iv))
iv <- - diag(1/iv.d) %*% iv %*% diag(1/iv.d)
q <- NULL
n <- nrow(v)
for (i in 1:(n-1))
  q <- rbind( q, c(v[i,1:i],iv[i,(i+1):n]) )
q <- rbind( q, v[n,] )
diag(q) <- round(diag(q))
q
}

frets.fun <- function( data, i )
{
  d <- data[i,]
  v <- pcorr( d )
  c(v[1,],v[2,],v[3,],v[4,])
}
frets.boot <- boot(log(as.matrix(frets)), frets.fun, R=999)
# we will concentrate on the partial correlation between head breadth
# for the first son and head length for the second. This is the 7th
# element in the output of frets.fun so we set index=7
jack.after.boot(frets.boot,useJ=FALSE,stinf=FALSE,index=7)

```

k3.linear

*Linear Skewness Estimate***Description**

Estimates the skewness of a statistic from its empirical influence values.

**Usage**

```
k3.linear(L, strata=NULL)
```

**Arguments**

L	Vector of the empirical influence values of a statistic. These will usually be calculated by a call to <code>empinf</code> .
strata	A numeric vector or factor specifying which observations (and hence which components of L) come from which strata.

**Value**

The skewness estimate calculated from L.

**References**

Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.



**See Also**

[empinf](#), [linear.approx](#), [var.linear](#)

**Examples**

```
# To estimate the skewness of the ratio of means for the city data.
ratio <- function(d,w)
  sum(d$x * w)/sum(d$u * w)
k3.linear(empinf(data=city, statistic=ratio))
```

---

linear.approx

*Linear Approximation of Bootstrap Replicates*

---

**Description**

This function takes a bootstrap object and for each bootstrap replicate it calculates the linear approximation to the statistic of interest for that bootstrap sample.

**Usage**

```
linear.approx(boot.out, L=NULL, index=1, type=NULL, t0=NULL,
             t=NULL, ...)
```

**Arguments**

<code>boot.out</code>	An object of class "boot" representing a nonparametric bootstrap. It will usually be created by the function <code>boot</code> .
<code>L</code>	A vector containing the empirical influence values for the statistic of interest. If it is not supplied then <code>L</code> is calculated through a call to <code>empinf</code> .
<code>index</code>	The index of the variable of interest within the output of <code>boot.out\$statistic</code> .
<code>type</code>	This gives the type of empirical influence values to be calculated. It is not used if <code>L</code> is supplied. The possible types of empirical influence values are described in the help for <code>empinf</code> .
<code>t0</code>	The observed value of the statistic of interest. The input value is used only if one of <code>t</code> or <code>L</code> is also supplied. The default value is <code>boot.out\$t0[index]</code> . If <code>t0</code> is supplied but neither <code>t</code> nor <code>L</code> are supplied then <code>t0</code> is set to <code>boot.out\$t0[index]</code> and a warning is generated.
<code>t</code>	A vector of bootstrap replicates of the statistic of interest. If <code>t0</code> is missing then <code>t</code> is not used, otherwise it is used to calculate the empirical influence values (if they are not supplied in <code>L</code> ).
<code>...</code>	Any extra arguments required by <code>boot.out\$statistic</code> . These are needed if <code>L</code> is not supplied as they are used by <code>empinf</code> to calculate empirical influence values.

**Details**

The linear approximation to a bootstrap replicate with frequency vector  $f$  is given by  $t_0 + \sum(L * f) / n$  in the one sample with an easy extension to the stratified case. The frequencies are found by calling `boot.array`.

**Value**

A vector of length `boot.out$R` with the linear approximations to the statistic of interest for each of the bootstrap samples.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

**See Also**

[boot](#), [empinf](#), [control](#)

**Examples**

```
# Using the city data let us look at the linear approximation to the
# ratio statistic and its logarithm. We compare these with the
# corresponding plots for the bigcity data

ratio <- function(d, w)
  sum(d$x * w)/sum(d$u * w)
city.boot <- boot(city, ratio, R=499, stype="w")
bigcity.boot <- boot(bigcity, ratio, R=499, stype="w")
par(pty="s")
par(mfrow=c(2,2))

# The first plot is for the city data ratio statistic.
city.lin1 <- linear.approx(city.boot)
lim <- range(c(city.boot$t,city.lin1))
plot(city.boot$t, city.lin1, xlim=lim,ylim=lim,
      main="Ratio; n=10", xlab="t*", ylab="tL*")
abline(0,1)

# Now for the log of the ratio statistic for the city data.
city.lin2 <- linear.approx(city.boot,t0=log(city.boot$t0),
                          t=log(city.boot$t))
lim <- range(c(log(city.boot$t),city.lin2))
plot(log(city.boot$t), city.lin2, xlim=lim, ylim=lim,
      main="Log(Ratio); n=10", xlab="t*", ylab="tL*")
abline(0,1)

# The ratio statistic for the bigcity data.
bigcity.lin1 <- linear.approx(bigcity.boot)
lim <- range(c(bigcity.boot$t,bigcity.lin1))
plot(bigcity.lin1,bigcity.boot$t, xlim=lim,ylim=lim,
      main="Ratio; n=49", xlab="t*", ylab="tL*")
abline(0,1)

# Finally the log of the ratio statistic for the bigcity data.
bigcity.lin2 <- linear.approx(bigcity.boot,t0=log(bigcity.boot$t0),
                             t=log(bigcity.boot$t))
lim <- range(c(log(bigcity.boot$t),bigcity.lin2))
plot(bigcity.lin2,log(bigcity.boot$t), xlim=lim,ylim=lim,
      main="Log(Ratio); n=49", xlab="t*", ylab="tL*")
abline(0,1)
```

```
par(mfrow=c(1,1))
```

---

```
lines.saddle.distn Add a Saddlepoint Approximation to a Plot
```

---

### Description

This function adds a line corresponding to a saddlepoint density or distribution function approximation to the current plot.

### Usage

```
## S3 method for class 'saddle.distn':
lines(x, dens = TRUE, h = function(u) u, J = function(u) 1,
      npts = 50, lty = 1, ...)
```

### Arguments

<code>x</code>	An object of class "saddle.distn" (see <a href="#">saddle.distn.object</a> representing a saddlepoint approximation to a distribution).
<code>dens</code>	A logical variable indicating whether the saddlepoint density (TRUE; the default) or the saddlepoint distribution function (FALSE) should be plotted.
<code>h</code>	Any transformation of the variable that is required. Its first argument must be the value at which the approximation is being performed and the function must be vectorized.
<code>J</code>	When <code>dens=TRUE</code> this function specifies the Jacobian for any transformation that may be necessary. The first argument of <code>J</code> must be the value at which the approximation is being performed and the function must be vectorized. If <code>h</code> is supplied <code>J</code> must also be supplied and both must have the same argument list.
<code>npts</code>	The number of points to be used for the plot. These points will be evenly spaced over the range of points used in finding the saddlepoint approximation.
<code>lty</code>	The line type to be used.
<code>...</code>	Any additional arguments to <code>h</code> and <code>J</code> .

### Details

The function uses `smooth.spline` to produce the saddlepoint curve. When `dens=TRUE` the spline is on the log scale and when `dens=FALSE` it is on the probit scale.

### Value

`sad.d` is returned invisibly.

### Side Effects

A line is added to the current plot.

### References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

**See Also**[saddle.distn](#)**Examples**

```

# In this example we show how a plot such as that in Figure 9.9 of
# Davison and Hinkley (1997) may be produced. Note the large number of
# bootstrap replicates required in this example.
expdata <- rexp(12)
vfun <- function(d, i)
{
  n <- length(d)
  (n-1)/n*var(d[i])
}
exp.boot <- boot(expdata,vfun, R = 9999)
exp.L <- (expdata-mean(expdata))^2 - exp.boot$t0
exp.tL <- linear.approx(exp.boot, L = exp.L)
hist(exp.tL, nclass = 50, prob = TRUE)
exp.t0 <- c(0, sqrt(var(exp.boot$t)))
exp.sp <- saddle.distn(A = exp.L/12, wdist = "m", t0 = exp.t0)

# The saddlepoint approximation in this case is to the density of
# t-t0 and so t0 must be added for the plot.
lines(exp.sp, h = function(u,t0) u+t0, J = function(u,t0) 1,
      t0 = exp.boot$t0)

```

logit

*Logit of Proportions***Description**

This function calculates the logit of proportions.

**Usage**

```
logit(p)
```

**Arguments**

**p** A numeric Splus object, all of whose values are in the range [0,1]. Missing values (NAs) are allowed.

**Details**

If any elements of **p** are outside the unit interval then an error message is generated. Values of **p** equal to 0 or 1 (to within machine precision) will return `-Inf` or `Inf` respectively. Any NAs in the input will also be NAs in the output.

**Value**

A numeric object of the same type as **p** containing the logits of the input values.

**See Also**[inv.logit](#)

---

 manaus

*Average Heights of the Rio Negro river at Manaus*


---

**Description**

The manaus time series is of class "ts" and has 1080 observations on one variable.

The data values are monthly averages of the daily stages (heights) of the Rio Negro at Manaus. Manaus is 18km upstream from the confluence of the Rio Negro with the Amazon but because of the tiny slope of the water surface and the lower courses of its flatland affluents, they may be regarded as a good approximation of the water level in the Amazon at the confluence. The data here cover 90 years from January 1903 until December 1992.

The Manaus gauge is tied in with an arbitrary bench mark of 100m set in the steps of the Municipal Prefecture; gauge readings are usually referred to sea level, on the basis of a mark on the steps leading to the Parish Church (Matriz), which is assumed to lie at an altitude of 35.874 m according to observations made many years ago under the direction of Samuel Pereira, an engineer in charge of the Manaus Sanitation Committee Whereas such an altitude cannot, by any means, be considered to be a precise datum point, observations have been provisionally referred to it. The measurements are in metres.

**Source**

The data were kindly made available by Professors H. O'Reilly Sternberg and D. R. Brillinger of the University of California at Berkeley.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Sternberg, H. O'R. (1987) Aggravation of floods in the Amazon river as a consequence of deforestation? *Geografiska Annaler*, **69A**, 201-219.

Sternberg, H. O'R. (1995) Waters and wetlands of Brazilian Amazonia: An uncertain future. In *The Fragile Tropics of Latin America: Sustainable Management of Changing Environments*, Nishizawa, T. and Uitto, J.I. (editors), United Nations University Press, 113-179.

---

 melanoma

*Survival from Malignant Melanoma*


---

**Description**

The melanoma data frame has 205 rows and 7 columns.

The data consist of measurements made on patients with malignant melanoma. Each patient had their tumour removed by surgery at the Department of Plastic Surgery, University Hospital of Odense, Denmark during the period 1962 to 1977. The surgery consisted of complete removal of the tumour together with about 2.5cm of the surrounding skin. Among the measurements taken were the thickness of the tumour and whether it was ulcerated or not. These are thought to be important prognostic variables in that patients with a thick and/or ulcerated tumour have an increased chance of death from melanoma. Patients were followed until the end of 1977.

**Usage**

melanoma

**Format**

This data frame contains the following columns:

`time` Survival time in days since the operation, possibly censored.

`status` The patients status at the end of the study. 1 indicates that they had died from melanoma, 2 indicates that they were still alive and 3 indicates that they had died from causes unrelated to their melanoma.

`sex` The patients sex; 1=male, 0=female.

`age` Age in years at the time of the operation.

`year` Year of operation.

`thickness` Tumour thickness in mm.

`ulcer` Indicator of ulceration; 1=present, 0=absent.

**Note**

This dataset is not related to the dataset in the **lattice** package with the same name.

**Source**

The data were obtained from

Andersen, P.K., Borgan, O., Gill, R.D. and Keiding, N. (1993) *Statistical Models Based on Counting Processes*. Springer-Verlag.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Venables, W.N. and Ripley, B.D. (1994) *Modern Applied Statistics with S-Plus*. Springer-Verlag.

---

motor

*Data from a Simulated Motorcycle Accident*

---

**Description**

The `motor` data frame has 94 rows and 4 columns. The rows are obtained by removing replicate values of `time` from the dataset `mcycle`. Two extra columns are added to allow for strata with a different residual variance in each stratum.

**Usage**

`motor`

**Format**

This data frame contains the following columns:

`times` The time in milliseconds since impact.

`accel` The recorded head acceleration (in g).

`strata` A numeric column indicating to which of the three strata (numbered 1, 2 and 3) the observations belong.

`v` An estimate of the residual variance for the observation. `v` is constant within the strata but a different estimate is used for each of the three strata.

**Source**

The data were obtained from

Silverman, B.W. (1985) Some aspects of the spline smoothing approach to non-parametric curve fitting. *Journal of the Royal Statistical Society, B*, **47**, 1–52.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Venables, W.N. and Ripley, B.D. (1994) *Modern Applied Statistics with S-Plus*. Springer-Verlag.

**See Also**

[mcycle](#)

---

neuro

*Neurophysiological Point Process Data*

---

**Description**

`neuro` is a matrix containing times of observed firing of a neuron in windows of 250ms either side of the application of a stimulus to a human subject. Each row of the matrix is a replication of the experiment and there were a total of 469 replicates.

**Note**

There are a lot of missing values in the matrix as different numbers of firings were observed in different replicates. The number of firings observed varied from 2 to 6.

**Source**

The data were collected and kindly made available by Dr. S.J. Boniface of the Neurophysiology Unit at the Radcliffe Infirmary, Oxford.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Ventura, V., Davison, A.C. and Boniface, S.J. (1997) A stochastic model for the effect of magnetic brain stimulation on a motoneurone. To appear in *Applied Statistics*.

---

`nitrofen`*Toxicity of Nitrofen in Aquatic Systems*

---

### Description

The `nitrofen` data frame has 50 rows and 5 columns.

Nitrofen is a herbicide that was used extensively for the control of broad-leaved and grass weeds in cereals and rice. Although it is relatively non-toxic to adult mammals, nitrofen is a significant tetragen and mutagen. It is also acutely toxic and reproductively toxic to cladoceran zooplankton. Nitrofen is no longer in commercial use in the U.S., having been the first pesticide to be withdrawn due to tetragenic effects.

The data here come from an experiment to measure the reproductive toxicity of nitrofen on a species of zooplankton (*Ceriodaphnia dubia*). 50 animals were randomized into batches of 10 and each batch was put in a solution with a measured concentration of nitrofen. Then the number of live offspring in each of the three broods to each animal was recorded.

### Usage

```
nitrofen
```

### Format

This data frame contains the following columns:

`conc` The nitrofen concentration in the solution (mug/litre).

`brood1` The number of live offspring in the first brood.

`brood2` The number of live offspring in the second brood.

`brood3` The number of live offspring in the third brood.

`total` The total number of live offspring in the first three broods.

### Source

The data were obtained from

Bailer, A.J. and Oris, J.T. (1994) Assessing toxicity of pollutants in aquatic systems. In *Case Studies in Biometry*. N. Lange, L. Ryan, L. Billard, D. Brillinger, L. Conquest and J. Greenhouse (editors), 25–40. John Wiley.

### References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.



---

`nodal`*Nodal Involvement in Prostate Cancer*

---

**Description**

The `nodal` data frame has 53 rows and 7 columns.

The treatment strategy for a patient diagnosed with cancer of the prostate depend highly on whether the cancer has spread to the surrounding lymph nodes. It is common to operate on the patient to get samples from the nodes which can then be analysed under a microscope but clearly it would be preferable if an accurate assessment of nodal involvement could be made without surgery.

For a sample of 53 prostate cancer patients, a number of possible predictor variables were measured before surgery. The patients then had surgery to determine nodal involvement. It was required to see if nodal involvement could be accurately predicted from the predictor variables and which ones were most important.

**Usage**

```
nodal
```

**Format**

This data frame contains the following columns:

`m` A column of ones.

`r` An indicator of nodal involvement.

`aged` The patients age dichotomized into less than 60 (0) and 60 or over 1.

`stage` A measurement of the size and position of the tumour observed by palpitation with the fingers via the rectum. A value of 1 indicates a more serious case of the cancer.

`grade` Another indicator of the seriousness of the cancer, this one is determined by a pathology reading of a biopsy taken by needle before surgery. A value of 1 indicates a more serious case of the cancer.

`xray` A third measure of the seriousness of the cancer taken from an X-ray reading. A value of 1 indicates a more serious case of the cancer.

`acid` The level of acid phosphatase in the blood serum.

**Source**

The data were obtained from

Brown, B.W. (1980) Prediction analysis for binary data. In *Biostatistics Casebook*. R.G. Miller, B. Efron, B.W. Brown and L.E. Moses (editors), 3–18. John Wiley.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

norm.ci

*Normal Approximation Confidence Intervals***Description**

Using the normal approximation to a statistic, calculate equi-tailed two-sided confidence intervals.

**Usage**

```
norm.ci(boot.out=NULL, conf=0.95, index=1, var.t0=NULL,
        t0=NULL, t=NULL, L=NULL, h=function(t) t,
        hdot=function(t) 1, hinv=function(t) t)
```

**Arguments**

<code>boot.out</code>	A bootstrap output object returned from a call to <code>boot</code> . If <code>t0</code> is missing then <code>boot.out</code> is a required argument. It is also required if both <code>var.t0</code> and <code>t</code> are missing.
<code>conf</code>	A scalar or vector containing the confidence level(s) of the required interval(s).
<code>index</code>	The index of the statistic of interest within the output of a call to <code>boot.out\$statistic</code> . It is not used if <code>boot.out</code> is missing, in which case <code>t0</code> must be supplied.
<code>var.t0</code>	The variance of the statistic of interest. If it is not supplied then <code>var(t)</code> is used.
<code>t0</code>	The observed value of the statistic of interest. If it is missing then it is taken from <code>boot.out</code> which is required in that case.
<code>t</code>	Bootstrap replicates of the variable of interest. These are used to estimate the variance of the statistic of interest if <code>var.t0</code> is not supplied. The default value is <code>boot.out\$t[, index]</code> .
<code>L</code>	The empirical influence values for the statistic of interest. These are used to calculate <code>var.t0</code> if neither <code>var.t0</code> nor <code>boot.out</code> are supplied. If a transformation is supplied through <code>h</code> then the influence values must be for the untransformed statistic <code>t0</code> .
<code>h</code>	A function defining a monotonic transformation, the intervals are calculated on the scale of <code>h(t)</code> and the inverse function <code>hinv</code> is applied to the resulting intervals. <code>h</code> must be a function of one variable only and must be vectorized. The default is the identity function.
<code>hdot</code>	A function of one argument returning the derivative of <code>h</code> . It is a required argument if <code>h</code> is supplied and is used for approximating the variance of <code>h(t0)</code> . The default is the constant function 1.
<code>hinv</code>	A function, like <code>h</code> , which returns the inverse of <code>h</code> . It is used to transform the intervals calculated on the scale of <code>h(t)</code> back to the original scale. The default is the identity function. If <code>h</code> is supplied but <code>hinv</code> is not, then the intervals returned will be on the transformed scale.

**Details**

It is assumed that the statistic of interest has an approximately normal distribution with variance `var.t0` and so a confidence interval of length  $2 * qnorm((1+conf)/2) * sqrt(var.t0)$  is found. If `boot.out` or `t` are supplied then the interval is bias-corrected using the bootstrap bias estimate, and so the interval would be centred at  $2 * t0 - mean(t)$ . Otherwise the interval is centred at `t0`.

**Value**

If `length(conf)` is 1 then a vector containing the confidence level and the endpoints of the interval is returned. Otherwise, the returned value is a matrix where each row corresponds to a different confidence level.

**Note**

This function is primarily designed to be called by `boot.ci` to calculate the normal approximation after a bootstrap but it can also be used without doing any bootstrap calculations as long as `t0` and `var.t0` can be supplied. See the examples below.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

**See Also**

[boot.ci](#)

**Examples**

```
# In Example 5.1 of Davison and Hinkley (1997), normal approximation
# confidence intervals are found for the air-conditioning data.
air.mean <- mean(aircondit$hours)
air.n <- nrow(aircondit)
air.v <- air.mean^2/air.n
norm.ci(t0=air.mean, var.t0=air.v)
exp(norm.ci(t0=log(air.mean), var.t0=1/air.n)[2:3])

# Now a more complicated example - the ratio estimate for the city data.
ratio <- function(d, w)
  sum(d$x * w)/sum(d$u * w)
city.v <- var.linear(empinf(data=city, statistic=ratio))
norm.ci(t0=ratio(city,rep(0.1,10)), var.t0=city.v)
```

**Description**

The `nuclear` data frame has 32 rows and 11 columns.

The data relate to the construction of 32 light water reactor (LWR) plants constructed in the U.S.A in the late 1960's and early 1970's. The data was collected with the aim of predicting the cost of construction of further LWR plants. 6 of the power plants had partial turnkey guarantees and it is possible that, for these plants, some manufacturers' subsidies may be hidden in the quoted capital costs.

**Usage**

```
nuclear
```

**Format**

This data frame contains the following columns:

`cost` The capital cost of construction in millions of dollars adjusted to 1976 base.

`date` The date on which the construction permit was issued. The data are measured in years since January 1 1990 to the nearest month.

`t1` The time between application for and issue of the construction permit.

`t2` The time between issue of operating license and construction permit.

`cap` The net capacity of the power plant (MWe).

`pr` A binary variable where 1 indicates the prior existence of a LWR plant at the same site.

`ne` A binary variable where 1 indicates that the plant was constructed in the north-east region of the U.S.A.

`ct` A binary variable where 1 indicates the use of a cooling tower in the plant.

`bw` A binary variable where 1 indicates that the nuclear steam supply system was manufactured by Babcock-Wilcox.

`cum.n` The cumulative number of power plants constructed by each architect-engineer.

`pt` A binary variable where 1 indicates those plants with partial turnkey guarantees.

**Source**

The data were obtained from

Cox, D.R. and Snell, E.J. (1981) *Applied Statistics: Principles and Examples*. Chapman and Hall.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

paulsen

*Neurotransmission in Guinea Pig Brains*

---

### Description

The `paulsen` data frame has 346 rows and 1 columns.

Sections were prepared from the brain of adult guinea pigs. Spontaneous currents that flowed into individual brain cells were then recorded and the peak amplitude of each current measured. The aim of the experiment was to see if the current flow was quantal in nature (i.e. that it is not a single burst but instead is built up of many smaller bursts of current). If the current was indeed quantal then it would be expected that the distribution of the current amplitude would be multimodal with modes at regular intervals. The modes would be expected to decrease in magnitude for higher current amplitudes.

### Usage

```
paulsen
```

### Format

This data frame contains the following column:

`y` The current flowing into individual brain cells. The currents are measured in pico-amperes.

### Source

The data were kindly made available by Dr. O. Paulsen from the Department of Pharmacology at the University of Oxford.

Paulsen, O. and Heggelund, P. (1994) The quantal size at retinogeniculate synapses determined from spontaneous and evoked EPSCs in guinea-pig thalamic slices. *Journal of Physiology*, **480**, 505–511.

### References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

plot.boot

*Plots of the Output of a Bootstrap Simulation*

---

### Description

This takes a bootstrap object and produces plots for the bootstrap replicates of the variable of interest.

### Usage

```
## S3 method for class 'boot':
plot(x, index=1, t0=NULL, t=NULL, jack=FALSE, qdist="norm",
     nclass=NULL, df, ...)
```

**Arguments**

x	An object of class "boot" returned from one of the bootstrap generation functions.
index	The index of the variable of interest within the output of <code>boot.out</code> . This is ignored if <code>t</code> and <code>t0</code> are supplied.
t0	The original value of the statistic. This defaults to <code>boot.out\$t0[index]</code> unless <code>t</code> is supplied when it defaults to <code>NULL</code> . In that case no vertical line is drawn on the histogram.
t	The bootstrap replicates of the statistic. Usually this will take on its default value of <code>boot.out\$t[,index]</code> , however it may be useful sometimes to supply a different set of values which are a function of <code>boot.out\$t</code> .
jack	A logical value indicating whether a jackknife-after-bootstrap plot is required. The default is not to produce such a plot.
qdist	The distribution against which the Q-Q plot should be drawn. At present "norm" (normal distribution - the default) and "chisq" (chi-squared distribution) are the only possible values.
nclass	An integer giving the number of classes to be used in the bootstrap histogram. The default is the integer between 10 and 100 closest to <code>ceiling(length(t)/25)</code> .
df	If <code>qdist</code> is "chisq" then this is the degrees of freedom for the chi-squared distribution to be used. It is a required argument in that case.
...	When <code>jack</code> is <code>TRUE</code> additional parameters to <code>jack.after.boot</code> can be supplied. See the help file for <code>jack.after.boot</code> for details of the possible parameters.

**Details**

This function will generally produce two side-by-side plots. The left plot will be a histogram of the bootstrap replicates. Usually the breaks of the histogram will be chosen so that `t0` is at a breakpoint and all intervals are of equal length. A vertical dotted line indicates the position of `t0`. This cannot be done if `t` is supplied but `t0` is not and so, in that case, the breakpoints are computed by `hist` using the `nclass` argument and no vertical line is drawn.

The second plot is a Q-Q plot of the bootstrap replicates. The order statistics of the replicates can be plotted against normal or chi-squared quantiles. In either case the expected line is also plotted. For the normal, this will have intercept `mean(t)` and slope `sqrt(var(t))` while for the chi-squared it has intercept 0 and slope 1.

If `jack` is `TRUE` a third plot is produced beneath these two. That plot is the jackknife-after-bootstrap plot. This plot may only be requested when nonparametric simulation has been used. See `jack.after.boot` for further details of this plot.

**Value**

`boot.out` is returned invisibly.

**Side Effects**

All screens are closed and cleared and a number of plots are produced on the current graphics device. Screens are closed but not cleared at termination of this function.

**See Also**

`boot`, `jack.after.boot`, `print.boot`

**Examples**

```
# We fit an exponential model to the air-conditioning data and use
# that for a parametric bootstrap. Then we look at plots of the
# resampled means.
air.rg <- function(data, mle)
  rexp(length(data), 1/mle)

air.boot <- boot(aircondit$hours, mean, R=999, sim="parametric",
  ran.gen=air.rg, mle=mean(aircondit$hours))
plot(air.boot)

# In the difference of means example for the last two series of the
# gravity data
grav1 <- gravity[as.numeric(gravity[,2])>=7,]
grav.fun <- function(dat, w)
{
  strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
  d <- dat[, 1]
  ns <- tabulate(strata)
  w <- w/tapply(w, strata, sum)[strata]
  mns <- tapply(d * w, strata, sum)
  mn2 <- tapply(d * d * w, strata, sum)
  s2hat <- sum((mn2 - mns^2)/ns)
  c(mns[2]-mns[1], s2hat)
}

grav.boot <- boot(grav1, grav.fun, R=499, stype="w", strata=grav1[,2])
plot(grav.boot)
# now suppose we want to look at the studentized differences.
grav.z <- (grav.boot$t[,1]-grav.boot$t0[1])/sqrt(grav.boot$t[,2])
plot(grav.boot, t=grav.z, t0=0)

# In this example we look at the one of the partial correlations for the
# head dimensions in the dataset frets.
pcorr <- function( x )
{
  # Function to find the correlations and partial correlations between
  # the four measurements.
  v <- cor(x);
  v.d <- diag(var(x));
  iv <- solve(v);
  iv.d <- sqrt(diag(iv));
  iv <- - diag(1/iv.d) %*% iv %*% diag(1/iv.d);
  q <- NULL;
  n <- nrow(v);
  for (i in 1:(n-1))
    q <- rbind( q, c(v[i,1:i], iv[i, (i+1):n]) );
  q <- rbind( q, v[n,] );
  diag(q) <- round(diag(q));
  q
}
```

```
frets.fun <- function( data, i )
{   d <- data[i,];
    v <- pcorr( d );
    c(v[1,],v[2,],v[3,],v[4,])
}
frets.boot <- boot(log(as.matrix(frets)), frets.fun, R=999)
plot(frets.boot, index=7, jack=TRUE, stinf=FALSE, useJ=FALSE)
```

---

poisons

*Animal Survival Times*

---

### Description

The `poisons` data frame has 48 rows and 3 columns.

The data form a 3x4 factorial experiment, the factors being three poisons and four treatments. Each combination of the two factors was used for four animals, the allocation to animals having been completely randomized.

### Usage

```
poisons
```

### Format

This data frame contains the following columns:

`time` The survival time of the animal in units of 10 hours.

`poison` A factor with levels 1, 2 and 3 giving the type of poison used.

`treat` A factor with levels A, B, C and D giving the treatment.

### Source

The data were obtained from

Box, G.E.P. and Cox, D.R. (1964) An analysis of transformations (with Discussion). *Journal of the Royal Statistical Society, B*, **26**, 211–252.

### References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.



polar

*Pole Positions of New Caledonian Laterites*

---

**Description**

The `polar` data frame has 50 rows and 2 columns.

The data are the pole positions from a paleomagnetic study of New Caledonian laterites.

**Usage**

```
polar
```

**Format**

This data frame contains the following columns:

`lat` The latitude (in degrees) of the pole position. Note that all latitudes are negative as the axis is taken to be in the lower hemisphere.

`long` The longitude (in degrees) of the pole position.

**Source**

The data were obtained from

Fisher, N.I., Lewis, T. and Embleton, B.J.J. (1987) *Statistical Analysis of Spherical Data*. Cambridge University Press.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

print.boot*Print a Summary of a Bootstrap Object*

---

**Description**

This is a method for the function `print` for objects of the class `"boot"`.

**Usage**

```
## S3 method for class 'boot':
print(x, digits = getOption("digits"),
      index = 1:ncol(boot.out$t), ...)
```

**Arguments**

<code>x</code>	A bootstrap output object of class "boot" generated by one of the bootstrap functions.
<code>digits</code>	The number of digits to be printed in the summary statistics.
<code>index</code>	Indices indicating for which elements of the bootstrap output summary statistics are required.
<code>...</code>	further arguments passed to or from other methods.

**Details**

For each statistic calculated in the bootstrap the original value and the bootstrap estimates of its bias and standard error are printed. If `boot.out$to` is missing (such as when it was created by a call to `tsboot` with `orig.t=FALSE`) the bootstrap mean and standard error are printed. If resampling was done using importance resampling weights, then the bootstrap estimates are reweighted as if uniform resampling had been done. The ratio importance sampling estimates are used and if there were a number of distributions then defensive mixture distributions are used. In this case an extra column with the mean of the observed bootstrap statistics is also printed.

**Value**

The bootstrap object is returned invisibly.

**See Also**

[boot](#), [censboot](#), [imp.moments](#), [plot.boot](#), [tilt.boot](#), [tsboot](#)

---

```
print.bootci
```

*Print Bootstrap Confidence Intervals*

---

**Description**

This is a method for the function `print()` to print objects of the class "bootci".

**Usage**

```
## S3 method for class 'bootci':
print(x, hinv = NULL, ...)
```

**Arguments**

<code>x</code>	The output from a call to <code>boot.ci</code> .
<code>hinv</code>	A transformation to be made to the interval end-points before they are printed.
<code>...</code>	further arguments passed to or from other methods.

**Details**

This function prints out the results from `boot.ci` in a "nice" format. It also notes whether the scale of the intervals is the original scale of the input to `boot.ci` or a different scale and whether the calculations were done on a transformed scale. It also looks at the order statistics that were used in calculating the intervals. If the smallest or largest values were used then it prints a message

```
Warning : Intervals used Extreme Quantiles
```

Such intervals should be considered very unstable and not relied upon for inferences. Even if the extreme values are not used, it is possible that the intervals are unstable if they used quantiles close to the extreme values. The function alerts the user to intervals which use the upper or lower 10 order statistics with the message

```
Some intervals may be unstable
```

**Value**

The object `ci.out` is returned invisibly.

**See Also**

[boot.ci](#)

---

`print.saddle.distn` *Print Quantiles of Saddlepoint Approximations*

---

**Description**

This is a method for the function `print()` to print objects of class `"saddle.distn"`.

**Usage**

```
## S3 method for class 'saddle.distn':  
print(x, ...)
```

**Arguments**

<code>x</code>	An object of class <code>"saddle.distn"</code> created by a call to <code>saddle.distn</code> .
<code>...</code>	further arguments passed to or from other methods.

**Details**

The quantiles of the saddlepoint approximation to the distribution are printed along with the original call and some other useful information.

**Value**

The input is returned invisibly.

**See Also**

[lines.saddle.distn](#), [saddle.distn](#)

---

print.simplex      *Print Solution to Linear Programming Problem*

---

### Description

This is a method for the function `print()` to print objects of class "simplex".

### Usage

```
## S3 method for class 'simplex':  
print(x, ...)
```

### Arguments

`x`                    An object of class "simplex" created by calling the function `simplex` to solve a linear programming problem.

`...`                further arguments passed to or from other methods.

### Details

The coefficients of the objective function are printed. If a solution to the linear programming problem was found then the solution and the optimal value of the objective function are printed. If a feasible solution was found but the maximum number of iterations was exceeded then the last feasible solution and the objective function value at that point are printed. If no feasible solution could be found then a message stating that is printed.

### Value

`x` is returned silently.

### See Also

[simplex](#)

---

remission                    *Cancer Remission and Cell Activity*

---

### Description

The `remission` data frame has 27 rows and 3 columns.

### Usage

```
remission
```

**Format**

This data frame contains the following columns:

- LI A measure of cell activity.
- m The number of patients in each group (all values are actually 1 here).
- r The number of patients (out of m) who went into remission.

**Source**

The data were obtained from

Freeman, D.H. (1987) *Applied Categorical Data Analysis*. Marcel Dekker.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

saddle

*Saddlepoint Approximations for Bootstrap Statistics*

---

**Description**

This function calculates a saddlepoint approximation to the distribution of a linear combination of  $\mathbf{W}$  at a particular point  $u$ , where  $\mathbf{W}$  is a vector of random variables. The distribution of  $\mathbf{W}$  may be multinomial (default), Poisson or binary. Other distributions are possible also if the adjusted cumulant generating function and its second derivative are given. Conditional saddlepoint approximations to the distribution of one linear combination given the values of other linear combinations of  $\mathbf{W}$  can be calculated for  $\mathbf{W}$  having binary or Poisson distributions.

**Usage**

```
saddle(A=NULL, u=NULL, wdist="m", type="simp", d=NULL, dl=1,
       init=rep(0.1, d), mu=rep(0.5, n), LR=FALSE, strata=NULL,
       K.adj=NULL, K2=NULL)
```

**Arguments**

- |       |   |
|-------|---|
| A     | A vector or matrix of known coefficients of the linear combinations of $\mathbf{W}$ . It is a required argument unless <code>K.adj</code> and <code>K2</code> are supplied, in which case it is ignored.  |
| u     | The value at which it is desired to calculate the saddlepoint approximation to the distribution of the linear combination of $\mathbf{W}$ . It is a required argument unless <code>K.adj</code> and <code>K2</code> are supplied, in which case it is ignored.  |
| wdist | The distribution of $\mathbf{W}$ . This can be one of "m" (multinomial), "p" (Poisson), "b" (binary) or "o" (other). If <code>K.adj</code> and <code>K2</code> are given <code>wdist</code> is set to "o".  |
| type  | The type of saddlepoint approximation. Possible types are "simp" for simple saddlepoint and "cond" for the conditional saddlepoint. When <code>wdist</code> is "o" or "m", <code>type</code> is automatically set to "simp", which is the only type of saddlepoint currently implemented for those distributions. |

d	This specifies the dimension of the whole statistic. This argument is required only when <code>wdist="o"</code> and defaults to 1 if not supplied in that case. For other distributions it is set to <code>ncol(A)</code> .
d1	When <code>type</code> is "cond" this is the dimension of the statistic of interest which must be less than <code>length(u)</code> . Then the saddlepoint approximation to the conditional distribution of the first <code>d1</code> linear combinations given the values of the remaining combinations is found. Conditional distribution function approximations can only be found if the value of <code>d1</code> is 1.
init	Used if <code>wdist</code> is either "m" or "o", this gives initial values to <code>nlmin</code> which is used to solve the saddlepoint equation.
mu	The values of the parameters of the distribution of <b>W</b> when <code>wdist</code> is "m", "p" or "b". <code>mu</code> must be of the same length as <b>W</b> (i.e. <code>nrow(A)</code> ). The default is that all values of <code>mu</code> are equal and so the elements of <b>W</b> are identically distributed.
LR	If TRUE then the Lugananni-Rice approximation to the cdf is used, otherwise the approximation used is based on Barndorff-Nielsen's $r^*$ .
strata	The strata for stratified data.
K.adj	The adjusted cumulant generating function used when <code>wdist</code> is "o". This is a function of a single parameter, <code>zeta</code> , which calculates $K(zeta) - u \cdot zeta$ , where $K(zeta)$ is the cumulant generating function of <b>W</b> .
K2	This is a function of a single parameter <code>zeta</code> which returns the matrix of second derivatives of $K(zeta)$ for use when <code>wdist</code> is "o". If <code>K.adj</code> is given then this must be given also. It is called only once with the calculated solution to the saddlepoint equation being passed as the argument. This argument is ignored if <code>K.adj</code> is not supplied.

### Details

If `wdist` is "o" or "m", the saddlepoint equations are solved using `nlmin` to minimize `K.adj` with respect to its parameter `zeta`. For the Poisson and binary cases, a generalized linear model is fitted such that the parameter estimates solve the saddlepoint equations. The response variable 'y' for the `glm` must satisfy the equation  $t(A) \cdot y = u(t())$  ( $t()$  being the transpose function). Such a vector can be found as a feasible solution to a linear programming problem. This is done by a call to `simplex`. The covariate matrix for the `glm` is given by `A`.

### Value

A list consisting of the following components

<code>spa</code>	The saddlepoint approximations. The first value is the density approximation and the second value is the distribution function approximation.
<code>zeta.hat</code>	The solution to the saddlepoint equation. For the conditional saddlepoint this is the solution to the saddlepoint equation for the numerator.
<code>zeta2.hat</code>	If <code>type</code> is "cond" this is the solution to the saddlepoint equation for the denominator. This component is not returned for any other value of <code>type</code> .

### References

Booth, J.G. and Butler, R.W. (1990) Randomization distributions and saddlepoint approximations in generalized linear models. *Biometrika*, **77**, 787–796.

Canty, A.J. and Davison, A.C. (1997) Implementation of saddlepoint approximations to resampling distributions. *Computing Science and Statistics; Proceedings of the 28th Symposium on the Interface*, 248–253.

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and their Application*. Cambridge University Press.

Jensen, J.L. (1995) *Saddlepoint Approximations*. Oxford University Press.

### See Also

[saddle.distn](#), [simplex](#)

### Examples

```
# To evaluate the bootstrap distribution of the mean failure time of
# air-conditioning equipment at 80 hours
saddle(A=aircondit$hours/12, u=80)

# Alternatively this can be done using a conditional poisson
saddle(A=cbind(aircondit$hours/12,1), u=c(80,12), wdist="p", type="cond")

# To use the Lugananni-Rice approximation to this
saddle(A=cbind(aircondit$hours/12,1), u=c(80,12), wdist="p", type="cond",
       LR = TRUE)

# Example 9.16 of Davison and Hinkley (1997) calculates saddlepoint
# approximations to the distribution of the ratio statistic for the
# city data. Since the statistic is not in itself a linear combination
# of random Variables, its distribution cannot be found directly.
# Instead the statistic is expressed as the solution to a linear
# estimating equation and hence its distribution can be found. We
# get the saddlepoint approximation to the pdf and cdf evaluated at
# t=1.25 as follows.
jacobian <- function(dat,t,zeta)
{
  p <- exp(zeta*(dat$x-t*dat$u))
  abs(sum(dat$u*p)/sum(p))
}
city.sp1 <- saddle(A=city$x-1.25*city$u, u=0)
city.sp1$spa[1] <- jacobian(city, 1.25, city.sp1$zeta.hat) * city.sp1$spa[1]
city.sp1
```

---

saddle.distn

*Saddlepoint Distribution Approximations for Bootstrap Statistics*

---

### Description

Approximate an entire distribution using saddlepoint methods. This function can calculate simple and conditional saddlepoint distribution approximations for a univariate quantity of interest. For the simple saddlepoint the quantity of interest is a linear combination of  $\mathbf{W}$  where  $\mathbf{W}$  is a vector of random variables. For the conditional saddlepoint we require the distribution of one linear combination given the values of any number of other linear combinations. The distribution of  $\mathbf{W}$  must be one of multinomial, Poisson or binary. The primary use of this function is to calculate quantiles of bootstrap distributions using saddlepoint approximations. Such quantiles are required by the function `control` to approximate the distribution of the linear approximation to a statistic.

**Usage**

```
saddle.distn(A, u=NULL, alpha=NULL, wdist="m",
             type="simp", npts=20, t=NULL, t0=NULL,
             init=rep(0.1, d), mu=rep(0.5, n), LR=FALSE,
             strata=NULL, ...)
```

**Arguments**

A	This is a matrix of known coefficients or a function which returns such a matrix. If a function then its first argument must be the point $t$ at which a saddlepoint is required. The most common reason for A being a function would be if the statistic is not itself a linear combination of the $\mathbf{W}$ but is the solution to a linear estimating equation.
u	If A is a function then u must also be a function returning a vector with length equal to the number of columns of the matrix returned by A. Usually all components other than the first will be constants as the other components are the values of the conditioning variables. If A is a matrix with more than one column (such as when <code>wdist="cond"</code> ) then u should be a vector with length one less than <code>ncol(A)</code> . In this case u specifies the values of the conditioning variables. If A is a matrix with one column or a vector then u is not used.
alpha	The alpha levels for the quantiles of the distribution which should be returned. By default the 0.1, 0.5, 1, 2.5, 5, 10, 20, 50, 80, 90, 95, 97.5, 99, 99.5 and 99.9 percentiles are calculated.
wdist	The distribution of $\mathbf{W}$ . Possible values are "m" (multinomial), "p" (Poisson), or "b" (binary).
type	The type of saddlepoint to be used. Possible values are "simp" (simple saddlepoint) and "cond" (conditional). If <code>wdist</code> is "m", <code>type</code> is set to "simp".
npts	The number of points at which the saddlepoint approximation should be calculated and then used to fit the spline.
t	A vector of points at which the saddlepoint approximations are calculated. These points should extend beyond the extreme quantiles required but still be in the possible range of the bootstrap distribution. The observed value of the statistic should not be included in $t$ as the distribution function approximation breaks down at that point. The points should, however cover the entire effective range of the distribution including close to the centre. If $t$ is supplied then <code>npts</code> is set to <code>length(t)</code> . When $t$ is not supplied, the function attempts to find the effective range of the distribution and then selects points to cover this range.
t0	If $t$ is not supplied then a vector of length 2 should be passed as <code>t0</code> . The first component of <code>t0</code> should be the centre of the distribution and the second should be an estimate of spread (such as a standard error). These two are then used to find the effective range of the distribution. The range finding mechanism does rely on an accurate estimate of location in <code>t0[1]</code> .
init	When <code>wdist</code> is "m", this vector should contain the initial values to be passed to <code>n1min</code> when it is called to solve the saddlepoint equations.
mu	The vector of parameter values for the distribution. The default is that the components of $\mathbf{W}$ are identically distributed.
LR	A logical flag. When <code>LR</code> is <code>TRUE</code> the Lugananni-Rice cdf approximations are calculated and used to fit the spline. Otherwise the cdf approximations used are based on Barndorff-Nielsen's $r^*$ .



strata	A vector giving the strata when the rows of A relate to stratified data. This is used only when wdist is "m".
...	When A and u are functions any additional arguments are passed unchanged each time one of them is called.

## Details

The range at which the saddlepoint is used is such that the cdf approximation at the endpoints is more extreme than required by the extreme values of `alpha`. The lower endpoint is found by evaluating the saddlepoint at the points `t0[1]-2*t0[2]`, `t0[1]-4*t0[2]`, `t0[1]-8*t0[2]` etc. until a point is found with a cdf approximation less than  $\min(\alpha)/10$ , then a bisection method is used to find the endpoint which has cdf approximation in the range  $(\min(\alpha)/1000, \min(\alpha)/10)$ . Then a number of, equally spaced, points are chosen between the lower endpoint and `t0[1]` until a total of `npts/2` approximations have been made. The remaining `npts/2` points are chosen to the right of `t0[1]` in a similar manner. Any points which are very close to the centre of the distribution are then omitted as the cdf approximations are not reliable at the centre. A smoothing spline is then fitted to the probit of the saddlepoint distribution function approximations at the remaining points and the required quantiles are predicted from the spline.

Sometimes the function will terminate with the message "Unable to find range". There are two main reasons why this may occur. One is that the distribution is too discrete and/or the required quantiles too extreme, this can cause the function to be unable to find a point within the allowable range which is beyond the extreme quantiles. Another possibility is that the value of `t0[2]` is too small and so too many steps are required to find the range. The first problem cannot be solved except by asking for less extreme quantiles, although for very discrete distributions the approximations may not be very good. In the second case using a larger value of `t0[2]` will usually solve the problem.

## Value

The returned value is an object of class "saddle.distn". See the help file for [saddle.distn.object](#) for a description of such an object.

## References

- Booth, J.G. and Butler, R.W. (1990) Randomization distributions and saddlepoint approximations in generalized linear models. *Biometrika*, **77**, 787–796.
- Canty, A.J. and Davison, A.C. (1997) Implementation of saddlepoint approximations to resampling distributions. *Computing Science and Statistics; Proceedings of the 28th Symposium on the Interface* 248–253.
- Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and their Application*. Cambridge University Press.
- Jensen, J.L. (1995) *Saddlepoint Approximations*. Oxford University Press.

## See Also

[lines.saddle.distn](#), [saddle](#), [saddle.distn.object](#), [smooth.spline](#)

## Examples

```
# The bootstrap distribution of the mean of the air-conditioning
# failure data: fails to find value on R (and probably on S too)
```

```

air.t0 <- c(mean(aircondit$hours), sqrt(var(aircondit$hours)/12))
## Not run: saddle.distn(A = aircondit$hours/12, t0 = air.t0)

# alternatively using the conditional poisson
saddle.distn(A = cbind(aircondit$hours/12, 1), u = 12, wdistr = "p",
             type = "cond", t0 = air.t0)

# Distribution of the ratio of a sample of size 10 from the bigcity
# data, taken from Example 9.16 of Davison and Hinkley (1997).
ratio <- function(d, w) sum(d$x * w) / sum(d$u * w)
city.v <- var.linear(empinf(data = city, statistic = ratio))
bigcity.t0 <- c(mean(bigcity$x) / mean(bigcity$u), sqrt(city.v))
Afn <- function(t, data) cbind(data$x - t * data$u, 1)
ufn <- function(t, data) c(0, 10)
saddle.distn(A = Afn, u = ufn, wdistr = "b", type = "cond",
             t0 = bigcity.t0, data = bigcity)

# From Example 9.16 of Davison and Hinkley (1997) again, we find the
# conditional distribution of the ratio given the sum of city$u.
Afn <- function(t, data) cbind(data$x - t * data$u, data$u, 1)
ufn <- function(t, data) c(0, sum(data$u), 10)
city.t0 <- c(mean(city$x) / mean(city$u), sqrt(city.v))
saddle.distn(A = Afn, u = ufn, wdistr = "p", type = "cond", t0 = city.t0,
             data = city)

```

---

saddle.distn.object

*Saddlepoint Distribution Approximation Objects*

---

## Description

Class of objects that result from calculating saddlepoint distribution approximations by a call to `saddle.distn`.

## Generation

This class of objects is returned from calls to the function `saddle.distn`.

## Methods

The class "saddle.distn" has methods for the functions `lines` and `print`.

## Structure

Objects of class "saddle.distn" are implemented as a list with the following components.

**quantiles** A matrix with 2 columns. The first column contains the probabilities  $\alpha$  and the second column contains the estimated quantiles of the distribution at those probabilities derived from the spline.

**points** A matrix of evaluations of the saddlepoint approximation. The first column contains the values of  $t$  which were used, the second and third contain the density and cdf approximations at those points and the rest of the columns contain the solutions to the saddlepoint equations. When `type` is "simp", there is only one of those. When `type` is "cond" there are  $2 * d - 1$  where  $d$  is the number of columns in  $A$  or the output of  $A(t, \dots \{ \})$ . The first  $d$  of these correspond to the numerator and the remainder correspond to the denominator.

**distn** An object of class `smooth.spline`. This corresponds to the spline fitted to the saddlepoint cdf approximations in points in order to approximate the entire distribution. For the structure of the object see `smooth.spline`.

**call** The original call to `saddle.distn` which generated the object.

**LR** A logical variable indicating whether the Lugananni-Rice approximations were used.

### See Also

`lines.saddle.distn`, `saddle.distn`, `print.saddle.distn`

---

salinity

*Water Salinity and River Discharge*

---

### Description

The `salinity` data frame has 28 rows and 4 columns.

Biweekly averages of the water salinity and river discharge in Pamlico Sound, North Carolina were recorded between the years 1972 and 1977. The data in this set consists only of those measurements in March, April and May.

### Usage

```
salinity
```

### Format

This data frame contains the following columns:

`sal` The average salinity of the water over two weeks.

`lag` The average salinity of the water lagged two weeks. Since only spring is used, the value of `lag` is not always equal to the previous value of `sal`.

`trend` A factor indicating in which of the 6 biweekly periods between March and May, the observations were taken. The levels of the factor are from 0 to 5 with 0 being the first two weeks in March.

`dis` The amount of river discharge during the two weeks for which `sal` is the average salinity.

### Source

The data were obtained from

Ruppert, D. and Carroll, R.J. (1980) Trimmed least squares estimation in the linear model. *Journal of the American Statistical Association*, **75**, 828–838.

### References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

simplex

*Simplex Method for Linear Programming Problems***Description**

This function will optimize the linear function  $a\%*\%x$  subject to the constraints  $A1\%*\%x \leq b1$ ,  $A2\%*\%x \geq b2$ ,  $A3\%*\%x = b3$  and  $x \geq 0$ . Either maximization or minimization is possible but the default is minimization.

**Usage**

```
simplex(a, A1 = NULL, b1 = NULL, A2 = NULL, b2 = NULL, A3 = NULL,
       b3 = NULL, maxi = FALSE, n.iter = n + 2 * m, eps = 1e-10)
```

**Arguments**

a	A vector of length n which gives the coefficients of the objective function.
A1	An m1 by n matrix of coefficients for the $\leq$ type of constraints.
b1	A vector of length m1 giving the right hand side of the $\leq$ constraints. This argument is required if A1 is given and ignored otherwise. All values in b1 must be non-negative.
A2	An m2 by n matrix of coefficients for the $\geq$ type of constraints.
b2	A vector of length m2 giving the right hand side of the $\geq$ constraints. This argument is required if A2 is given and ignored otherwise. All values in b2 must be non-negative. Note that the constraints $x \geq 0$ are included automatically and so should not be repeated here.
A3	An m3 by n matrix of coefficients for the equality constraints.
b3	A vector of length m3 giving the right hand side of equality constraints. This argument is required if A3 is given and ignored otherwise. All values in b3 must be non-negative.
maxi	A logical flag which specifies minimization if FALSE (default) and maximization otherwise. If maxi is TRUE then the maximization problem is recast as a minimization problem by changing the objective function coefficients to their negatives.
n.iter	The maximum number of iterations to be conducted in each phase of the simplex method. The default is $n+2*(m1+m2+m3)$ .
eps	The floating point tolerance to be used in tests of equality.

**Details**

The method employed by this function is the two phase tableau simplex method. If there are  $\geq$  or equality constraints an initial feasible solution is not easy to find. To find a feasible solution an artificial variable is introduced into each  $\geq$  or equality constraint and an auxiliary objective function is defined as the sum of these artificial variables. If a feasible solution to the set of constraints exists then the auxiliary objective will be minimized when all of the artificial variables are 0. These are then discarded and the original problem solved starting at the solution to the auxiliary problem. If the only constraints are of the  $\leq$  form, the origin is a feasible solution and so the first stage can be omitted.

**Value**

An object of class "simplex": see [simplex.object](#).

**Note**

The method employed here is suitable only for relatively small systems. Also if possible the number of constraints should be reduced to a minimum in order to speed up the execution time which is approximately proportional to the cube of the number of constraints. In particular if there are any constraints of the form  $x[i] \geq b2[i]$  they should be omitted by setting  $x[i] = x[i] - b2[i]$ , changing all the constraints and the objective function accordingly and then transforming back after the solution has been found.

**References**

Gill, P.E., Murray, W. and Wright, M.H. (1991) *Numerical Linear Algebra and Optimization Vol. 1*. Addison-Wesley.

Press, W.H., Teukolsky, S.A., Vetterling, W.T. and Flannery, B.P. (1992) *Numerical Recipes: The Art of Scientific Computing (Second Edition)*. Cambridge University Press.

**Examples**

```
# This example is taken from Exercise 7.5 of Gill, Murray,  
# and Wright (1991).  
enj <- c(200, 6000, 3000, -200)  
fat <- c(800, 6000, 1000, 400)  
vitx <- c(50, 3, 150, 100)  
vity <- c(10, 10, 75, 100)  
vitz <- c(150, 35, 75, 5)  
simplex(a = enj, A1 = fat, b1 = 13800, A2 = rbind(vitx, vity, vitz),  
       b2 = c(600, 300, 550), maxi = TRUE)
```

---

simplex.object

*Linear Programming Solution Objects*

---

**Description**

Class of objects that result from solving a linear programming problem using `simplex`.

**Generation**

This class of objects is returned from calls to the function `simplex`.

**Methods**

The class "saddle.distn" has a method for the function `print`.

## Structure

Objects of class "simplex" are implemented as a list with the following components.

**soln** The values of  $x$  which optimize the objective function under the specified constraints provided those constraints are jointly feasible.

**solved** This indicates whether the problem was solved. A value of  $-1$  indicates that no feasible solution could be found. A value of  $0$  that the maximum number of iterations was reached without termination of the second stage. This may indicate an unbounded function or simply that more iterations are needed. A value of  $1$  indicates that an optimal solution has been found.

**value** The value of the objective function at `soln`.

**val.aux** This is `NULL` if a feasible solution is found. Otherwise it is a positive value giving the value of the auxiliary objective function when it was minimized.

**obj** The original coefficients of the objective function.

**a** The objective function coefficients re-expressed such that the basic variables have coefficient zero.

**a.aux** This is `NULL` if a feasible solution is found. Otherwise it is the re-expressed auxiliary objective function at the termination of the first phase of the simplex method.

**A** The final constraint matrix which is expressed in terms of the non-basic variables. If a feasible solution is found then this will have dimensions  $m_1+m_2+m_3$  by  $n+m_1+m_2$ , where the final  $m_1+m_2$  columns correspond to slack and surplus variables. If no feasible solution is found there will be an additional  $m_1+m_2+m_3$  columns for the artificial variables introduced to solve the first phase of the problem.

**basic** The indices of the basic (non-zero) variables in the solution. Indices between  $n+1$  and  $n+m_1$  correspond to slack variables, those between  $n+m_1+1$  and  $n+m_2$  correspond to surplus variables and those greater than  $n+m_2$  are artificial variables. Indices greater than  $n+m_2$  should occur only if `solved` is  $-1$  as the artificial variables are discarded in the second stage of the simplex method.

**slack** The final values of the  $m_1$  slack variables which arise when the " $\leq$ " constraints are re-expressed as the equalities  $A_1 * x + \text{slack} = b_1$ .

**surplus** The final values of the  $m_2$  surplus variables which arise when the " $\leq$ " constraints are re-expressed as the equalities  $A_2 * x - \text{surplus} = b_2$ .

**artificial** This is `NULL` if a feasible solution can be found. If no solution can be found then this contains the values of the  $m_1+m_2+m_3$  artificial variables which minimize their sum subject to the original constraints. A feasible solution exists only if all of the artificial variables can be made  $0$  simultaneously.

## See Also

[print.simplex](#), [simplex](#)

## Description

This function uses the method of frequency smoothing to find a distribution on a data set which has a required value, `theta`, of the statistic of interest. The method results in distributions which vary smoothly with `theta`.

## Usage

```
smooth.f(theta, boot.out, index=1, t=boot.out$t[, index], width=0.5)
```

## Arguments

<code>theta</code>	The required value for the statistic of interest. If <code>theta</code> is a vector, a separate distribution will be found for each element of <code>theta</code> .
<code>boot.out</code>	A bootstrap output object returned by a call to <code>boot</code> .
<code>index</code>	The index of the variable of interest in the output of <code>boot.out\$statistic</code> . This argument is ignored if <code>t</code> is supplied. <code>index</code> must be a scalar.
<code>t</code>	The bootstrap values of the statistic of interest. This must be a vector of length <code>boot.out\$R</code> and the values must be in the same order as the bootstrap replicates in <code>boot.out</code> .
<code>width</code>	The standardized width for the kernel smoothing. The smoothing uses a value of <code>width*s</code> for epsilon, where <code>s</code> is the bootstrap estimate of the standard error of the statistic of interest. <code>width</code> should take a value in the range (0.2, 1) to produce a reasonable smoothed distribution. If <code>width</code> is too large then the distribution becomes closer to uniform.

## Details

The new distributional weights are found by applying a normal kernel smoother to the observed values of `t` weighted by the observed frequencies in the bootstrap simulation. The resulting distribution may not have parameter value exactly equal to the required value `theta` but it will typically have a value which is close to `theta`. The details of how this method works can be found in Davison, Hinkley and Worton (1995) and Section 3.9.2 of Davison and Hinkley (1997).

## Value

If `length(theta)` is 1 then a vector with the same length as the data set `boot.out$data` is returned. The value in position `i` is the probability to be given to the data point in position `i` so that the distribution has parameter value approximately equal to `theta`. If `length(theta)` is bigger than 1 then the returned value is a matrix with `length(theta)` rows each of which corresponds to a distribution with the parameter value approximately equal to the corresponding value of `theta`.

## References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Davison, A.C., Hinkley, D.V. and Worton, B.J. (1995) Accurate and efficient construction of bootstrap likelihoods. *Statistics and Computing*, **5**, 257–264.

## See Also

[boot](#), [exp.tilt](#), [tilt.boot](#)

**Examples**

```

# Example 9.8 of Davison and Hinkley (1997) requires tilting the resampling
# distribution of the studentized statistic to be centred at the observed
# value of the test statistic 1.84. In the book exponential tilting was used
# but it is also possible to use smooth.f.
grav1 <- gravity[as.numeric(gravity[,2])>=7,]
grav.fun <- function(dat, w, orig)
{
  strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
  d <- dat[, 1]
  ns <- tabulate(strata)
  w <- w/tapply(w, strata, sum)[strata]
  mns <- tapply(d * w, strata, sum)
  mn2 <- tapply(d * d * w, strata, sum)
  s2hat <- sum((mn2 - mns^2)/ns)
  c(mns[2]-mns[1], s2hat, (mns[2]-mns[1]-orig)/sqrt(s2hat))
}
grav.z0 <- grav.fun(grav1,rep(1,26),0)
grav.boot <- boot(grav1, grav.fun, R=499, stype="w",
                 strata=grav1[,2], orig=grav.z0[1])
grav.sm <- smooth.f(grav.z0[3], grav.boot, index=3)

# Now we can run another bootstrap using these weights
grav.boot2 <- boot(grav1, grav.fun, R=499, stype="w",
                 strata=grav1[,2], orig=grav.z0[1],
                 weights=grav.sm)

# Estimated p-values can be found from these as follows
mean(grav.boot$t[,3] >= grav.z0[3])
imp.prob(grav.boot2,t0=-grav.z0[3],t=-grav.boot2$t[,3])

# Note that for the importance sampling probability we must
# multiply everything by -1 to ensure that we find the correct
# probability. Raw resampling is not reliable for probabilities
# greater than 0.5. Thus
1-imp.prob(grav.boot2,index=3,t0=grav.z0[3])$raw
# can give very strange results (negative probabilities).

```

---

sunspot

*Annual Mean Sunspot Numbers*


---

**Description**

sunspot is a time series and contains 289 observations.

The Zurich sunspot numbers have been analyzed in almost all books on time series analysis as well as numerous papers. The data set, usually attributed to Rudolf Wolf, consists of means of daily relative numbers of sunspot sightings. The relative number for a day is given by  $k(f+10g)$  where  $g$  is the number of sunspot groups observed,  $f$  is the total number of spots within the groups and  $k$  is a scaling factor relating the observer and telescope to a baseline. The relative numbers are then averaged to give an annual figure. See Inzenman (1983) for a discussion of the relative numbers. The figures are for the years 1700-1988.



**Source**

The data were obtained from

Tong, H. (1990) *Nonlinear Time Series: A Dynamical System Approach*. Oxford University Press

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Inzenman, A.J. (1983) J.R. Wolf and H.A. Wolfer: An historical note on the Zurich sunspot relative numbers. *Journal of the Royal Statistical Society, A*, **146**, 311-318.

Waldmeir, M. (1961) *The Sunspot Activity in the Years 1610-1960*. Schulthess and Co.

---

survival

*Survival of Rats after Radiation Doses*

---

**Description**

The `survival` data frame has 14 rows and 2 columns.

The data measured the survival percentages of batches of rats who were given varying doses of radiation. At each of 6 doses there were two or three replications of the experiment.

**Usage**

```
survival
```

**Format**

This data frame contains the following columns:

`dose` The dose of radiation administered (rads).

`surv` The survival rate of the batches expressed as a percentage.

**Source**

The data were obtained from

Efron, B. (1988) Computer-intensive methods in statistical regression. *SIAM Review*, **30**, 421-449.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

`tau`*Tau Particle Decay Modes*

---

**Description**

The `tau` data frame has 60 rows and 2 columns.

The tau particle is a heavy electron-like particle discovered in the 1970's by Martin Perl at the Stanford Linear Accelerator Center. Soon after its production the tau particle decays into various collections of more stable particles. About 86% of the time the decay involves just one charged particle. This rate has been measured independently 13 times.

The one-charged-particle event is made up of four major modes of decay as well as a collection of other events. The four main types of decay are denoted `rho`, `pi`, `e` and `mu`. These rates have been measured independently 6, 7, 14 and 19 times respectively. Due to physical constraints each experiment can only estimate the composite one-charged-particle decay rate or the rate of one of the major modes of decay.

Each experiment consists of a major research project involving many years work. One of the goals of the experiments was to estimate the rate of decay due to events other than the four main modes of decay. These are uncertain events and so cannot themselves be observed directly.

**Usage**`tau`**Format**

This data frame contains the following columns:

`rate` The decay rate expressed as a percentage.

`decay` The type of decay measured in the experiment. It is a factor with levels `1`, `rho`, `pi`, `e` and `mu`.

**Source**

The data were obtained from

Efron, B. (1992) Jackknife-after-bootstrap standard errors and influence functions (with Discussion). *Journal of the Royal Statistical Society, B*, **54**, 83–127.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

Hayes, K.G., Perl, M.L. and Efron, B. (1989) Application of the bootstrap statistical method to the tau-decay-mode problem. *Physical Review, D*, **39**, 274-279.

tilt.boot

*Non-parametric Tilted Bootstrap***Description**

This function will run an initial bootstrap with equal resampling probabilities (if required) and will use the output of the initial run to find resampling probabilities which put the value of the statistic at required values. It then runs an importance resampling bootstrap using the calculated probabilities as the resampling distribution.

**Usage**

```
tilt.boot(data, statistic, R, sim="ordinary", stype="i",
          strata=rep(1, n), L=NULL, theta=NULL,
          alpha=c(0.025, 0.975), tilt=TRUE, width=0.5,
          index=1, ...)
```

**Arguments**

data	The data as a vector, matrix or data frame. If it is a matrix or data frame then each row is considered as one (multivariate) observation.
statistic	A function which when applied to data returns a vector containing the statistic(s) of interest. It must take at least two arguments. The first argument will always be data and the second should be a vector of indices, weights or frequencies describing the bootstrap sample. Any other arguments must be supplied to tilt.boot and will be passed unchanged to statistic each time it is called.
R	The number of bootstrap replicates required. This will generally be a vector, the first value stating how many uniform bootstrap simulations are to be performed at the initial stage. The remaining values of R are the number of simulations to be performed resampling from each reweighted distribution. The first value of R must always be present, a value of 0 implying that no uniform resampling is to be carried out. Thus length(R) should always equal 1+length(theta).
sim	This is a character string indicating the type of bootstrap simulation required. There are only two possible values that this can take: "ordinary" and "balanced". If other simulation types are required for the initial un-weighted bootstrap then it will be necessary to run boot, calculate the weights appropriately, and run boot again using the calculated weights.
stype	A character string indicating the type of second argument expected by statistic. The possible values that stype can take are "i" (indices), "w" (weights) and "f" (frequencies).
strata	An integer vector or factor representing the strata for multi-sample problems.
L	The empirical influence values for the statistic of interest. They are used only for exponential tilting when tilt is TRUE. If tilt is TRUE and they are not supplied then tilt.boot uses empinf to calculate them.
theta	The required parameter value(s) for the tilted distribution(s). There should be one value of theta for each of the non-uniform distributions. If R[1] is 0 theta is a required argument. Otherwise theta values can be estimated from the initial uniform bootstrap and the values in alpha.

alpha	The alpha level to which tilting is required. This parameter is ignored if <code>R[1]</code> is 0 or if <code>theta</code> is supplied, otherwise it is used to find the values of <code>theta</code> as quantiles of the initial uniform bootstrap. In this case <code>R[1]</code> should be large enough that $\min(c(\text{alpha}, 1-\text{alpha})) * R[1] > 5$ , if this is not the case then a warning is generated to the effect that the <code>theta</code> are extreme values and so the tilted output may be unreliable.
tilt	A logical variable which if <code>TRUE</code> (the default) indicates that exponential tilting should be used, otherwise local frequency smoothing ( <code>smooth.f</code> ) is used. If <code>tilt</code> is <code>FALSE</code> then <code>R[1]</code> must be positive. In fact in this case the value of <code>R[1]</code> should be fairly large (in the region of 500 or more).
width	This argument is used only if <code>tilt</code> is <code>FALSE</code> , in which case it is passed unchanged to <code>smooth.f</code> as the standardized bandwidth for the smoothing operation. The value should generally be in the range (0.2, 1). See <code>smooth.f</code> for more details.
index	The index of the statistic of interest in the output from <code>statistic</code> . By default the first element of the output of <code>statistic</code> is used.
...	Any additional arguments required by <code>statistic</code> . These are passed unchanged to <code>statistic</code> each time it is called.

### Value

An object of class "boot" with the following components

t0	The observed value of the statistic on the original data.
t	The values of the bootstrap replicates of the statistic. There will be <code>sum(R)</code> of these, the first <code>R[1]</code> corresponding to the uniform bootstrap and the remainder to the tilted bootstrap(s).
R	The input vector of the number of bootstrap replicates.
data	The original data as supplied.
statistic	The <code>statistic</code> function as supplied.
sim	The simulation type used in the bootstrap(s), it can either be "ordinary" or "balanced".
stype	The type of statistic supplied, it is the same as the input value <code>stype</code> .
call	A copy of the original call to <code>tilt.boot</code> .
strata	The strata as supplied.
weights	The matrix of weights used. If <code>R[1]</code> is greater than 0 then the first row will be the uniform weights and each subsequent row the tilted weights. If <code>R[1]</code> equals 0 then the uniform weights are omitted and only the tilted weights are output.
theta	The values of <code>theta</code> used for the tilted distributions. These are either the input values or the values derived from the uniform bootstrap and <code>alpha</code> .

### References

- Booth, J.G., Hall, P. and Wood, A.T.A. (1993) Balanced importance resampling for the bootstrap. *Annals of Statistics*, **21**, 286–298.
- Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.
- Hinkley, D.V. and Shi, S. (1989) Importance sampling and the nested bootstrap. *Biometrika*, **76**, 435–446.

**See Also**

[boot](#), [exp.tilt](#), [Imp.Estimates](#), [imp.weights](#), [smooth.f](#)

**Examples**

```
# Note that these examples can take a while to run.

# Example 9.9 of Davison and Hinkley (1997).
grav1 <- gravity[as.numeric(gravity[,2])>=7,]
grav.fun <- function(dat, w, orig)
{
  strata <- tapply(dat[, 2], as.numeric(dat[, 2]))
  d <- dat[, 1]
  ns <- tabulate(strata)
  w <- w/tapply(w, strata, sum)[strata]
  mns <- tapply(d * w, strata, sum)
  mn2 <- tapply(d * d * w, strata, sum)
  s2hat <- sum((mn2 - mns^2)/ns)
  c(mns[2]-mns[1], s2hat, (mns[2]-mns[1]-orig)/sqrt(s2hat))
}
grav.z0 <- grav.fun(grav1, rep(1,26), 0)
tilt.boot(grav1, grav.fun, R=c(249,375,375), stype="w",
          strata=grav1[,2], tilt=TRUE, index=3, orig=grav.z0[1])

# Example 9.10 of Davison and Hinkley (1997) requires a balanced
# importance resampling bootstrap to be run. In this example we
# show how this might be run.
acme.fun <- function(data, i, bhat)
{
  d <- data[i,]
  n <- nrow(d)
  d.lm <- glm(d$acme~d$market)
  beta.b <- coef(d.lm)[2]
  d.diag <- glm.diag(d.lm)
  SSx <- (n-1)*var(d$market)
  tmp <- (d$market-mean(d$market))*d.diag$res*d.diag$sd
  sr <- sqrt(sum(tmp^2))/SSx
  c(beta.b, sr, (beta.b-bhat)/sr)
}
acme.b <- acme.fun(acme, 1:nrow(acme), 0)
acme.boot1 <- tilt.boot(acme, acme.fun, R=c(499, 250, 250),
                      stype="i", sim="balanced", alpha=c(0.05, 0.95),
                      tilt=TRUE, index=3, bhat=acme.b[1])
```

**Description**

Generate R bootstrap replicates of a statistic applied to a time series. The replicate time series can be generated using fixed or random block lengths or can be model based replicates.

**Usage**

```
tsboot(tseries, statistic, R, l=NULL, sim="model", endcorr=TRUE,
       n.sim=NROW(tseries), orig.t=TRUE, ran.gen,
       ran.args=NULL, norm=TRUE, ...)
```

**Arguments**

<code>tseries</code>	A univariate or multivariate time series.
<code>statistic</code>	A function which when applied to <code>tseries</code> returns a vector containing the statistic(s) of interest. Each time <code>statistic</code> is called it is passed a time series of length <code>n.sim</code> which is of the same class as the original <code>tseries</code> . Any other arguments which <code>statistic</code> takes must remain constant for each bootstrap replicate and should be supplied through the <code>...</code> argument to <code>tsboot</code> .
<code>R</code>	A positive integer giving the number of bootstrap replicates required.
<code>sim</code>	The type of simulation required to generate the replicate time series. The possible input values are "model" (model based resampling), "fixed" (block resampling with fixed block lengths of <code>l</code> ), "geom" (block resampling with block lengths having a geometric distribution with mean <code>l</code> ) or "scramble" (phase scrambling).
<code>l</code>	If <code>sim</code> is "fixed" then <code>l</code> is the fixed block length used in generating the replicate time series. If <code>sim</code> is "geom" then <code>l</code> is the mean of the geometric distribution used to generate the block lengths. <code>l</code> should be a positive integer less than the length of <code>tseries</code> . This argument is not required when <code>sim</code> is "model" but it is required for all other simulation types.
<code>endcorr</code>	A logical variable indicating whether end corrections are to be applied when <code>sim</code> is "fixed". When <code>sim</code> is "geom", <code>endcorr</code> is automatically set to TRUE; <code>endcorr</code> is not used when <code>sim</code> is "model" or "scramble".
<code>n.sim</code>	The length of the simulated time series. Typically this will be equal to the length of the original time series but there are situations when it will be larger. One obvious situation is if prediction is required. Another situation in which <code>n.sim</code> is larger than the original length is if <code>tseries</code> is a residual time series from fitting some model to the original time series. In this case, <code>n.sim</code> would usually be the length of the original time series.
<code>orig.t</code>	A logical variable which indicates whether <code>statistic</code> should be applied to <code>tseries</code> itself as well as the bootstrap replicate series. If <code>statistic</code> is expecting a longer time series than <code>tseries</code> or if applying <code>statistic</code> to <code>tseries</code> will not yield any useful information then <code>orig.t</code> should be set to FALSE.
<code>ran.gen</code>	This is a function of three arguments. The first argument is a time series. If <code>sim</code> is "model" then it will always be <code>tseries</code> that is passed. For other simulation types it is the result of selecting <code>n.sim</code> observations from <code>tseries</code> by some scheme and converting the result back into a time series of the same form as <code>tseries</code> (although of length <code>n.sim</code> ). The second argument to <code>ran.gen</code> is always the value <code>n.sim</code> , and the third argument is <code>ran.args</code> , which is used to supply any other objects needed by <code>ran.gen</code> . If <code>sim</code> is "model" then the generation of the replicate time series will be done in <code>ran.gen</code> (for example through use of <code>arima.sim</code> ). For the other simulation types <code>ran.gen</code> is used for 'post-blackening'. The default is that the function simply returns the time series passed to it.

<code>ran.args</code>	This will be supplied to <code>ran.gen</code> each time it is called. If <code>ran.gen</code> needs any extra arguments then they should be supplied as components of <code>ran.args</code> . Multiple arguments may be passed by making <code>ran.args</code> a list. If <code>ran.args</code> is <code>NULL</code> then it should not be used within <code>ran.gen</code> but note that <code>ran.gen</code> must still have its third argument.
<code>norm</code>	A logical argument indicating whether normal margins should be used for phase scrambling. If <code>norm</code> is <code>FALSE</code> then margins corresponding to the exact empirical margins are used.
<code>...</code>	Any extra arguments to <code>statistic</code> may be supplied here.

### Details

If `sim` is "fixed" then each replicate time series is found by taking blocks of length `l`, from the original time series and putting them end-to-end until a new series of length `n.sim` is created. When `sim` is "geom" a similar approach is taken except that now the block lengths are generated from a geometric distribution with mean 1. Post-blackening can be carried out on these replicate time series by including the function `ran.gen` in the call to `tsboot` and having `tseries` as a time series of residuals.

Model based resampling is very similar to the parametric bootstrap and all simulation must be in one of the user specified functions. This avoids the complicated problem of choosing the block length but relies on an accurate model choice being made.

Phase scrambling is described in Section 8.2.4 of Davison and Hinkley (1997). The types of statistic for which this method produces reasonable results is very limited and the other methods seem to do better in most situations. Other types of resampling in the frequency domain can be accomplished using the function `boot` with the argument `sim="parametric"`.

### Value

An object of class "boot" with the following components.

<code>t0</code>	If <code>orig.t</code> is <code>TRUE</code> then <code>t0</code> is the result of <code>statistic(tseries, ...)</code> otherwise it is <code>NULL</code> .
<code>t</code>	The results of applying <code>statistic</code> to the replicate time series.
<code>R</code>	The value of <code>R</code> as supplied to <code>tsboot</code> .
<code>tseries</code>	The original time series.
<code>statistic</code>	The function <code>statistic</code> as supplied.
<code>sim</code>	The simulation type used in generating the replicates.
<code>endcorr</code>	The value of <code>endcorr</code> used. The value is meaningful only when <code>sim</code> is "fixed"; it is ignored for model based simulation or phase scrambling and is always set to <code>TRUE</code> if <code>sim</code> is "geom".
<code>n.sim</code>	The value of <code>n.sim</code> used.
<code>l</code>	The value of <code>l</code> used for block based resampling. This will be <code>NULL</code> if block based resampling was not used.
<code>ran.gen</code>	The <code>ran.gen</code> function used for generating the series or for "post-blackening".
<code>ran.args</code>	The extra arguments passed to <code>ran.gen</code> .
<code>call</code>	The original call to <code>tsboot</code> .

## References

- Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.
- Kunsch, H.R. (1989) The jackknife and the bootstrap for general stationary observations. *Annals of Statistics*, **17**, 1217–1241.
- Politis, D.N. and Romano, J.P. (1994) The stationary bootstrap. *Journal of the American Statistical Association*, **89**, 1303–1313.

## See Also

[boot](#), [arima.sim](#)

## Examples

```
lynx.fun <- function(tsb)
{   ar.fit <- ar(tsb, order.max=25)
    c(ar.fit$order, mean(tsb), tsb)
}

# the stationary bootstrap with mean block length 20
lynx.1 <- tsboot(log(lynx), lynx.fun, R=99, l=20, sim="geom")

# the fixed block bootstrap with length 20
lynx.2 <- tsboot(log(lynx), lynx.fun, R=99, l=20, sim="fixed")

# Now for model based resampling we need the original model
# Note that for all of the bootstraps which use the residuals as their
# data, we set orig.t to FALSE since the function applied to the residual
# time series will be meaningless.
lynx.ar <- ar(log(lynx))
lynx.model <- list(order=c(lynx.ar$order,0,0),ar=lynx.ar$ar)
lynx.res <- lynx.ar$resid[!is.na(lynx.ar$resid)]
lynx.res <- lynx.res - mean(lynx.res)

lynx.sim <- function(res,n.sim, ran.args) {
# random generation of replicate series using arima.sim
  rgl <- function(n, res)
    sample(res, n, replace=TRUE)
  ts.orig <- ran.args$ts
  ts.mod <- ran.args$model
  mean(ts.orig)+ts(arima.sim(model=ts.mod, n=n.sim,
                             rand.gen=rgl, res=as.vector(res)))
}

lynx.3 <- tsboot(lynx.res, lynx.fun, R=99, sim="model", n.sim=114,
                orig.t=FALSE, ran.gen=lynx.sim,
                ran.args=list(ts=log(lynx), model=lynx.model))

# For "post-blackening" we need to define another function
lynx.black <- function(res, n.sim, ran.args)
{   ts.orig <- ran.args$ts
    ts.mod <- ran.args$model
    mean(ts.orig) + ts(arima.sim(model=ts.mod,n=n.sim,innov=res))
}
```



```

# Now we can run apply the two types of block resampling again but this
# time applying post-blackening.
lynx.1b <- tsboot(lynx.res, lynx.fun, R=99, l=20, sim="fixed",
                 n.sim=114, orig.t=FALSE, ran.gen=lynx.black,
                 ran.args=list(ts=log(lynx), model=lynx.model))

lynx.2b <- tsboot(lynx.res, lynx.fun, R=99, l=20, sim="geom",
                 n.sim=114, orig.t=FALSE, ran.gen=lynx.black,
                 ran.args=list(ts=log(lynx), model=lynx.model))

# To compare the observed order of the bootstrap replicates we
# proceed as follows.
table(lynx.1$t[,1])
table(lynx.1b$t[,1])
table(lynx.2$t[,1])
table(lynx.2b$t[,1])
table(lynx.3$t[,1])
# Notice that the post-blackened and model-based bootstraps preserve
# the true order of the model (11) in many more cases than the others.

```

---

tuna

*Tuna Sighting Data*


---

### Description

The `tuna` data frame has 64 rows and 1 columns.

The data come from an aerial line transect survey of Southern Bluefin Tuna in the Great Australian Bight. An aircraft with two spotters on board flies randomly allocated line transects. Each school of tuna sighted is counted and its perpendicular distance from the transect measured. The survey was conducted in summer when tuna tend to stay on the surface.

### Usage

```
tuna
```

### Format

This data frame contains the following column:

- y The perpendicular distance, in miles, from the transect for 64 independent sightings of tuna schools.

### Source

The data were obtained from

Chen, S.X. (1996) Empirical likelihood confidence intervals for nonparametric density estimation. *Biometrika*, **83**, 329–341.

### References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

urine	<i>Urine Analysis Data</i>
-------	----------------------------

---

### Description

The `urine` data frame has 79 rows and 7 columns.

79 urine specimens were analyzed in an effort to determine if certain physical characteristics of the urine might be related to the formation of calcium oxalate crystals.

### Usage

```
urine
```

### Format

This data frame contains the following columns:

`r` Indicator of the presence of calcium oxalate crystals.

`gravity` The specific gravity of the urine.

`ph` The pH reading of the urine.

`osmo` The osmolarity of the urine. Osmolarity is proportional to the concentration of molecules in solution.

`cond` The conductivity of the urine. Conductivity is proportional to the concentration of charged ions in solution.

`urea` The urea concentration in millimoles per litre.

`calc` The calcium concentration in millimoles per litre.

### Source

The data were obtained from

Andrews, D.F. and Herzberg, A.M. (1985) *Data: A Collection of Problems from Many Fields for the Student and Research Worker*. Springer-Verlag.

### References

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

---

var.linear	<i>Linear Variance Estimate</i>
------------	---------------------------------

---

**Description**

Estimates the variance of a statistic from its empirical influence values.

**Usage**

```
var.linear(L, strata=NULL)
```

**Arguments**

L	Vector of the empirical influence values of a statistic. These will usually be calculated by a call to <code>empinf</code> .
strata	A numeric vector or factor specifying which observations (and hence empirical influence values) come from which strata.

**Value**

The variance estimate calculated from L.

**References**

Davison, A. C. and Hinkley, D. V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.

**See Also**

[empinf](#), [linear.approx](#), [k3.linear](#)

**Examples**

```
# To estimate the variance of the ratio of means for the city data.
ratio <- function(d,w)
  sum(d$x * w) / sum(d$u * w)
var.linear(empinf(data=city, statistic=ratio))
```

---

wool	<i>Australian Relative Wool Prices</i>
------	--

---

**Description**

`wool` is a time series of class "ts" and contains 309 observations.

Each week that the market is open the Australian Wool Corporation set a floor price which determines their policy on intervention and is therefore a reflection of the overall price of wool for the week in question. Actual prices paid can vary considerably about the floor price. The series here is the log of the ratio between the price for fine grade wool and the floor price, each market week between July 1976 and Jun 1984.

**Source**

The data were obtained from

Diggle, P.J. (1990) *Time Series: A Biostatistical Introduction*. Oxford University Press.

**References**

Davison, A.C. and Hinkley, D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press.



## Chapter 14

# The `class` package

---

`batchSOM`

*Self-Organizing Maps: Batch Algorithm*

---

### Description

Kohonen's Self-Organizing Maps are a crude form of multidimensional scaling.

### Usage

```
batchSOM(data, grid = somgrid(), radii, init)
```

### Arguments

<code>data</code>	a matrix or data frame of observations, scaled so that Euclidean distance is appropriate.
<code>grid</code>	A grid for the representatives: see <code>somgrid</code> .
<code>radii</code>	the radii of the neighbourhood to be used for each pass: one pass is run for each element of <code>radii</code> .
<code>init</code>	the initial representatives. If missing, chosen (without replacement) randomly from <code>data</code> .

### Details

The batch SOM algorithm of Kohonen(1995, section 3.14) is used.

### Value

An object of class "SOM" with components

<code>grid</code>	the grid, an object of class "somgrid".
<code>codes</code>	a matrix of representatives.

### References

Kohonen, T. (1995) *Self-Organizing Maps*. Springer-Verlag.  
Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.  
Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[somgrid](#), [SOM](#)

**Examples**

```
require(graphics)
data(crabs, package = "MASS")

lcrabs <- log(crabs[, 4:8])
crabs.grp <- factor(c("B", "b", "O", "o")[rep(1:4, rep(50,4))])
gr <- somgrid(topo = "hexagonal")
crabs.som <- batchSOM(lcrabs, gr, c(4, 4, 2, 2, 1, 1, 1, 0, 0))
plot(crabs.som)

bins <- as.numeric(knn1(crabs.som$code, lcrabs, 0:47))
plot(crabs.som$grid, type = "n")
symbols(crabs.som$grid$pts[, 1], crabs.som$grid$pts[, 2],
        circles = rep(0.4, 48), inches = FALSE, add = TRUE)
text(crabs.som$grid$pts[bins, ] + rnorm(400, 0, 0.1),
     as.character(crabs.grp))
```

---

condense

*Condense training set for k-NN classifier*

---

**Description**

Condense training set for k-NN classifier

**Usage**

```
condense(train, class, store, trace = TRUE)
```

**Arguments**

train	matrix for training set
class	vector of classifications for test set
store	initial store set. Default one randomly chosen element of the set.
trace	logical. Trace iterations?

**Details**

The store set is used to 1-NN classify the rest, and misclassified patterns are added to the store set. The whole set is checked until no additions occur.

**Value**

Index vector of cases to be retained (the final store set).

## References

- P. A. Devijver and J. Kittler (1982) *Pattern Recognition. A Statistical Approach*. Prentice-Hall, pp. 119–121.
- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

## See Also

`reduce.nn`, `multiedit`

## Examples

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test  <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl    <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
keep  <- condense(train, cl)
knn(train[keep, , drop=FALSE], test, cl[keep])
keep2 <- reduce.nn(train, keep, cl)
knn(train[keep2, , drop=FALSE], test, cl[keep2])
```

---

knn

*k-Nearest Neighbour Classification*

---

## Description

k-nearest neighbour classification for test set from training set. For each row of the test set, the k nearest (in Euclidean distance) training set vectors are found, and the classification is decided by majority vote, with ties broken at random. If there are ties for the kth nearest vector, all candidates are included in the vote.

## Usage

```
knn(train, test, cl, k = 1, l = 0, prob = FALSE, use.all = TRUE)
```

## Arguments

<code>train</code>	matrix or data frame of training set cases.
<code>test</code>	matrix or data frame of test set cases. A vector will be interpreted as a row vector for a single case.
<code>cl</code>	factor of true classifications of training set
<code>k</code>	number of neighbours considered.
<code>l</code>	minimum vote for definite decision, otherwise <code>doubt</code> . (More precisely, less than k-1 dissenting votes are allowed, even if k is increased by ties.)
<code>prob</code>	If this is true, the proportion of the votes for the winning class are returned as attribute <code>prob</code> .
<code>use.all</code>	controls handling of ties. If true, all distances equal to the kth largest are included. If false, a random selection of distances equal to the kth is chosen to use exactly k neighbours.



**Value**

Factor of classifications of test set. `doubt` will be returned as NA.

**References**

- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.  
 Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[knn1](#), [knn.cv](#)

**Examples**

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
knn(train, test, cl, k = 3, prob=TRUE)
attributes(.Last.value)
```

---

knn.cv

*k-Nearest Neighbour Cross-Validatory Classification*


---

**Description**

k-nearest neighbour cross-validatory classification from training set.

**Usage**

```
knn.cv(train, cl, k = 1, l = 0, prob = FALSE, use.all = TRUE)
```

**Arguments**

<code>train</code>	matrix or data frame of training set cases.
<code>cl</code>	factor of true classifications of training set
<code>k</code>	number of neighbours considered.
<code>l</code>	minimum vote for definite decision, otherwise <code>doubt</code> . (More precisely, less than $k-1$ dissenting votes are allowed, even if $k$ is increased by ties.)
<code>prob</code>	If this is true, the proportion of the votes for the winning class are returned as attribute <code>prob</code> .
<code>use.all</code>	controls handling of ties. If true, all distances equal to the $k$ th largest are included. If false, a random selection of distances equal to the $k$ th is chosen to use exactly $k$ neighbours.

**Details**

This uses leave-one-out cross validation. For each row of the training set `train`, the  $k$  nearest (in Euclidean distance) other training set vectors are found, and the classification is decided by majority vote, with ties broken at random. If there are ties for the  $k$ th nearest vector, all candidates are included in the vote.

**Value**

Factor of classifications of training set. `doubt` will be returned as NA.

**References**

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[knn](#)

**Examples**

```
train <- rbind(iris3[, , 1], iris3[, , 2], iris3[, , 3])
cl <- factor(c(rep("s", 50), rep("c", 50), rep("v", 50)))
knn.cv(train, cl, k = 3, prob = TRUE)
attributes(.Last.value)
```

---

knn1

*1-nearest neighbour classification*

---

**Description**

Nearest neighbour classification for test set from training set. For each row of the test set, the nearest (by Euclidean distance) training set vector is found, and its classification used. If there is more than one nearest, a majority vote is used with ties broken at random.

**Usage**

```
knn1(train, test, cl)
```

**Arguments**

<code>train</code>	matrix or data frame of training set cases.
<code>test</code>	matrix or data frame of test set cases. A vector will be interpreted as a row vector for a single case.
<code>cl</code>	factor of true classification of training set.

**Value**

Factor of classifications of test set.

**References**

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[knn](#)

## Examples

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
knn1(train, test, cl)
```

---

lvq1

*Learning Vector Quantization I*

---

## Description

Moves examples in a codebook to better represent the training set.

## Usage

```
lvq1(x, cl, codebk, niter = 100 * nrow(codebk$x), alpha = 0.03)
```

## Arguments

<code>x</code>	a matrix or data frame of examples
<code>cl</code>	a vector or factor of classifications for the examples
<code>codebk</code>	a codebook
<code>niter</code>	number of iterations
<code>alpha</code>	constant for training

## Details

Selects `niter` examples at random with replacement, and adjusts the nearest example in the codebook for each.

## Value

A codebook, represented as a list with components `x` and `cl` giving the examples and classes.

## References

- Kohonen, T. (1990) The self-organizing map. *Proc. IEEE* **78**, 1464–1480.
- Kohonen, T. (1995) *Self-Organizing Maps*. Springer, Berlin.
- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

## See Also

[lvqinit](#), [olvq1](#), [lvq2](#), [lvq3](#), [lvqtest](#)

**Examples**

```

train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test  <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl    <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
cd    <- lvqinit(train, cl, 10)
lvqtest(cd, train)
cd0   <- olvq1(train, cl, cd)
lvqtest(cd0, train)
cd1   <- lvq1(train, cl, cd0)
lvqtest(cd1, train)

```

lvq2

*Learning Vector Quantization 2.1***Description**

Moves examples in a codebook to better represent the training set.

**Usage**

```

lvq2(x, cl, codebk, niter = 100 * nrow(codebk$x), alpha = 0.03,
     win = 0.3)

```

**Arguments**

<code>x</code>	a matrix or data frame of examples
<code>cl</code>	a vector or factor of classifications for the examples
<code>codebk</code>	a codebook
<code>niter</code>	number of iterations
<code>alpha</code>	constant for training
<code>win</code>	a tolerance for the closeness of the two nearest vectors.

**Details**

Selects `niter` examples at random with replacement, and adjusts the nearest two examples in the codebook if one is correct and the other incorrect.

**Value**

A codebook, represented as a list with components `x` and `cl` giving the examples and classes.

**References**

- Kohonen, T. (1990) The self-organizing map. *Proc. IEEE* **78**, 1464–1480.
- Kohonen, T. (1995) *Self-Organizing Maps*. Springer, Berlin.
- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

`lvqinit`, `lvq1`, `olvq1`, `lvq3`, `lvqtest`

**Examples**

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test  <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl    <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
cd    <- lvqinit(train, cl, 10)
lvqtest(cd, train)
cd0   <- olvq1(train, cl, cd)
lvqtest(cd0, train)
cd2   <- lvq2(train, cl, cd0)
lvqtest(cd2, train)
```

---

lvq3

*Learning Vector Quantization 3*


---

**Description**

Moves examples in a codebook to better represent the training set.

**Usage**

```
lvq3(x, cl, codebk, niter = 100*nrow(codebk$x), alpha = 0.03,
     win = 0.3, epsilon = 0.1)
```

**Arguments**

<code>x</code>	a matrix or data frame of examples
<code>cl</code>	a vector or factor of classifications for the examples
<code>codebk</code>	a codebook
<code>niter</code>	number of iterations
<code>alpha</code>	constant for training
<code>win</code>	a tolerance for the closeness of the two nearest vectors.
<code>epsilon</code>	proportion of move for correct vectors

**Details**

Selects `niter` examples at random with replacement, and adjusts the nearest two examples in the codebook for each.

**Value**

A codebook, represented as a list with components `x` and `cl` giving the examples and classes.

## References

- Kohonen, T. (1990) The self-organizing map. *Proc. IEEE* **78**, 1464–1480.
- Kohonen, T. (1995) *Self-Organizing Maps*. Springer, Berlin.
- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

## See Also

`lvqinit`, `lvq1`, `olvq1`, `lvq2`, `lvqtest`

## Examples

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
cd <- lvqinit(train, cl, 10)
lvqtest(cd, train)
cd0 <- olvq1(train, cl, cd)
lvqtest(cd0, train)
cd3 <- lvq3(train, cl, cd0)
lvqtest(cd3, train)
```

---

lvqinit

*Initialize a LVQ Codebook*

---

## Description

Construct an initial codebook for LVQ methods.

## Usage

```
lvqinit(x, cl, size, prior, k = 5)
```

## Arguments

- |                    |   |
|--------------------|---|
| <code>x</code>     | a matrix or data frame of training examples, $n$ by $p$ .   |
| <code>cl</code>    | the classifications for the training examples. A vector or factor of length $n$ .   |
| <code>size</code>  | the size of the codebook. Defaults to $\min(\text{round}(0.4 \cdot n_{\text{g}} \cdot (n_{\text{g}} - 1 + p/2)), 0), n)$ where $n_{\text{g}}$ is the number of classes. |
| <code>prior</code> | Probabilities to represent classes in the codebook. Default proportions in the training set.  |
| <code>k</code>     | $k$ used for $k$ -NN test of correct classification. Default is 5.  |

## Details

Selects `size` examples from the training set without replacement with proportions proportional to the prior or the original proportions.

## Value

A codebook, represented as a list with components `x` and `cl` giving the examples and classes.

**References**

- Kohonen, T. (1990) The self-organizing map. *Proc. IEEE* **78**, 1464–1480.
- Kohonen, T. (1995) *Self-Organizing Maps*. Springer, Berlin.
- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[lvq1](#), [lvq2](#), [lvq3](#), [olvq1](#), [lvqtest](#)

**Examples**

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
cd <- lvqinit(train, cl, 10)
lvqtest(cd, train)
cd1 <- olvq1(train, cl, cd)
lvqtest(cd1, train)
```

---

lvqtest

*Classify Test Set from LVQ Codebook*

---

**Description**

Classify a test set by 1-NN from a specified LVQ codebook.

**Usage**

```
lvqtest(codebk, test)
```

**Arguments**

codebk	codebook object returned by other LVQ software
test	matrix of test examples

**Details**

Uses 1-NN to classify each test example against the codebook.

**Value**

Factor of classification for each row of  $x$

**References**

- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[lvqinit](#), [olvq1](#)

**Examples**

```
# The function is currently defined as
function(codebk, test) knn1(codebk$x, test, codebk$cl)
```

---

multiedit

*Multiedit for k-NN Classifier*

---

**Description**

Multiedit for k-NN classifier

**Usage**

```
multiedit(x, class, k = 1, V = 3, I = 5, trace = TRUE)
```

**Arguments**

x	matrix of training set.
class	vector of classification of training set.
k	number of neighbours used in k-NN.
V	divide training set into V parts.
I	number of null passes before quitting.
trace	logical for statistics at each pass.

**Value**

Index vector of cases to be retained.

**References**

- P. A. Devijver and J. Kittler (1982) *Pattern Recognition. A Statistical Approach*. Prentice-Hall, p. 115.
- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[condense](#), [reduce.nn](#)



**Examples**

```

tr <- sample(1:50, 25)
train <- rbind(iris3[tr,,1], iris3[tr,,2], iris3[tr,,3])
test <- rbind(iris3[-tr,,1], iris3[-tr,,2], iris3[-tr,,3])
cl <- factor(c(rep(1,25),rep(2,25), rep(3,25)), labels=c("s", "c", "v"))
table(cl, knn(train, test, cl, 3))
ind1 <- multiedit(train, cl, 3)
length(ind1)
table(cl, knn(train[ind1, , drop=FALSE], test, cl[ind1], 1))
ntrain <- train[ind1,]; ncl <- cl[ind1]
ind2 <- condense(ntrain, ncl)
length(ind2)
table(cl, knn(ntrain[ind2, , drop=FALSE], test, ncl[ind2], 1))

```

olvq1

*Optimized Learning Vector Quantization 1***Description**

Moves examples in a codebook to better represent the training set.

**Usage**

```
olvq1(x, cl, codebk, niter = 40 * nrow(codebk$x), alpha = 0.3)
```

**Arguments**

x	a matrix or data frame of examples
cl	a vector or factor of classifications for the examples
codebk	a codebook
niter	number of iterations
alpha	constant for training

**Details**

Selects `niter` examples at random with replacement, and adjusts the nearest example in the codebook for each.

**Value**

A codebook, represented as a list with components `x` and `cl` giving the examples and classes.

**References**

- Kohonen, T. (1990) The self-organizing map. *Proc. IEEE* **78**, 1464–1480.
- Kohonen, T. (1995) *Self-Organizing Maps*. Springer, Berlin.
- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[lvqinit](#), [lvqtest](#), [lvq1](#), [lvq2](#), [lvq3](#)

**Examples**

```
train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
cd <- lvqinit(train, cl, 10)
lvqtest(cd, train)
cd1 <- olvq1(train, cl, cd)
lvqtest(cd1, train)
```

---

reduce.nn

*Reduce Training Set for a k-NN Classifier*

---

**Description**

Reduce training set for a k-NN classifier. Used after condense.

**Usage**

```
reduce.nn(train, ind, class)
```

**Arguments**

train	matrix for training set
ind	Initial list of members of the training set (from condense).
class	vector of classifications for test set

**Details**

All the members of the training set are tried in random order. Any which when dropped do not cause any members of the training set to be wrongly classified are dropped.

**Value**

Index vector of cases to be retained.

**References**

- Gates, G.W. (1972) The reduced nearest neighbor rule. *IEEE Trans. Information Theory* **IT-18**, 431–432.
- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[condense](#), [multiedit](#)

**Examples**

```

train <- rbind(iris3[1:25,,1], iris3[1:25,,2], iris3[1:25,,3])
test  <- rbind(iris3[26:50,,1], iris3[26:50,,2], iris3[26:50,,3])
cl    <- factor(c(rep("s",25), rep("c",25), rep("v",25)))
keep  <- condense(train, cl)
knn(train[keep,], test, cl[keep])
keep2 <- reduce.nn(train, keep, cl)
knn(train[keep2,], test, cl[keep2])

```

SOM

*Self-Organizing Maps: Online Algorithm***Description**

Kohonen's Self-Organizing Maps are a crude form of multidimensional scaling.

**Usage**

```
SOM(data, grid = somgrid(), rlen = 10000, alpha, radii, init)
```

**Arguments**

<code>data</code>	a matrix or data frame of observations, scaled so that Euclidean distance is appropriate.
<code>grid</code>	A grid for the representatives: see <code>somgrid</code> .
<code>rlen</code>	the number of updates: used only in the defaults for <code>alpha</code> and <code>radii</code> .
<code>alpha</code>	the amount of change: one update is done for each element of <code>alpha</code> . Default is to decline linearly from 0.05 to 0 over <code>rlen</code> updates.
<code>radii</code>	the radii of the neighbourhood to be used for each update: must be the same length as <code>alpha</code> . Default is to decline linearly from 4 to 1 over <code>rlen</code> updates.
<code>init</code>	the initial representatives. If missing, chosen (without replacement) randomly from <code>data</code> .

**Details**

`alpha` and `radii` can also be lists, in which case each component is used in turn, allowing two- or more phase training.

**Value**

An object of class "SOM" with components

<code>grid</code>	the grid, an object of class "somgrid".
<code>codes</code>	a matrix of representatives.

## References

- Kohonen, T. (1995) *Self-Organizing Maps*. Springer-Verlag
- Kohonen, T., Hynninen, J., Kangas, J. and Laaksonen, J. (1996) *SOM PAK: The self-organizing map program package*. Laboratory of Computer and Information Science, Helsinki University of Technology, Technical Report A31.
- Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.
- Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

## See Also

[somgrid](#), [batchSOM](#)

## Examples

```
require(graphics)
data(crabs, package = "MASS")

lcrabs <- log(crabs[, 4:8])
crabs.grp <- factor(c("B", "b", "O", "o")[rep(1:4, rep(50,4))])
gr <- somgrid(topo = "hexagonal")
crabs.som <- SOM(lcrabs, gr)
plot(crabs.som)

## 2-phase training
crabs.som2 <- SOM(lcrabs, gr,
  alpha = list(seq(0.05, 0, len = 1e4), seq(0.02, 0, len = 1e5)),
  radii = list(seq(8, 1, len = 1e4), seq(4, 1, len = 1e5)))
plot(crabs.som2)
```

---

somgrid

*Plot SOM Fits*

---

## Description

Plotting functions for SOM results.

## Usage

```
somgrid(xdim = 8, ydim = 6, topo = c("rectangular", "hexagonal"))

## S3 method for class 'somgrid':
plot(x, type = "p", ...)

## S3 method for class 'SOM':
plot(x, ...)
```

## Arguments

`xdim`, `ydim` dimensions of the grid

`topo` the topology of the grid.

`x` an object inheriting from class "somgrid" or "SOM".

`type`, `...` graphical parameters.

**Details**

The class "somgrid" records the coordinates of the grid to be used for (batch or on-line) SOM: this has a plot method.

The plot method for class "SOM" plots a [stars](#) plot of the representative at each grid point.

**Value**

For somgrid, an object of class "somgrid", a list with components

pts                    a two-column matrix giving locations for the grid points.  
xdim, ydim, topo        as in the arguments to somgrid.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[batchSOM](#), [SOM](#)

## Chapter 15

# The `cluster` package

---

`agnes`

*Agglomerative Nesting (Hierarchical Clustering)*

---

### Description

Computes agglomerative hierarchical clustering of the dataset.

### Usage

```
agnes(x, diss = inherits(x, "dist"), metric = "euclidean",
      stand = FALSE, method = "average", par.method,
      keep.diss = n < 100, keep.data = !diss)
```

### Arguments

<code>x</code>	<p>data matrix or data frame, or dissimilarity matrix, depending on the value of the <code>diss</code> argument.</p> <p>In case of a matrix or data frame, each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (NAs) are allowed.</p> <p>In case of a dissimilarity matrix, <code>x</code> is typically the output of <code>daisy</code> or <code>dist</code>. Also a vector with length <math>n*(n-1)/2</math> is allowed (where <code>n</code> is the number of observations), and will be interpreted in the same way as the output of the above-mentioned functions. Missing values (NAs) are not allowed.</p>
<code>diss</code>	<p>logical flag: if TRUE (default for <code>dist</code> or <code>dissimilarity</code> objects), then <code>x</code> is assumed to be a dissimilarity matrix. If FALSE, then <code>x</code> is treated as a matrix of observations by variables.</p>
<code>metric</code>	<p>character string specifying the metric to be used for calculating dissimilarities between observations. The currently available options are "euclidean" and "manhattan". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences. If <code>x</code> is already a dissimilarity matrix, then this argument will be ignored.</p>
<code>stand</code>	<p>logical flag: if TRUE, then the measurements in <code>x</code> are standardized before calculating the dissimilarities. Measurements are standardized for each variable</p>

	(column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation. If $x$ is already a dissimilarity matrix, then this argument will be ignored.
<code>method</code>	character string defining the clustering method. The six methods implemented are "average" ([unweighted pair-]group average method, UPGMA), "single" (single linkage), "complete" (complete linkage), "ward" (Ward's method), "weighted" (weighted average linkage) and its generalization "flexible" which uses (a constant version of) the Lance-Williams formula and the <code>par.method</code> argument. Default is "average".
<code>par.method</code>	if <code>method == "flexible"</code> , numeric vector of length 1, 3, or 4, see in the details section.
<code>keep.diss</code> , <code>keep.data</code>	logicals indicating if the dissimilarities and/or input data $x$ should be kept in the result. Setting these to <code>FALSE</code> can give much smaller results and hence even save memory allocation <i>time</i> .

## Details

`agnes` is fully described in chapter 5 of Kaufman and Rousseeuw (1990). Compared to other agglomerative clustering methods such as `hclust`, `agnes` has the following features: (a) it yields the agglomerative coefficient (see `agnes.object`) which measures the amount of clustering structure found; and (b) apart from the usual tree it also provides the banner, a novel graphical display (see `plot.agnes`).

The `agnes`-algorithm constructs a hierarchy of clusterings.

At first, each observation is a small cluster by itself. Clusters are merged until only one large cluster remains which contains all the observations. At each stage the two *nearest* clusters are combined to form one larger cluster.

For `method="average"`, the distance between two clusters is the average of the dissimilarities between the points in one cluster and the points in the other cluster.

In `method="single"`, we use the smallest dissimilarity between a point in the first cluster and a point in the second cluster (nearest neighbor method).

When `method="complete"`, we use the largest dissimilarity between a point in the first cluster and a point in the second cluster (furthest neighbor method).

The `method = "flexible"` allows (and requires) more details: The Lance-Williams formula specifies how dissimilarities are computed when clusters are agglomerated (equation (32) in K.&R., p.237). If clusters  $C_1$  and  $C_2$  are agglomerated into a new cluster, the dissimilarity between their union and another cluster  $Q$  is given by

$$D(C_1 \cup C_2, Q) = \alpha_1 * D(C_1, Q) + \alpha_2 * D(C_2, Q) + \beta * D(C_1, C_2) + \gamma * |D(C_1, Q) - D(C_2, Q)|,$$

where the four coefficients  $(\alpha_1, \alpha_2, \beta, \gamma)$  are specified by the vector `par.method`:

If `par.method` is of length 1, say  $= \alpha$ , `par.method` is extended to give the "Flexible Strategy" (K. & R., p.236 f) with Lance-Williams coefficients  $(\alpha_1 = \alpha_2 = \alpha, \beta = 1 - 2\alpha, \gamma = 0)$ .

If of length 3,  $\gamma = 0$  is used.

**Care** and expertise is probably needed when using `method = "flexible"` particularly for the case when `par.method` is specified of longer length than one. The *weighted average* (`method="weighted"`) is the same as `method="flexible"`, `par.method = 0.5`.

## Value

an object of class "agnes" representing the clustering. See `agnes.object` for details.

## BACKGROUND

Cluster analysis divides a dataset into groups (clusters) of observations that are similar to each other.

**Hierarchical methods** like `agnes`, `diana`, and `mona` construct a hierarchy of clusterings, with the number of clusters ranging from one to the number of observations.

**Partitioning methods** like `pam`, `clara`, and `fanny` require that the number of clusters be given by the user.

## References

Kaufman, L. and Rousseeuw, P.J. (1990). *Finding Groups in Data: An Introduction to Cluster Analysis*. Wiley, New York.

Anja Struyf, Mia Hubert & Peter J. Rousseeuw (1996): Clustering in an Object-Oriented Environment. *Journal of Statistical Software*, **1**. <http://www.stat.ucla.edu/journals/jss/>

Struyf, A., Hubert, M. and Rousseeuw, P.J. (1997). Integrating Robust Clustering Techniques in S-PLUS, *Computational Statistics and Data Analysis*, **26**, 17–37.

Lance, G.N., and W.T. Williams (1966). A General Theory of Classifactory Sorting Strategies, I. Hierarchical Systems. *Computer J.* **9**, 373–380.

## See Also

`agnes.object`, `daisy`, `diana`, `dist`, `hclust`, `plot.agnes`, `twins.object`.

## Examples

```
data(votes.repub)
agn1 <- agnes(votes.repub, metric = "manhattan", stand = TRUE)
agn1
plot(agn1)

op <- par(mfrow=c(2,2))
agn2 <- agnes(daisy(votes.repub), diss = TRUE, method = "complete")
plot(agn2)
agnS <- agnes(votes.repub, method = "flexible", par.meth = 0.6)
plot(agnS)
par(op)

data(agriculture)
## Plot similar to Figure 7 in ref
## Not run: plot(agnes(agriculture), ask = TRUE)
```

## Description

The objects of class "agnes" represent an agglomerative hierarchical clustering of a dataset.



**Value**

A legitimate `agnes` object is a list with the following components:

<code>order</code>	a vector giving a permutation of the original observations to allow for plotting, in the sense that the branches of a clustering tree will not cross.
<code>order.lab</code>	a vector similar to <code>order</code> , but containing observation labels instead of observation numbers. This component is only available if the original observations were labelled.
<code>height</code>	a vector with the distances between merging clusters at the successive stages.
<code>ac</code>	the agglomerative coefficient, measuring the clustering structure of the dataset. For each observation $i$ , denote by $m(i)$ its dissimilarity to the first cluster it is merged with, divided by the dissimilarity of the merger in the final step of the algorithm. The <code>ac</code> is the average of all $1 - m(i)$ . It can also be seen as the average width (or the percentage filled) of the banner plot. Because <code>ac</code> grows with the number of observations, this measure should not be used to compare datasets of very different sizes.
<code>merge</code>	an $(n-1)$ by 2 matrix, where $n$ is the number of observations. Row $i$ of <code>merge</code> describes the merging of clusters at step $i$ of the clustering. If a number $j$ in the row is negative, then the single observation $ j $ is merged at this stage. If $j$ is positive, then the merger is with the cluster formed at stage $j$ of the algorithm.
<code>diss</code>	an object of class "dissimilarity" (see <a href="#">dissimilarity.object</a> ), representing the total dissimilarity matrix of the dataset.
<code>data</code>	a matrix containing the original or standardized measurements, depending on the <code>stand</code> option of the function <code>agnes</code> . If a dissimilarity matrix was given as input structure, then this component is not available.

**GENERATION**

This class of objects is returned from [agnes](#).

**METHODS**

The "agnes" class has methods for the following generic functions: `print`, `summary`, `plot`.

**INHERITANCE**

The class "agnes" inherits from "twins". Therefore, the generic functions [pltree](#) and [as.hclust](#) are available for agnes objects. After applying `as.hclust()`, all *its* methods are available, of course.

**See Also**

[agnes](#), [diana](#), [as.hclust](#), [hclust](#), [plot.agnes](#), [twins.object](#).

---

`agriculture`*European Union Agricultural Workforces*

---

### Description

Gross National Product (GNP) per capita and percentage of the population working in agriculture for each country belonging to the European Union in 1993.

### Usage

```
data(agriculture)
```

### Format

A data frame with 12 observations on 2 variables:

```
  [,1] x numeric per capita GNP
  [,2] y numeric percentage in agriculture
```

The row names of the data frame indicate the countries.

### Details

The data seem to show two clusters, the “more agricultural” one consisting of Greece, Portugal, Spain, and Ireland.

### Source

Eurostat (European Statistical Agency, 1994): *Cijfers en feiten: Een statistisch portret van de Europese Unie*.

### References

Anja Struyf, Mia Hubert & Peter J. Rousseeuw (1996): Clustering in an Object-Oriented Environment. *Journal of Statistical Software*, **1**. <http://www.stat.ucla.edu/journals/jss/>

### See Also

[agnes](#), [daisy](#), [diana](#).

### Examples

```
data(agriculture)

## Compute the dissimilarities using Euclidean metric and without
## standardization
daisy(agriculture, metric = "euclidean", stand = FALSE)

## 2nd plot is similar to Figure 3 in Struyf et al (1996)
plot(pam(agriculture, 2))

## Plot similar to Figure 7 in Struyf et al (1996)
```

```
## Not run: plot(agnes(agriculture), ask = TRUE)

## Plot similar to Figure 8 in Struyf et al (1996)
## Not run: plot(diana(agriculture), ask = TRUE)
```

---

animals

*Attributes of Animals*

---

### Description

This data set considers 6 binary attributes for 20 animals.

### Usage

```
data(animals)
```

### Format

A data frame with 20 observations on 6 variables:

[ , 1]	war	warm-blooded
[ , 2]	fly	can fly
[ , 3]	ver	vertebrate
[ , 4]	end	endangered
[ , 5]	gro	live in groups
[ , 6]	hai	have hair

All variables are encoded as 1 = 'no', 2 = 'yes'.

### Details

This dataset is useful for illustrating monothetic (only a single variable is used for each split) hierarchical clustering.

### Source

Leonard Kaufman and Peter J. Rousseeuw (1990): *Finding Groups in Data* (pp 297ff). New York: Wiley.

### References

Anja Struyf, Mia Hubert & Peter J. Rousseeuw (1996): Clustering in an Object-Oriented Environment. *Journal of Statistical Software*, **1**. <http://www.stat.ucla.edu/journals/jss/>

### Examples

```
data(animals)
apply(animals, 2, table) # simple overview
```

```

ma <- mona(animals)
ma
## Plot similar to Figure 10 in Struyf et al (1996)
plot(ma)

```

---

 bannerplot

*Plot Banner (of Hierarchical Clustering)*


---

## Description

Draws a “banner”, i.e. basically a horizontal `barplot` visualizing the (agglomerative or divisive) hierarchical clustering or an other binary dendrogram structure.

## Usage

```

bannerplot(x, w = rev(x$height), fromLeft = TRUE,
           main=NULL, sub=NULL, xlab = "Height", adj = 0,
           col = c(2, 0), border = 0, axes = TRUE, frame.plot = axes,
           rev.xax = !fromLeft, xax.pretty = TRUE,
           labels = NULL, nmax.lab = 35, max.strlen = 5,
           yax.do = axes && length(x$order) <= nmax.lab,
           yaxRight = fromLeft, y.mar = 2.4 + max.strlen/2.5, ...)

```

## Arguments

<code>x</code>	a list with components <code>order</code> , <code>order.lab</code> and <code>height</code> when <code>w</code> , the next argument is not specified.
<code>w</code>	non-negative numeric vector of bar widths.
<code>fromLeft</code>	logical, indicating if the banner is from the left or not.
<code>main, sub</code>	main and sub titles, see <code>title</code> .
<code>xlab</code>	x axis label (with ‘correct’ default e.g. for <code>plot.agnes</code> ).
<code>adj</code>	passed to <code>title(main, sub)</code> for string adjustment.
<code>col</code>	vector of length 2, for two horizontal segments.
<code>border</code>	color for bar border; now defaults to background (no border).
<code>axes</code>	logical indicating if axes (and labels) should be drawn at all.
<code>frame.plot</code>	logical indicating the banner should be framed; mainly used when <code>border = 0</code> (as per default).
<code>rev.xax</code>	logical indicating if the x axis should be reversed (as in <code>plot.diana</code> ).
<code>xax.pretty</code>	logical or integer indicating if <code>pretty()</code> should be used for the x axis. <code>xax.pretty = FALSE</code> is mainly for back compatibility.
<code>labels</code>	labels to use on y-axis; the default is constructed from <code>x</code> .
<code>nmax.lab</code>	integer indicating the number of labels which is considered too large for single-name labelling the banner plot.
<code>max.strlen</code>	positive integer giving the length to which strings are truncated in banner plot labeling.
<code>yax.do</code>	logical indicating if a y axis and banner labels should be drawn.

`yaxRight`      logical indicating if the y axis is on the right or left.  
`y.mar`            positive number specifying the margin width to use when banners are labeled (along a y-axis). The default adapts to the string width and optimally would also depend on the font.  
`...`              graphical parameters (see [par](#)) may also be supplied as arguments to this function.

**Note**

This is mainly a utility called from `plot.agnes`, `plot.diana` and `plot.mona`.

**Author(s)**

Martin Maechler (from original code of Kaufman and Rousseeuw).

**Examples**

```
data(agriculture)
bannerplot(agnes(agriculture), main = "Bannerplot")
```

---

`chorSub`
*Subset of C-horizon of Kola Data*


---

**Description**

This is a small rounded subset of the C-horizon data `chorizon` from package **mvoutlier**.

**Usage**

```
data(chorSub)
```

**Format**

A data frame with 61 observations on 10 variables. The variables contain scaled concentrations of chemical elements.

**Details**

This data set was produced from `chorizon` via these statements:

```
data(chorizon, package = "mvoutlier")
chorSub <- round(100*scale(chorizon[,101:110]))[190:250,]
storage.mode(chorSub) <- "integer"
colnames(chorSub) <- gsub("_.*", "", colnames(chorSub))
```

**Source**

Kola Project (1993-1998)

**See Also**

`chorizon` in package **mvoutlier** and other Kola data in the same package.

**Examples**

```
data(chorSub)
summary(chorSub)
pairs(chorSub, gap= .1)# some outliers
```

clara *Clustering Large Applications*

**Description**

Computes a "clara" object, a list representing a clustering of the data into k clusters.

**Usage**

```
clara(x, k, metric = "euclidean", stand = FALSE, samples = 5,
      sampsize = min(n, 40 + 2 * k), trace = 0, medoids.x = TRUE,
      keep.data = medoids.x, rngR = FALSE)
```

**Arguments**

- x data matrix or data frame, each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (NAs) are allowed.
- k integer, the number of clusters. It is required that  $0 < k < n$  where  $n$  is the number of observations (i.e.,  $n = \text{nrow}(x)$ ).
- metric character string specifying the metric to be used for calculating dissimilarities between observations. The currently available options are "euclidean" and "manhattan". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences.
- stand logical, indicating if the measurements in  $x$  are standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation.
- samples integer, number of samples to be drawn from the dataset.
- sampsize integer, number of observations in each sample. `sampsize` should be higher than the number of clusters ( $k$ ) and at most the number of observations ( $n = \text{nrow}(x)$ ).
- trace integer indicating a *trace level* for diagnostic output during the algorithm.
- medoids.x logical indicating if the medoids should be returned, identically to some rows of the input data  $x$ . If FALSE, `keep.data` must be false as well, and the medoid indices, i.e., row numbers of the medoids will still be returned (`i.med` component), and the algorithm saves space by needing one copy less of  $x$ .
- keep.data logical indicating if the (*scaled* if `stand` is true) data should be kept in the result.  
Setting this to FALSE saves memory (and hence time), but disables `clusplot()` ing of the result. Use `medoids.x = FALSE` to save even more memory.
- rngR logical indicating if R's random number generator should be used instead of the primitive clara()-builtin one. If true, this also means that each call to `clara()` returns a different result – though only slightly different in good situations.

## Details

`clara` is fully described in chapter 3 of Kaufman and Rousseeuw (1990). Compared to other partitioning methods such as `pam`, it can deal with much larger datasets. Internally, this is achieved by considering sub-datasets of fixed size (`sampsize`) such that the time and storage requirements become linear in  $n$  rather than quadratic.

Each sub-dataset is partitioned into  $k$  clusters using the same algorithm as in `pam`.

Once  $k$  representative objects have been selected from the sub-dataset, each observation of the entire dataset is assigned to the nearest medoid.

The sum of the dissimilarities of the observations to their closest medoid is used as a measure of the quality of the clustering. The sub-dataset for which the sum is minimal, is retained. A further analysis is carried out on the final partition.

Each sub-dataset is forced to contain the medoids obtained from the best sub-dataset until then. Randomly drawn observations are added to this set until `sampsize` has been reached.

## Value

an object of class "clara" representing the clustering. See `clara.object` for details.

## Note

By default, the random sampling is implemented with a *very* simple scheme (with period  $2^{16} = 65536$ ) inside the Fortran code, independently of R's random number generation, and as a matter of fact, deterministically. Alternatively, we recommend setting `rngR = TRUE` which uses R's random number generators. Then, `clara()` results are made reproducible typically by using `set.seed()` before calling `clara`.

The storage requirement of `clara` computation (for small  $k$ ) is about  $O(n \times p) + O(j^2)$  where  $j = \text{sampsize}$ , and  $(n, p) = \text{dim}(x)$ . The CPU computing time (again assuming small  $k$ ) is about  $O(n \times p \times j^2 \times N)$ , where  $N = \text{samples}$ .

For "small" datasets, the function `pam` can be used directly. What can be considered *small*, is really a function of available computing power, both memory (RAM) and speed. Originally (1990), "small" meant less than 100 observations; in 1997, the authors said "*small (say with fewer than 200 observations)*"; as of 2006, you can use `pam` with several thousand observations.

## Author(s)

Kaufman and Rousseeuw (see `agnes`), originally. All arguments from `trace` on, and most R documentation and all tests by Martin Maechler.

## See Also

`agnes` for background and references; `clara.object`, `pam`, `partition.object`, `plot.partition`.

## Examples

```
## generate 500 objects, divided into 2 clusters.
x <- rbind(cbind(rnorm(200,0,8), rnorm(200,0,8)),
           cbind(rnorm(300,50,8), rnorm(300,50,8)))
clarax <- clara(x, 2)
clarax
clarax$clusinfo
plot(clarax)
```

```
## `xclara' is an artificial data set with 3 clusters of 1000 bivariate
## objects each.
data(xclara)
(clx3 <- clara(xclara, 3))
## Plot similar to Figure 5 in Struyf et al (1996)
## Not run: plot(clx3, ask = TRUE)

## Try 100 times *different* random samples -- for reliability:
nSim <- 100
nCl <- 3 # = no.classes
set.seed(421) # (reproducibility)
cl <- matrix(NA, nrow(xclara), nSim)
for(i in 1:nSim)
  cl[,i] <- clara(xclara, nCl, medoids.x = FALSE, rngR = TRUE)$cluster
tcl <- apply(cl, 1, tabulate, nbins = nCl)
## those that are not always in same cluster (5 out of 3000 for this seed):
(iDoubt <- which(apply(tcl, 2, function(n) all(n < nSim))))
if(length(iDoubt)) { # (not for all seeds)
  tabD <- tcl[,iDoubt, drop=FALSE]
  dimnames(tabD) <- list(cluster = paste(1:nCl), obs = format(iDoubt))
  t(tabD) # how many times in which clusters
}
```

---

clara.object

*Clustering Large Applications (CLARA) Object*

---

### Description

The objects of class "clara" represent a partitioning of a large dataset into clusters and are typically returned from [clara](#).

### Value

A legitimate clara object is a list with the following components:

sample	labels or case numbers of the observations in the best sample, that is, the sample used by the clara algorithm for the final partition.
medoids	the medoids or representative objects of the clusters. It is a matrix with in each row the coordinates of one medoid. Possibly NULL, namely when the object resulted from clara(*, medoids.x=FALSE). Use the following i.med in that case.
i.med	the <i>indices</i> of the medoids above: medoids <- x[i.med,] where x is the original data matrix in clara(x,*).
clustering	the clustering vector, see <a href="#">partition.object</a> .
objective	the objective function for the final clustering of the entire dataset.
clusinfo	matrix, each row gives numerical information for one cluster. These are the cardinality of the cluster (number of observations), the maximal and average dissimilarity between the observations in the cluster and the cluster's medoid. The last column is the maximal dissimilarity between the observations in the



	cluster and the cluster's medoid, divided by the minimal dissimilarity between the cluster's medoid and the medoid of any other cluster. If this ratio is small, the cluster is well-separated from the other clusters.
diss	dissimilarity (maybe NULL), see <a href="#">partition.object</a> .
silinfo	list with silhouette width information for the best sample, see <a href="#">partition.object</a> .
call	generating call, see <a href="#">partition.object</a> .
data	matrix, possibly standardized, or NULL, see <a href="#">partition.object</a> .

### Methods, Inheritance

The "clara" class has methods for the following generic functions: `print`, `summary`.

The class "clara" inherits from "partition". Therefore, the generic functions `plot` and `clusplot` can be used on a clara object.

### See Also

[clara](#), [dissimilarity.object](#), [partition.object](#), [plot.partition](#).

---

clusplot

*Cluster Plot - Generic Function*

---

### Description

Draws a 2-dimensional "clusplot" on the current graphics device. This is a generic function with a default and `partition` method.

### Usage

```
clusplot(x, ...)
```

### Arguments

<code>x</code>	an R object.
<code>...</code>	additional arguments for <a href="#">methods</a> . Graphical parameters (see <a href="#">par</a> ) may also be supplied as arguments to this function.

### Side Effects

a 2-dimensional clusplot is created on the current graphics device.

### See Also

(for references and examples) [clusplot.default](#), [clusplot.partition](#), [partition.object](#), [pam](#), [fanny](#), [clara](#).

---

clusplot.default     *Bivariate Cluster Plot (clusplot) Default Method*


---

### Description

Creates a bivariate plot visualizing a partition (clustering) of the data. All observation are represented by points in the plot, using principal components or multidimensional scaling. Around each cluster an ellipse is drawn.

### Usage

```
## Default S3 method:
clusplot(x, clus, diss = FALSE, cor = TRUE, stand = FALSE,
         lines = 2, shade = FALSE, color = FALSE,
         labels= 0, plotchar = TRUE,
         col.p = "dark green", col.txt = col.p,
         col.clus = if(color) c(2, 4, 6, 3) else 5,
         span = TRUE, xlim = NULL, ylim = NULL,
         main = paste("CLUSPLOT(", deparse(substitute(x)), ")"),
         sub = paste("These two components explain",
                    round(100 * var.dec, digits = 2), "% of the point variability."),
         verbose = getOption("verbose"),
         ...)
```

### Arguments

<code>x</code>	matrix or data frame, or dissimilarity matrix, depending on the value of the <code>diss</code> argument.  In case of a matrix (alike), each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (NAs) are allowed. They are replaced by the median of the corresponding variable. When some variables or some observations contain only missing values, the function stops with a warning message.  In case of a dissimilarity matrix, <code>x</code> is the output of <code>daisy</code> or <code>dist</code> or a symmetric matrix. Also, a vector of length $n * (n - 1) / 2$ is allowed (where $n$ is the number of observations), and will be interpreted in the same way as the output of the above-mentioned functions. Missing values (NAs) are not allowed.
<code>clus</code>	a vector of length $n$ representing a clustering of <code>x</code> . For each observation the vector lists the number or name of the cluster to which it has been assigned. <code>clus</code> is often the clustering component of the output of <code>pam</code> , <code>fanny</code> or <code>clara</code> .
<code>diss</code>	logical indicating if <code>x</code> will be considered as a dissimilarity matrix or a matrix of observations by variables (see <code>x</code> argument above).
<code>cor</code>	logical flag, only used when working with a data matrix ( <code>diss = FALSE</code> ). If TRUE, then the variables are scaled to unit variance.
<code>stand</code>	logical flag: if true, then the representations of the $n$ observations in the 2-dimensional plot are standardized.
<code>lines</code>	integer out of 0, 1, 2, used to obtain an idea of the distances between ellipses. The distance between two ellipses E1 and E2 is measured along the line connecting the centers $m1$ and $m2$ of the two ellipses.

In case E1 and E2 overlap on the line through  $m1$  and  $m2$ , no line is drawn. Otherwise, the result depends on the value of `lines`: If

**lines = 0**, no distance lines will appear on the plot;  
**lines = 1**, the line segment between  $m1$  and  $m2$  is drawn;  
**lines = 2**, a line segment between the boundaries of E1 and E2 is drawn (along the line connecting  $m1$  and  $m2$ ).

shade	logical flag: if TRUE, then the ellipses are shaded in relation to their density. The density is the number of points in the cluster divided by the area of the ellipse.
color	logical flag: if TRUE, then the ellipses are colored with respect to their density. With increasing density, the colors are light blue, light green, red and purple. To see these colors on the graphics device, an appropriate color scheme should be selected (we recommend a white background).
labels	integer code, currently one of 0,1,2,3,4 and 5. If <b>labels= 0</b> , no labels are placed in the plot; <b>labels= 1</b> , points and ellipses can be identified in the plot (see <code>identify</code> ); <b>labels= 2</b> , all points and ellipses are labelled in the plot; <b>labels= 3</b> , only the points are labelled in the plot; <b>labels= 4</b> , only the ellipses are labelled in the plot. <b>labels= 5</b> , the ellipses are labelled in the plot, and points can be identified. The levels of the vector <code>clus</code> are taken as labels for the clusters. The labels of the points are the rownames of <code>x</code> if <code>x</code> is matrix like. Otherwise ( <code>diss = TRUE</code> ), <code>x</code> is a vector, point labels can be attached to <code>x</code> as a "Labels" attribute ( <code>attr(x, "Labels")</code> ), as is done for the output of <code>daisy</code> . A possible <code>names</code> attribute of <code>clus</code> will not be taken into account.
plotchar	logical flag: if TRUE, then the plotting symbols differ for points belonging to different clusters.
span	logical flag: if TRUE, then each cluster is represented by the ellipse with smallest area containing all its points. (This is a special case of the minimum volume ellipsoid.) If FALSE, the ellipse is based on the mean and covariance matrix of the same points. While this is faster to compute, it often yields a much larger ellipse. There are also some special cases: When a cluster consists of only one point, a tiny circle is drawn around it. When the points of a cluster fall on a straight line, <code>span=FALSE</code> draws a narrow ellipse around it and <code>span=TRUE</code> gives the exact line segment.
col.p	color code(s) used for the observation points.
col.txt	color code(s) used for the labels (if <code>labels &gt;= 2</code> ).
col.clus	color code for the ellipses (and their labels); only one if <code>color</code> is false (as per default).
xlim, ylim	numeric vectors of length 2, giving the x- and y- ranges as in <code>plot.default</code> .
main	main title for the plot; by default, one is constructed.
sub	sub title for the plot; by default, one is constructed.
verbose	a logical indicating, if there should be extra diagnostic output; mainly for 'debugging'.
...	Further graphical parameters may also be supplied, see <code>par</code> .

## Details

clusplot uses the functions `princomp` and `cmdscale`. These functions are data reduction techniques. They will represent the data in a bivariate plot. Ellipses are then drawn to indicate the clusters. The further layout of the plot is determined by the optional arguments.

## Value

An invisible list with components:

Distances	When <code>lines</code> is 1 or 2 we obtain a $k$ by $k$ matrix ( $k$ is the number of clusters). The element in $[i, j]$ is the distance between ellipse $i$ and ellipse $j$ . If <code>lines = 0</code> , then the value of this component is NA.
Shading	A vector of length $k$ (where $k$ is the number of clusters), containing the amount of shading per cluster. Let $y$ be a vector where element $i$ is the ratio between the number of points in cluster $i$ and the area of ellipse $i$ . When the cluster $i$ is a line segment, $y[i]$ and the density of the cluster are set to NA. Let $z$ be the sum of all the elements of $y$ without the NAs. Then we put <code>shading = y/z * 37 + 3</code> .

## Side Effects

a visual display of the clustering is plotted on the current graphics device.

## Note

When we have 4 or fewer clusters, then the `color=TRUE` gives every cluster a different color. When there are more than 4 clusters, clusplot uses the function `pam` to cluster the densities into 4 groups such that ellipses with nearly the same density get the same color. `col.clus` specifies the colors used.

The `col.p` and `col.txt` arguments, added for R, are recycled to have length the number of observations. If `col.p` has more than one value, using `color = TRUE` can be confusing because of a mix of point and ellipse colors.

## References

Pison, G., Struyf, A. and Rousseeuw, P.J. (1999) Displaying a Clustering with CLUSPLOT, *Computational Statistics and Data Analysis*, **30**, 381–392.

A version of this is available as technical report from <http://www.agoras.ua.ac.be/abstract/Disclu99.htm>

Kaufman, L. and Rousseeuw, P.J. (1990). *Finding Groups in Data: An Introduction to Cluster Analysis*. Wiley, New York.

Struyf, A., Hubert, M. and Rousseeuw, P.J. (1997). Integrating Robust Clustering Techniques in S-PLUS, *Computational Statistics and Data Analysis*, **26**, 17-37.

## See Also

`princomp`, `cmdscale`, `pam`, `clara`, `daisy`, `par`, `identify`, `cov.mve`, `clusplot.partition`.

**Examples**

```
## plotting votes.diss(dissimilarity) in a bivariate plot and
## partitioning into 2 clusters
data(votes.repub)
votes.diss <- daisy(votes.repub)
votes.clus <- pam(votes.diss, 2, diss = TRUE)$clustering
clusplot(votes.diss, votes.clus, diss = TRUE, shade = TRUE)
clusplot(votes.diss, votes.clus, diss = TRUE,
         col.p = votes.clus, labels = 4)# color points and label ellipses

clusplot(votes.diss, votes.clus, diss = TRUE, span = FALSE)# simple ellipses

if(interactive()) { # uses identify() *interactively* :
  clusplot(votes.diss, votes.clus, diss = TRUE, shade = TRUE, labels = 1)
  clusplot(votes.diss, votes.clus, diss = TRUE, labels = 5)# ident. only points
}

## plotting iris (data frame) in a 2-dimensional plot and partitioning
## into 3 clusters.
data(iris)
iris.x <- iris[, 1:4]
cl3 <- pam(iris.x, 3)$clustering
op <- par(mfrow= c(2,2))
clusplot(iris.x, cl3, color = TRUE)
U <- par("usr")
## zoom in :
rect(0,-1, 2,1, border = "orange", lwd=2)
clusplot(iris.x, cl3, color = TRUE, xlim = c(0,2), ylim = c(-1,1))
box(col="orange",lwd=2); mtext("sub region", font = 4, cex = 2)
## or zoom out :
clusplot(iris.x, cl3, color = TRUE, xlim = c(-4,4), ylim = c(-4,4))
mtext("`super' region", font = 4, cex = 2)
rect(U[1],U[3], U[2],U[4], lwd=2, lty = 3)

# reset graphics
par(op)
```

---

clusplot.partition *Bivariate Clusplot of a Partitioning Object*

---

**Description**

Clusplot (Clustering Plot) method for an object of class partition.

**Usage**

```
## S3 method for class 'partition':
clusplot(x, main = NULL, dist = NULL, ...)
```

**Arguments**

x                    an object of class "partition", e.g. created by the functions [pam](#), [clara](#), or [fanny](#).

main	title for the plot; when NULL (by default), a title is constructed, using <code>x\$call</code> .
dist	when <code>x</code> does not have a <code>diss</code> nor a data component, e.g., for <code>pam(dist(*), keep.diss=FALSE)</code> , <code>dist</code> must specify the dissimilarity for the clusplot.
...	all optional arguments available for the <code>clusplot.default</code> function (except for the <code>diss</code> one) may also be supplied to this function. Graphical parameters (see <code>par</code> ) may also be supplied as arguments to this function.

## Details

This `clusplot.partition()` method relies on `clusplot.default`.

If the clustering algorithms `pam`, `fanny` and `clara` are applied to a data matrix of observations-by-variables then a clusplot of the resulting clustering can always be drawn. When the data matrix contains missing values and the clustering is performed with `pam` or `fanny`, the dissimilarity matrix will be given as input to `clusplot`. When the clustering algorithm `clara` was applied to a data matrix with NAs then `clusplot` will replace the missing values as described in `clusplot.default`, because a dissimilarity matrix is not available.

## Value

An invisible list with components

Distances	When option <code>lines</code> is 1 or 2 we obtain a <code>k</code> by <code>k</code> matrix ( <code>k</code> is the number of clusters). The element at row <code>j</code> and column <code>s</code> is the distance between ellipse <code>j</code> and ellipse <code>s</code> . If <code>lines=0</code> , then the value of this component is NA.
Shading	A vector of length <code>k</code> (where <code>k</code> is the number of clusters), containing the amount of shading per cluster. Let <code>y</code> be a vector where element <code>i</code> is the ratio between the number of objects in cluster <code>i</code> and the area of ellipse <code>i</code> . When the cluster <code>i</code> is a line segment, <code>y[i]</code> and the density of the cluster are set to NA. Let <code>z</code> be the sum of all the elements of <code>y</code> without the NAs. Then we put <code>shading = y/z * 37 + 3</code> .

## See Also

`clusplot.default` for references; `partition.object`, `pam`, `pam.object`, `clara`, `clara.object`, `fanny`, `fanny.object`, `par`.

## Examples

```
## generate 25 objects, divided into 2 clusters.
x <- rbind(cbind(rnorm(10,0,0.5), rnorm(10,0,0.5)),
           cbind(rnorm(15,5,0.5), rnorm(15,5,0.5)))
clusplot(pam(x, 2))
## add noise, and try again :
x4 <- cbind(x, rnorm(25), rnorm(25))
clusplot(pam(x4, 2))
```

coef.hclust

*Agglomerative Coefficient for 'hclust' Objects***Description**

Computes the “agglomerative coefficient”, measuring the clustering structure of the dataset.

For each observation  $i$ , denote by  $m(i)$  its dissimilarity to the first cluster it is merged with, divided by the dissimilarity of the merger in the final step of the algorithm. The agglomerative coefficient is the average of all  $1 - m(i)$ . It can also be seen as the average width (or the percentage filled) of the banner plot.

Because it grows with the number of observations, this measure should not be used to compare datasets of very different sizes.

**Usage**

```
coef.hclust(object, ...)
## S3 method for class 'hclust':
coef(object, ...)
## S3 method for class 'twins':
coef(object, ...)
```

**Arguments**

object	an object of class "hclust" or "twins", i.e., typically the result of <code>hclust(.)</code> , <code>agnes(.)</code> , or <code>diana(.)</code> . Since <code>coef.hclust</code> only uses <code>object\$heights</code> , and <code>object\$merge</code> , <code>object</code> can be any list-like object with appropriate <code>merge</code> and <code>heights</code> components.
...	currently unused potential further arguments

**Value**

a number specifying the *agglomerative* (or *divisive* for `diana` objects) coefficient as defined by Kaufman and Rousseeuw, see `agnes.object` \$ `ac` or `diana.object` \$ `dc`.

**Examples**

```
data(agriculture)
aa <- agnes(agriculture)
coef(aa) # really just extracts aa$ac
coef(as.hclust(aa)) # recomputes
```

daisy

*Dissimilarity Matrix Calculation***Description**

Compute all the pairwise dissimilarities (distances) between observations in the data set. The original variables may be of mixed types.

**Usage**

```
daisy(x, metric = c("euclidean", "manhattan", "gower"),
      stand = FALSE, type = list())
```

**Arguments**

- |                     |   |
|---------------------|---|
| <code>x</code>      | numeric matrix or data frame. Dissimilarities will be computed between the rows of <code>x</code> . Columns of mode <code>numeric</code> (i.e. all columns when <code>x</code> is a matrix) will be recognized as interval scaled variables, columns of class <code>factor</code> will be recognized as nominal variables, and columns of class <code>ordered</code> will be recognized as ordinal variables. Other variable types should be specified with the <code>type</code> argument. Missing values (NAs) are allowed.   |
| <code>metric</code> | character string specifying the metric to be used. The currently available options are "euclidean" (the default), "manhattan" and "gower". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences.<br><br>"Gower's distance" is chosen by metric "gower" or automatically if some columns of <code>x</code> are not numeric. Also known as Gower's coefficient (1971), expressed as a dissimilarity, this implies that a particular standardisation will be applied to each variable, and the "distance" between two units is the sum of all the variable-specific distances, see the details section. |
| <code>stand</code>  | logical flag: if TRUE, then the measurements in <code>x</code> are standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation.<br><br>If not all columns of <code>x</code> are numeric, <code>stand</code> will be ignored and Gower's standardization (based on the <a href="#">range</a> ) will be applied in any case, see argument <code>metric</code> , above, and the details section.  |
| <code>type</code>   | list for specifying some (or all) of the types of the variables (columns) in <code>x</code> . The list may contain the following components: "ordratio" (ratio scaled variables to be treated as ordinal variables), "logratio" (ratio scaled variables that must be logarithmically transformed), "asymm" (asymmetric binary) and "symm" (symmetric binary variables). Each component's value is a vector, containing the names or the numbers of the corresponding columns of <code>x</code> . Variables not mentioned in the <code>type</code> list are interpreted as usual (see argument <code>x</code> ).   |

**Details**

`daisy` is fully described in chapter 1 of Kaufman and Rousseeuw (1990). Compared to `dist` whose input must be numeric variables, the main feature of `daisy` is its ability to handle other



variable types as well (e.g. nominal, ordinal, (a)symmetric binary) even when different types occur in the same data set.

The handling of nominal, ordinal, and (a)symmetric binary data is achieved by using the general dissimilarity coefficient of Gower (1971). If `x` contains any columns of these data-types, both arguments `metric` and `stand` will be ignored and Gower's coefficient will be used as the metric. This can also be activated for purely numeric data by `metric = "gower"`. With that, each variable (column) is first standardized by dividing each entry by the range of the corresponding variable.

Note that setting the type to `symm` (symmetric binary) gives the same dissimilarities as using `nominal` (which is chosen for non-ordered factors) only when no missing values are present, and more efficiently.

Note that `daisy` now gives a warning when 2-valued numerical variables don't have an explicit `type` specified, because the reference authors recommend to consider using `asymm`.

In the `daisy` algorithm, missing values in a row of `x` are not included in the dissimilarities involving that row. There are two main cases,

1. If all variables are interval scaled, the metric is "euclidean", and `ng` is the number of columns in which neither row `i` and `j` have NAs, then the dissimilarity `d(i,j)` returned is  $\sqrt{\text{ncol}(x)/ng}$  times the Euclidean distance between the two vectors of length `ng` shortened to exclude NAs. The rule is similar for the "manhattan" metric, except that the coefficient is  $\text{ncol}(x)/ng$ . If `ng` is zero, the dissimilarity is NA.

2. When some variables have a type other than interval scaled, the dissimilarity between two rows is the weighted sum of the contributions of each variable.

The weight becomes zero when that variable is missing in either or both rows, or when the variable is asymmetric binary and both values are zero. In all other situations, the weight of the variable is 1.

The contribution of a nominal or binary variable to the total dissimilarity is 0 if both values are equal, 1 otherwise. The contribution of other variables is the absolute difference of both values, divided by the total range of that variable. Ordinal variables are first converted to ranks.

If `nok` is the number of nonzero weights, the dissimilarity is multiplied by the factor  $1/nok$  and thus ranges between 0 and 1. If `nok = 0`, the dissimilarity is set to NA.

## Value

an object of class "dissimilarity" containing the dissimilarities among the rows of `x`. This is typically the input for the functions `pam`, `fanny`, `agnes` or `diana`. For more details, see [dissimilarity.object](#).

## Background

Dissimilarities are used as inputs to cluster analysis and multidimensional scaling. The choice of metric may have a large impact.

## References

Gower, J. C. (1971) A general coefficient of similarity and some of its properties, *Biometrics* **27**, 857–874.

Kaufman, L. and Rousseeuw, P.J. (1990) *Finding Groups in Data: An Introduction to Cluster Analysis*. Wiley, New York.

Struyf, A., Hubert, M. and Rousseeuw, P.J. (1997) Integrating Robust Clustering Techniques in S-PLUS, *Computational Statistics and Data Analysis* **26**, 17–37.

**See Also**

[dissimilarity.object](#), [dist](#), [pam](#), [fanny](#), [clara](#), [agnes](#), [diana](#).

**Examples**

```
data(agriculture)
## Example 1 in ref:
## Dissimilarities using Euclidean metric and without standardization
d.agr <- daisy(agriculture, metric = "euclidean", stand = FALSE)
d.agr
as.matrix(d.agr)[,"DK"] # via as.matrix.dist(.)
## compare with
as.matrix(daisy(agriculture, metric = "gower"))

data(flower)
## Example 2 in ref
summary(df11 <- daisy(flower, type = list(asymm = 3)))
summary(df12 <- daisy(flower, type = list(asymm = c(1, 3), ordratio = 7)))
## this failed earlier:
summary(df13 <- daisy(flower,
  type = list(asymm = c("V1", "V3"), symm= 2,
    ordratio= 7, logratio= 8)))
```

---

diana

*Divisive ANAlysis Clustering*

---

**Description**

Computes a divisive hierarchical clustering of the dataset returning an object of class `diana`.

**Usage**

```
diana(x, diss = inherits(x, "dist"), metric = "euclidean", stand = FALSE,
  keep.diss = n < 100, keep.data = !diss)
```

**Arguments**

<code>x</code>	<p>data matrix or data frame, or dissimilarity matrix or object, depending on the value of the <code>diss</code> argument.</p> <p>In case of a matrix or data frame, each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (NAs) <i>are</i> allowed.</p> <p>In case of a dissimilarity matrix, <code>x</code> is typically the output of <a href="#">daisy</a> or <a href="#">dist</a>. Also a vector of length <math>n*(n-1)/2</math> is allowed (where <math>n</math> is the number of observations), and will be interpreted in the same way as the output of the above-mentioned functions. Missing values (NAs) are <i>not</i> allowed.</p>
<code>diss</code>	<p>logical flag: if TRUE (default for <code>dist</code> or <code>dissimilarity</code> objects), then <code>x</code> will be considered as a dissimilarity matrix. If FALSE, then <code>x</code> will be considered as a matrix of observations by variables.</p>

<code>metric</code>	character string specifying the metric to be used for calculating dissimilarities between observations. The currently available options are "euclidean" and "manhattan". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences. If <code>x</code> is already a dissimilarity matrix, then this argument will be ignored.
<code>stand</code>	logical; if true, the measurements in <code>x</code> are standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable's mean value and dividing by the variable's mean absolute deviation. If <code>x</code> is already a dissimilarity matrix, then this argument will be ignored.
<code>keep.diss, keep.data</code>	logicals indicating if the dissimilarities and/or input data <code>x</code> should be kept in the result. Setting these to <code>FALSE</code> can give much smaller results and hence even save memory allocation <i>time</i> .

### Details

`diana` is fully described in chapter 6 of Kaufman and Rousseeuw (1990). It is probably unique in computing a divisive hierarchy, whereas most other software for hierarchical clustering is agglomerative. Moreover, `diana` provides (a) the divisive coefficient (see `diana.object`) which measures the amount of clustering structure found; and (b) the banner, a novel graphical display (see `plot.diana`).

The `diana`-algorithm constructs a hierarchy of clusterings, starting with one large cluster containing all  $n$  observations. Clusters are divided until each cluster contains only a single observation.

At each stage, the cluster with the largest diameter is selected. (The diameter of a cluster is the largest dissimilarity between any two of its observations.)

To divide the selected cluster, the algorithm first looks for its most disparate observation (i.e., which has the largest average dissimilarity to the other observations of the selected cluster). This observation initiates the "splinter group". In subsequent steps, the algorithm reassigns observations that are closer to the "splinter group" than to the "old party". The result is a division of the selected cluster into two new clusters.

### Value

an object of class "diana" representing the clustering; this class has methods for the following generic functions: `print`, `summary`, `plot`.

Further, the class "diana" inherits from "twins". Therefore, the generic function `pltree` can be used on a `diana` object, and an `as.hclust` method is available.

A legitimate `diana` object is a list with the following components:

<code>order</code>	a vector giving a permutation of the original observations to allow for plotting, in the sense that the branches of a clustering tree will not cross.
<code>order.lab</code>	a vector similar to <code>order</code> , but containing observation labels instead of observation numbers. This component is only available if the original observations were labelled.
<code>height</code>	a vector with the diameters of the clusters prior to splitting.
<code>dc</code>	the divisive coefficient, measuring the clustering structure of the dataset. For each observation $i$ , denote by $d(i)$ the diameter of the last cluster to which it belongs (before being split off as a single observation), divided by the diameter of the whole dataset. The <code>dc</code> is the average of all $1 - d(i)$ . It can also be

	seen as the average width (or the percentage filled) of the banner plot. Because <code>dc</code> grows with the number of observations, this measure should not be used to compare datasets of very different sizes.
<code>merge</code>	an (n-1) by 2 matrix, where n is the number of observations. Row <i>i</i> of <code>merge</code> describes the split at step n-i of the clustering. If a number <i>j</i> in row <i>r</i> is negative, then the single observation $ j $ is split off at stage n-r. If <i>j</i> is positive, then the cluster that will be splitted at stage n-j (described by row <i>j</i> ), is split off at stage n-r.
<code>diss</code>	an object of class "dissimilarity", representing the total dissimilarity matrix of the dataset.
<code>data</code>	a matrix containing the original or standardized measurements, depending on the <code>stand</code> option of the function <code>agnes</code> . If a dissimilarity matrix was given as input structure, then this component is not available.

**See Also**

`agnes` also for background and references; `cutree` (and `as.hclust`) for grouping extraction; `daisy`, `dist`, `plot.diana`, `twins.object`.

**Examples**

```
data(votes.repub)
dv <- diana(votes.repub, metric = "manhattan", stand = TRUE)
print(dv)
plot(dv)

## Cut into 2 groups:
dv2 <- cutree(as.hclust(dv), k = 2)
table(dv2) # 8 and 42 group members
rownames(votes.repub)[dv2 == 1]

## For two groups, does the metric matter ?
dv0 <- diana(votes.repub, stand = TRUE) # default: Euclidean
dv.2 <- cutree(as.hclust(dv0), k = 2)
table(dv2 == dv.2) ## identical group assignments

data(agriculture)
## Plot similar to Figure 8 in ref
## Not run: plot(diana(agriculture), ask = TRUE)
```

---

dissimilarity.object

*Dissimilarity Matrix Object*

---

**Description**

Objects of class "dissimilarity" representing the dissimilarity matrix of a dataset.

**Value**

The dissimilarity matrix is symmetric, and hence its lower triangle (column wise) is represented as a vector to save storage space. If the object, is called `do`, and `n` the number of observations, i.e., `n <- attr(do, "Size")`, then for  $i < j \leq n$ , the dissimilarity between (row)  $i$  and  $j$  is `do[n*(i-1) - i*(i-1)/2 + j-i]`. The length of the vector is  $n*(n-1)/2$ , i.e., of order  $n^2$ .

"dissimilarity" objects also inherit from class `dist` and can use `dist` methods, in particular, `as.matrix`, such that  $d_{ij}$  from above is just `as.matrix(do)[i, j]`.

The object has the following attributes:

Size	the number of observations in the dataset.
Metric	the metric used for calculating the dissimilarities. Possible values are "euclidean", "manhattan", "mixed" (if variables of different types were present in the dataset), and "unspecified".
Labels	optionally, contains the labels, if any, of the observations of the dataset.
NA.message	optionally, if a dissimilarity could not be computed, because of too many missing values for some observations of the dataset.
Types	when a mixed metric was used, the types for each variable as one-letter codes (as in the book, e.g. p.54): <ul style="list-style-type: none"> <li><b>A</b> Asymmetric binary</li> <li><b>S</b> Symmetric binary</li> <li><b>N</b> Nominal (factor)</li> <li><b>O</b> Ordinal (ordered factor)</li> <li><b>I</b> Interval scaled (numeric)</li> <li><b>T</b> raTio to be log transformed (positive numeric)</li> </ul>
	.

**GENERATION**

`daisy` returns this class of objects. Also the functions `pam`, `clara`, `fanny`, `agnes`, and `diana` return a `dissimilarity` object, as one component of their return objects.

**METHODS**

The "dissimilarity" class has methods for the following generic functions: `print`, `summary`.

**See Also**

`daisy`, `dist`, `pam`, `clara`, `fanny`, `agnes`, `diana`.

ellipsoidhull

Compute the Ellipsoid Hull or Spanning Ellipsoid of a Point Set

**Description**

Compute the “ellipsoid hull” or “spanning ellipsoid”, i.e. the ellipsoid of minimal volume (‘area’ in 2D) such that all given points lie just inside or on the boundary of the ellipsoid.

**Usage**

```
ellipsoidhull(x, tol=0.01, maxit=5000,
             ret.wt = FALSE, ret.sqdist = FALSE, ret.pr = FALSE)
## S3 method for class 'ellipsoid':
print(x, digits = max(1, getOption("digits") - 2), ...)
```

**Arguments**

`x` the  $n$   $p$ -dimensional points as numeric  $n \times p$  matrix.

`tol` convergence tolerance for Titterington’s algorithm. Setting this to much smaller values may drastically increase the number of iterations needed, and you may want to increase `maxit` as well.

`maxit` integer giving the maximal number of iteration steps for the algorithm.

`ret.wt`, `ret.sqdist`, `ret.pr` logicals indicating if additional information should be returned, `ret.wt` specifying the *weights*, `ret.sqdist` the *squared distances* and `ret.pr` the final **probabilities** in the algorithms.

`digits, ...` the usual arguments to `print` methods.

**Details**

The “spanning ellipsoid” algorithm is said to stem from Titterington(1976), in Pison et al(1999) who use it for `clusplot.default`.

The problem can be seen as a special case of the “Min.Vol.” ellipsoid of which a more flexible and general implementation is `cov.mve` in the MASS package.

**Value**

an object of class "ellipsoid", basically a `list` with several components, comprising at least

`cov`  $p \times p$  covariance matrix description the ellipsoid.

`loc`  $p$ -dimensional location of the ellipsoid center.

`d2` average squared radius. Further,  $d2 = t^2$ , where  $t$  is “the value of a t-statistic on the ellipse boundary” (from `ellipse` in the **ellipse** package), and hence, more usefully,  $d2 = qchisq(alpha, df = p)$ , where `alpha` is the confidence level for  $p$ -variate normally distributed data with location and covariance `loc` and `cov` to lie inside the ellipsoid.

`wt` the vector of weights iff `ret.wt` was true.

`sqdist` the vector of squared distances iff `ret.sqdist` was true.

`prob` the vector of algorithm probabilities iff `ret.pr` was true.

<code>it</code>	number of iterations used.
<code>tol, maxit</code>	just the input argument, see above.
<code>eps</code>	the achieved tolerance which is the maximal squared radius minus $p$ .
<code>ierr</code>	error code as from the algorithm; 0 means <i>ok</i> .
<code>conv</code>	logical indicating if the converged. This is defined as <code>it &lt; maxit &amp;&amp; ierr == 0</code> .

### Author(s)

Martin Maechler did the present class implementation; Rousseeuw et al did the underlying code.

### References

Pison, G., Struyf, A. and Rousseeuw, P.J. (1999) Displaying a Clustering with CLUSPLOT, *Computational Statistics and Data Analysis*, **30**, 381–392.

A version of this is available as technical report from <http://www.agoras.ua.ac.be/abstract/Disclu99.htm>

D.M. Titterton (1976) Algorithms for computing D-optimal design on finite design spaces. In *Proc. of the 1976 Conf. on Information Science and Systems*, 213–216; John Hopkins University.

### See Also

`predict.ellipsoid` which is also the `predict` method for `ellipsoid` objects. `volume.ellipsoid` for an example of ‘manual’ `ellipsoid` object construction; further `ellipse` from package **ellipse** and `ellipsePoints` from package **sfsmisc**. `chull` for the convex hull, `clusplot` which makes use of this; `cov.mve`.

### Examples

```
x <- rnorm(100)
xy <- unname(cbind(x, rnorm(100) + 2*x + 10))
exy <- ellipsoidhull(xy)
exy # >> calling print.ellipsoid()

plot(xy)
lines(predict(exy))
points(rbind(exy$loc), col = "red", cex = 3, pch = 13)

exy <- ellipsoidhull(xy, tol = 1e-7, ret.wt = TRUE, ret.sq = TRUE)
str(exy) # had small `tol`, hence many iterations
(ii <- which(zapsmall(exy $ wt) > 1e-6)) # only about 4 to 6 points
round(exy$wt[ii], 3); sum(exy$wt[ii]) # sum to 1
```

### Description

Computes a fuzzy clustering of the data into  $k$  clusters.

**Usage**

```
fanny(x, k, diss = inherits(x, "dist"), memb.exp = 2,
      metric = c("euclidean", "manhattan", "SqEuclidean"),
      stand = FALSE, iniMem.p = NULL, cluster.only = FALSE,
      keep.diss = !diss && !cluster.only && n < 100,
      keep.data = !diss && !cluster.only,
      maxit = 500, tol = 1e-15, trace.lev = 0)
```

**Arguments**

- |                      |  |
|----------------------|--|
| x                    | data matrix or data frame, or dissimilarity matrix, depending on the value of the <code>diss</code> argument.<br><br>In case of a matrix or data frame, each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (NAs) are allowed.<br><br>In case of a dissimilarity matrix, x is typically the output of <code>daisy</code> or <code>dist</code> . Also a vector of length $n*(n-1)/2$ is allowed (where n is the number of observations), and will be interpreted in the same way as the output of the above-mentioned functions. Missing values (NAs) are not allowed. |
| k                    | integer giving the desired number of clusters. It is required that $0 < k < n/2$ where n is the number of observations.  |
| diss                 | logical flag: if TRUE (default for <code>dist</code> or <code>dissimilarity</code> objects), then x is assumed to be a dissimilarity matrix. If FALSE, then x is treated as a matrix of observations by variables.   |
| memb.exp             | number r strictly larger than 1 specifying the <i>membership exponent</i> used in the fit criterion; see the ‘Details’ below. Default: 2 which used to be hardwired inside FANNY.  |
| metric               | character string specifying the metric to be used for calculating dissimilarities between observations. Options are "euclidean" (default), "manhattan", and "SqEuclidean". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences, and "SqEuclidean", the <i>squared</i> euclidean distances are sum-of-squares of differences. Using this last option is equivalent (but somewhat slower) to computing so called “fuzzy C-means”.<br>If x is already a dissimilarity matrix, then this argument will be ignored.   |
| stand                | logical; if true, the measurements in x are standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable’s mean value and dividing by the variable’s mean absolute deviation. If x is already a dissimilarity matrix, then this argument will be ignored.  |
| iniMem.p             | numeric $n \times k$ matrix or NULL (by default); can be used to specify a starting membership matrix, i.e., a matrix of non-negative numbers, each row summing to one.  |
| cluster.only         | logical; if true, no silhouette information will be computed and returned, see details.  |
| keep.diss, keep.data | logicals indicating if the dissimilarities and/or input data x should be kept in the result. Setting these to FALSE can give smaller results and hence also save memory allocation <i>time</i> .   |



<code>maxit, tol</code>	maximal number of iterations and default tolerance for convergence (relative convergence of the fit criterion) for the FANNY algorithm. The defaults <code>maxit = 500</code> and <code>tol = 1e-15</code> used to be hardwired inside the algorithm.
<code>trace.lev</code>	integer specifying a trace level for printing diagnostics during the C-internal algorithm. Default 0 does not print anything; higher values print increasingly more.

## Details

In a fuzzy clustering, each observation is “spread out” over the various clusters. Denote by  $u_{iv}$  the membership of observation  $i$  to cluster  $v$ .

The memberships are nonnegative, and for a fixed observation  $i$  they sum to 1. The particular method `fanny` stems from chapter 4 of Kaufman and Rousseeuw (1990) (see the references in `daisy`) and has been extended by Martin Maechler to allow user specified `memb.exp`, `iniMem.p`, `maxit`, `tol`, etc.

Fanny aims to minimize the objective function

$$\sum_{v=1}^k \frac{\sum_{i=1}^n \sum_{j=1}^n u_{iv}^r u_{jv}^r d(i, j)}{2 \sum_{j=1}^n u_{jv}^r}$$

where  $n$  is the number of observations,  $k$  is the number of clusters,  $r$  is the membership exponent `memb.exp` and  $d(i, j)$  is the dissimilarity between observations  $i$  and  $j$ .

Note that  $r \rightarrow 1$  gives increasingly crisper clusterings whereas  $r \rightarrow \infty$  leads to complete fuzziness. Kaufman & Rousseeuw (1990), p.191 note that values too close to 1 can lead to slow convergence. Further note that even the default,  $r = 2$  can lead to complete fuzziness, i.e., memberships  $u_{iv} \equiv 1/k$ . In that case a warning is signalled and the user is advised to choose a smaller `memb.exp (= r)`.

Compared to other fuzzy clustering methods, `fanny` has the following features: (a) it also accepts a dissimilarity matrix; (b) it is more robust to the spherical cluster assumption; (c) it provides a novel graphical display, the silhouette plot (see `plot.partition`).

## Value

an object of class "fanny" representing the clustering. See `fanny.object` for details.

## See Also

`agnes` for background and references; `fanny.object`, `partition.object`, `plot.partition`, `daisy`, `dist`.

## Examples

```
## generate 10+15 objects in two clusters, plus 3 objects lying
## between those clusters.
x <- rbind(cbind(rnorm(10, 0, 0.5), rnorm(10, 0, 0.5)),
           cbind(rnorm(15, 5, 0.5), rnorm(15, 5, 0.5)),
           cbind(rnorm( 3, 3.2, 0.5), rnorm( 3, 3.2, 0.5)))
fannyx <- fanny(x, 2)
## Note that observations 26:28 are "fuzzy" (closer to # 2):
fannyx
summary(fannyx)
plot(fannyx)

(fan.x.15 <- fanny(x, 2, memb.exp = 1.5)) # 'crispier' for obs. 26:28
```

```
(fanny(x, 2, memb.exp = 3))           # more fuzzy in general

data(ruspini)
f4 <- fanny(ruspini, 4)
stopifnot(rle(f4$clustering)$lengths == c(20,23,17,15))
plot(f4, which = 1)
## Plot similar to Figure 6 in Stryuf et al (1996)
plot(fanny(ruspini, 5))
```

fanny.object

*Fuzzy Analysis (FANNY) Object***Description**

The objects of class "fanny" represent a fuzzy clustering of a dataset.

**Value**

A legitimate fanny object is a list with the following components:

membership	matrix containing the memberships for each pair consisting of an observation and a cluster.
memb.exp	the membership exponent used in the fitting criterion.
coeff	Dunn's partition coefficient $F(k)$ of the clustering, where $k$ is the number of clusters. $F(k)$ is the sum of all <i>squared</i> membership coefficients, divided by the number of observations. Its value is between $1/k$ and 1. The normalized form of the coefficient is also given. It is defined as $(F(k) - 1/k)/(1 - 1/k)$ , and ranges between 0 and 1. A low value of Dunn's coefficient indicates a very fuzzy clustering, whereas a value close to 1 indicates a near-crisp clustering.
clustering	the clustering vector of the nearest crisp clustering, see <a href="#">partition.object</a> .
k.crisp	integer ( $\leq k$ ) giving the number of <i>crisp</i> clusters; can be less than $k$ , where it's recommended to decrease <code>memb.exp</code> .
objective	named vector containing the minimal value of the objective function reached by the FANNY algorithm and the relative convergence tolerance <code>tol</code> used.
convergence	named vector with <code>iterations</code> , the number of iterations needed and <code>converged</code> indicating if the algorithm converged (in <code>maxit</code> iterations within convergence tolerance <code>tol</code> ).
diss	an object of class "dissimilarity", see <a href="#">partition.object</a> .
call	generating call, see <a href="#">partition.object</a> .
silinfo	list with silhouette information of the nearest crisp clustering, see <a href="#">partition.object</a> .
data	matrix, possibly standardized, or NULL, see <a href="#">partition.object</a> .

**GENERATION**

These objects are returned from [fanny](#).

**METHODS**

The "fanny" class has methods for the following generic functions: `print`, `summary`.

**INHERITANCE**

The class "fanny" inherits from "partition". Therefore, the generic functions `plot` and `clusplot` can be used on a fanny object.

**See Also**

`fanny`, `print.fanny`, `dissimilarity.object`, `partition.object`,  
`plot.partition`.

---

flower

*Flower Characteristics*

---

**Description**

8 characteristics for 18 popular flowers.

**Usage**

```
data(flower)
```

**Format**

A data frame with 18 observations on 8 variables:

[ , "V1"]	factor	winters
[ , "V2"]	factor	shadow
[ , "V3"]	factor	tubers
[ , "V4"]	factor	color
[ , "V5"]	ordered	soil
[ , "V6"]	ordered	preference
[ , "V7"]	numeric	height
[ , "V8"]	numeric	distance

**V1** winters, is binary and indicates whether the plant may be left in the garden when it freezes.

**V2** shadow, is binary and shows whether the plant needs to stand in the shadow.

**V3** tubers, is asymmetric binary and distinguishes between plants with tubers and plants that grow in any other way.

**V4** color, is nominal and specifies the flower's color (1 = white, 2 = yellow, 3 = pink, 4 = red, 5 = blue).

**V5** soil, is ordinal and indicates whether the plant grows in dry (1), normal (2), or wet (3) soil.

**V6** preference, is ordinal and gives someone's preference ranking going from 1 to 18.

**V7** height, is interval scaled, the plant's height in centimeters.

**V8** distance, is interval scaled, the distance in centimeters that should be left between the plants.

**Source**

The reference below.

**References**

Anja Struyf, Mia Hubert & Peter J. Rousseeuw (1996): Clustering in an Object-Oriented Environment. *Journal of Statistical Software*, **1**. <http://www.stat.ucla.edu/journals/jss/>

**Examples**

```
data(flower)
## Example 2 in ref
daisy(flower, type = list(asymm = 3))
daisy(flower, type = list(asymm = c(1, 3), ordratio = 7))
```

---

lower.to.upper.tri.inds

*Permute Indices for Triangular Matrices*

---

**Description**

Compute index vectors for extracting or reordering of lower or upper triangular matrices that are stored as contiguous vectors.

**Usage**

```
lower.to.upper.tri.inds(n)
upper.to.lower.tri.inds(n)
```

**Arguments**

n                    integer larger than 1.

**Value**

integer vector containing a permutation of  $1:N$  where  $N = n(n-1)/2$ .

**Note**

these functions are mainly for internal use in the cluster package, and may not remain available (unless we see a good reason).

**See Also**

[upper.tri](#), [lower.tri](#) with a related purpose.

**Examples**

```

m5 <- matrix(NA, 5, 5)
m <- m5; m[lower.tri(m)] <- upper.to.lower.tri.inds(5); m
m <- m5; m[upper.tri(m)] <- lower.to.upper.tri.inds(5); m

stopifnot(lower.to.upper.tri.inds(2) == 1,
          lower.to.upper.tri.inds(3) == 1:3,
          upper.to.lower.tri.inds(3) == 1:3,
          sort(upper.to.lower.tri.inds(5)) == 1:10,
          sort(lower.to.upper.tri.inds(6)) == 1:15)

```

mona

*MONothetic Analysis Clustering of Binary Variables***Description**

Returns a list representing a divisive hierarchical clustering of a dataset with binary variables only.

**Usage**

```
mona(x)
```

**Arguments**

**x** data matrix or data frame in which each row corresponds to an observation, and each column corresponds to a variable. All variables must be binary. A limited number of missing values (NAs) is allowed. Every observation must have at least one value different from NA. No variable should have half of its values missing. There must be at least one variable which has no missing values. A variable with all its non-missing values identical, is not allowed.

**Details**

`mona` is fully described in chapter 7 of Kaufman and Rousseeuw (1990). It is "monothetic" in the sense that each division is based on a single (well-chosen) variable, whereas most other hierarchical methods (including `agnes` and `diana`) are "polythetic", i.e. they use all variables together.

The `mona`-algorithm constructs a hierarchy of clusterings, starting with one large cluster. Clusters are divided until all observations in the same cluster have identical values for all variables.

At each stage, all clusters are divided according to the values of one variable. A cluster is divided into one cluster with all observations having value 1 for that variable, and another cluster with all observations having value 0 for that variable.

The variable used for splitting a cluster is the variable with the maximal total association to the other variables, according to the observations in the cluster to be splitted. The association between variables  $f$  and  $g$  is given by  $a(f,g)*d(f,g) - b(f,g)*c(f,g)$ , where  $a(f,g)$ ,  $b(f,g)$ ,  $c(f,g)$ , and  $d(f,g)$  are the numbers in the contingency table of  $f$  and  $g$ . [That is,  $a(f,g)$  (resp.  $d(f,g)$ ) is the number of observations for which  $f$  and  $g$  both have value 0 (resp. value 1);  $b(f,g)$  (resp.  $c(f,g)$ ) is the number of observations for which  $f$  has value 0 (resp. 1) and  $g$  has value 1 (resp. 0).] The total association of a variable  $f$  is the sum of its associations to all variables.

This algorithm does not work with missing values, therefore the data are revised, e.g. all missing values are filled in. To do this, the same measure of association between variables is used as in the algorithm. When variable  $f$  has missing values, the variable  $g$  with the largest absolute association

to `f` is looked up. When the association between `f` and `g` is positive, any missing value of `f` is replaced by the value of `g` for the same observation. If the association between `f` and `g` is negative, then any missing value of `f` is replaced by the value of `1-g` for the same observation.

### Value

an object of class "mona" representing the clustering. See `mona.object` for details.

### See Also

`agnes` for background and references; `mona.object`, `plot.mona`.

### Examples

```
data(animals)
ma <- mona(animals)
ma
## Plot similar to Figure 10 in Struyf et al (1996)
plot(ma)
```

---

`mona.object`

*Monothetic Analysis (MONA) Object*

---

### Description

The objects of class "mona" represent the divisive hierarchical clustering of a dataset with only binary variables (measurements). This class of objects is returned from `mona`.

### Value

A legitimate `mona` object is a list with the following components:

<code>data</code>	matrix with the same dimensions as the original data matrix, but with factors coded as 0 and 1, and all missing values replaced.
<code>order</code>	a vector giving a permutation of the original observations to allow for plotting, in the sense that the branches of a clustering tree will not cross.
<code>order.lab</code>	a vector similar to <code>order</code> , but containing observation labels instead of observation numbers. This component is only available if the original observations were labelled.
<code>variable</code>	vector of length <code>n-1</code> where <code>n</code> is the number of observations, specifying the variables used to separate the observations of <code>order</code> .
<code>step</code>	vector of length <code>n-1</code> where <code>n</code> is the number of observations, specifying the separation steps at which the observations of <code>order</code> are separated.

### METHODS

The "mona" class has methods for the following generic functions: `print`, `summary`, `plot`.

### See Also

`mona` for examples etc, `plot.mona`.

pam

*Partitioning Around Medoids***Description**

Partitioning (clustering) of the data into  $k$  clusters “around medoids”, a more robust version of K-means.

**Usage**

```
pam(x, k, diss = inherits(x, "dist"), metric = "euclidean",
    medoids = NULL, stand = FALSE, cluster.only = FALSE,
    do.swap = TRUE,
    keep.diss = !diss && !cluster.only && n < 100,
    keep.data = !diss && !cluster.only, trace.lev = 0)
```

**Arguments**

- |              |  |
|--------------|--|
| x            | data matrix or data frame, or dissimilarity matrix or object, depending on the value of the <code>diss</code> argument.<br><br>In case of a matrix or data frame, each row corresponds to an observation, and each column corresponds to a variable. All variables must be numeric. Missing values (NAs) are allowed—as long as every pair of observations has at least one case not missing.<br><br>In case of a dissimilarity matrix, <code>x</code> is typically the output of <code>daisy</code> or <code>dist</code> . Also a vector of length $n*(n-1)/2$ is allowed (where $n$ is the number of observations), and will be interpreted in the same way as the output of the above-mentioned functions. Missing values (NAs) are <i>not</i> allowed. |
| k            | positive integer specifying the number of clusters, less than the number of observations.  |
| diss         | logical flag: if TRUE (default for <code>dist</code> or <code>dissimilarity</code> objects), then <code>x</code> will be considered as a dissimilarity matrix. If FALSE, then <code>x</code> will be considered as a matrix of observations by variables.  |
| metric       | character string specifying the metric to be used for calculating dissimilarities between observations.<br><br>The currently available options are "euclidean" and "manhattan". Euclidean distances are root sum-of-squares of differences, and manhattan distances are the sum of absolute differences. If <code>x</code> is already a dissimilarity matrix, then this argument will be ignored.  |
| medoids      | NULL (default) or length- $k$ vector of integer indices (in $1:n$ ) specifying initial medoids instead of using the ‘ <i>build</i> ’ algorithm.  |
| stand        | logical; if true, the measurements in <code>x</code> are standardized before calculating the dissimilarities. Measurements are standardized for each variable (column), by subtracting the variable’s mean value and dividing by the variable’s mean absolute deviation. If <code>x</code> is already a dissimilarity matrix, then this argument will be ignored.  |
| cluster.only | logical; if true, only the clustering will be computed and returned, see details.  |

<code>do.swap</code>	logical indicating if the <b>swap</b> phase should happen. The default, <code>TRUE</code> , correspond to the original algorithm. On the other hand, the <b>swap</b> phase is much more computer intensive than the <b>build</b> one for large $n$ , so can be skipped by <code>do.swap = FALSE</code> .
<code>keep.diss, keep.data</code>	logicals indicating if the dissimilarities and/or input data $x$ should be kept in the result. Setting these to <code>FALSE</code> can give much smaller results and hence even save memory allocation <i>time</i> .
<code>trace.lev</code>	integer specifying a trace level for printing diagnostics during the build and swap phase of the algorithm. Default 0 does not print anything; higher values print increasingly more.

### Details

`pam` is fully described in chapter 2 of Kaufman and Rousseeuw (1990). Compared to the `k-means` approach in `kmeans`, the function `pam` has the following features: (a) it also accepts a dissimilarity matrix; (b) it is more robust because it minimizes a sum of dissimilarities instead of a sum of squared euclidean distances; (c) it provides a novel graphical display, the silhouette plot (see `plot.partition`) (d) it allows to select the number of clusters using `mean(silhouette(pr))` on the result `pr <- pam(..)`, or directly its component `pr$silinfo$avg.width`, see also [pam.object](#).

When `cluster.only` is true, the result is simply a (possibly named) integer vector specifying the clustering, i.e.,

`pam(x, k, cluster.only=TRUE)` is the same as  
`pam(x, k)$clustering` but computed more efficiently.

The `pam`-algorithm is based on the search for  $k$  representative objects or medoids among the observations of the dataset. These observations should represent the structure of the data. After finding a set of  $k$  medoids,  $k$  clusters are constructed by assigning each observation to the nearest medoid. The goal is to find  $k$  representative objects which minimize the sum of the dissimilarities of the observations to their closest representative object.

By default, when `medoids` are not specified, the algorithm first looks for a good initial set of medoids (this is called the **build** phase). Then it finds a local minimum for the objective function, that is, a solution such that there is no single switch of an observation with a medoid that will decrease the objective (this is called the **swap** phase).

When the `medoids` are specified, their order does *not* matter; in general, the algorithms have been designed to not depend on the order of the observations.

### Value

an object of class "pam" representing the clustering. See [?pam.object](#) for details.

### Note

For large datasets, `pam` may need too much memory or too much computation time since both are  $O(n^2)$ . Then, `clara()` is preferable, see its documentation.

### See Also

[agnes](#) for background and references; [pam.object](#), [clara](#), [daisy](#), [partition.object](#), [plot.partition](#), [dist](#).



**Examples**

```
## generate 25 objects, divided into 2 clusters.
x <- rbind(cbind(rnorm(10,0,0.5), rnorm(10,0,0.5)),
           cbind(rnorm(15,5,0.5), rnorm(15,5,0.5)))
pamx <- pam(x, 2)
pamx
summary(pamx)
plot(pamx)
## use obs. 1 & 16 as starting medoids -- same result (typically)
(p2m <- pam(x, 2, medoids = c(1,16)))

p3m <- pam(x, 3, trace = 2)
## rather stupid initial medoids:
(p3m. <- pam(x, 3, medoids = 3:1, trace = 1))

pam(daisy(x, metric = "manhattan"), 2, diss = TRUE)

data(ruspini)
## Plot similar to Figure 4 in Stryuf et al (1996)
## Not run: plot(pam(ruspini, 4), ask = TRUE)
```

pam.object

*Partitioning Around Medoids (PAM) Object***Description**

The objects of class "pam" represent a partitioning of a dataset into clusters.

**Value**

A legitimate pam object is a list with the following components:

medoids	the medoids or representative objects of the clusters. If a dissimilarity matrix was given as input to pam, then a vector of numbers or labels of observations is given, else medoids is a matrix with in each row the coordinates of one medoid.
id.med	integer vector of <i>indices</i> giving the medoid observation numbers.
clustering	the clustering vector, see <a href="#">partition.object</a> .
objective	the objective function after the first and second step of the pam algorithm.
isolation	vector with length equal to the number of clusters, specifying which clusters are isolated clusters (L- or L*-clusters) and which clusters are not isolated. A cluster is an L*-cluster iff its diameter is smaller than its separation. A cluster is an L-cluster iff for each observation <i>i</i> the maximal dissimilarity between <i>i</i> and any other observation of the cluster is smaller than the minimal dissimilarity between <i>i</i> and any observation of another cluster. Clearly each L*-cluster is also an L-cluster.
clusinfo	matrix, each row gives numerical information for one cluster. These are the cardinality of the cluster (number of observations), the maximal and average dissimilarity between the observations in the cluster and the cluster's medoid,

the diameter of the cluster (maximal dissimilarity between two observations of the cluster), and the separation of the cluster (minimal dissimilarity between an observation of the cluster and an observation of another cluster).

silinfo list with silhouette width information, see [partition.object](#).  
 diss dissimilarity (maybe NULL), see [partition.object](#).  
 call generating call, see [partition.object](#).  
 data (possibly standardized) see [partition.object](#).

## GENERATION

These objects are returned from [pam](#).

## METHODS

The "pam" class has methods for the following generic functions: print, summary.

## INHERITANCE

The class "pam" inherits from "partition". Therefore, the generic functions plot and clusplot can be used on a pam object.

## See Also

[pam](#), [dissimilarity.object](#), [partition.object](#), [plot.partition](#).

## Examples

```
## Use the silhouette widths for assessing the best number of clusters,
## following a one-dimensional example from Christian Hennig :
##
x <- c(rnorm(50), rnorm(50,mean=5), rnorm(30,mean=15))
asw <- numeric(20)
## Note that "k=1" won't work!
for (k in 2:20)
  asw[k] <- pam(x, k) $ silinfo $ avg.width
k.best <- which.max(asw)
cat("silhouette-optimal number of clusters:", k.best, "\n")

plot(1:20, asw, type="h", main = "pam() clustering assessment",
     xlab="k (# clusters)", ylab = "average silhouette width")
axis(1, k.best, paste("best",k.best,sep="\n"), col = "red", col.axis = "red")
```

---

partition.object    *Partitioning Object*

---

## Description

The objects of class "partition" represent a partitioning of a dataset into clusters.

**Value**

a "partition" object is a list with the following (and typically more) components:

clustering	the clustering vector. An integer vector of length $n$ , the number of observations, giving for each observation the number ('id') of the cluster to which it belongs.
call	the matched <code>call</code> generating the object.
silinfo	a list with all <i>silhouette</i> information, only available when the number of clusters is non-trivial, i.e., $1 < k < n$ and then has the following components, see <code>silhouette</code> <p><b>widths</b> an (<math>n \times 3</math>) matrix, as returned by <code>silhouette()</code>, with for each observation <math>i</math> the cluster to which <math>i</math> belongs, as well as the neighbor cluster of <math>i</math> (the cluster, not containing <math>i</math>, for which the average dissimilarity between its observations and <math>i</math> is minimal), and the silhouette width <math>s(i)</math> of the observation.</p> <p><b>clus.avg.widths</b> the average silhouette width per cluster.</p> <p><b>avg.width</b> the average silhouette width for the dataset, i.e., simply the average of <math>s(i)</math> over all observations <math>i</math>.</p> <p>This information is also needed to construct a <i>silhouette plot</i> of the clustering, see <code>plot.partition</code>.</p> <p>Note that <code>avg.width</code> can be maximized over different clusterings (e.g. with varying number of clusters) to choose an <i>optimal</i> clustering.</p>
objective	value of criterion maximized during the partitioning algorithm, may more than one entry for different stages.
diss	an object of class "dissimilarity", representing the total dissimilarity matrix of the dataset (or relevant subset, e.g. for <code>clara</code> ).
data	a matrix containing the original or standardized data. This might be missing to save memory or when a dissimilarity matrix was given as input structure to the clustering method.

**GENERATION**

These objects are returned from `pam`, `clara` or `fanny`.

**METHODS**

The "partition" class has a method for the following generic functions: `plot`, `clusplot`.

**INHERITANCE**

The following classes inherit from class "partition": "pam", "clara" and "fanny".

See `pam.object`, `clara.object` and `fanny.object` for details.

**See Also**

`pam`, `clara`, `fanny`.

---

 plantTraits

*Plant Species Traits Data*


---

**Description**

This dataset constitutes a description of 136 plant species according to biological attributes (morphological or reproductive)

**Usage**

```
data(plantTraits)
```

**Format**

A data frame with 136 observations on the following 31 variables.

pdias Diaspore mass (mg)

longindex Seed bank longevity

durflow Flowering duration

height Plant height, an ordered factor with levels 1 < 2 < ... < 8.

begflow Time of first flowering, an ordered factor with levels 1 < 2 < 3 < 4 < 5 < 6 < 7 < 8 < 9

mycor Mycorrhizas, an ordered factor with levels 0never < 1 sometimes < 2always

vegaer aerial vegetative propagation, an ordered factor with levels 0never < 1 present but limited < 2important.

vegsout underground vegetative propagation, an ordered factor with 3 levels identical to vegaer above.

autopoll selfing pollination, an ordered factor with levels 0never < 1rare < 2 often < the rule3

insects insect pollination, an ordered factor with 5 levels 0 < ... < 4.

wind wind pollination, an ordered factor with 5 levels 0 < ... < 4.

lign a binary factor with levels 0:1, indicating if plant is woody.

piq a binary factor indicating if plant is thorny.

ros a binary factor indicating if plant is rosette.

semiros semi-rosette plant, a binary factor (0: no; 1: yes).

leafy leafy plant, a binary factor.

suman summer annual, a binary factor.

winan winter annual, a binary factor.

monocarp monocarpic perennial, a binary factor.

polycarp polycarpic perennial, a binary factor.

seasaes seasonal aestival leaves, a binary factor.

seashiv seasonal hibernal leaves, a binary factor.

seasver seasonal vernal leaves, a binary factor.

everalw leaves always evergreen, a binary factor.

everparti leaves partially evergreen, a binary factor.

elaiio fruits with an elaiosome (dispersed by ants), a binary factor.

endozoo endozoochorous fruits, a binary factor.  
 epizoo epizoochorous fruits, a binary factor.  
 aquat aquatic dispersal fruits, a binary factor.  
 windgl wind dispersed fruits, a binary factor.  
 unsp unspecialized mechanism of seed dispersal, a binary factor.

### Details

Most of factor attributes are not disjunctive. For example, a plant can be usually pollinated by insects but sometimes self-pollination can occurred.

### Source

Vallet, Jeanne (2005) *Structuration de communautés végétales et analyse comparative de traits biologiques le long d'un gradient d'urbanisation*. Mémoire de Master 2 'Ecologie-Biodiversité-Evolution'; Université Paris Sud XI, 30p.+ annexes (in french)

### Examples

```
data(plantTraits)

## Calculation of a dissimilarity matrix
library(cluster)
dai.b <- daisy(plantTraits,
              type = list(ordratio = 4:11, symm = 12:13, asymm = 14:31))

## Hierarchical classification
agn.trts <- agnes(dai.b, method="ward")
plot(agn.trts, which.plots = 2, cex= 0.6)
plot(agn.trts, which.plots = 1)
cutree6 <- cutree(agn.trts, k=6)
cutree6

## Principal Coordinate Analysis
cmds dai.b <- cmdscale(dai.b, k=6)
plot(cmdsdai.b[, 1:2], asp = 1, col = cutree6)
```

---

plot.agnes

*Plots of an Agglomerative Hierarchical Clustering*

---

### Description

Creates plots for visualizing an agnes object.

### Usage

```
## S3 method for class 'agnes':
plot(x, ask = FALSE, which.plots = NULL, main = NULL,
     sub = paste("Agglomerative Coefficient = ", round(x$ac, digits = 2)),
     adj = 0, nmax.lab = 35, max.strlen = 5, xax.pretty = TRUE, ...)
```

**Arguments**

<code>x</code>	an object of class "agnes", typically created by <code>agnes(.)</code> .
<code>ask</code>	logical; if true and <code>which.plots</code> is NULL, <code>plot.agnes</code> operates in interactive mode, via <code>menu</code> .
<code>which.plots</code>	integer vector or NULL (default), the latter producing both plots. Otherwise, <code>which.plots</code> must contain integers of 1 for a <i>banner</i> plot or 2 for a dendrogram or "clustering tree".
<code>main, sub</code>	main and sub title for the plot, with convenient defaults. See documentation for these arguments in <code>plot.default</code> .
<code>adj</code>	for label adjustment in <code>bannerplot()</code> .
<code>nmax.lab</code>	integer indicating the number of labels which is considered too large for single-name labelling the banner plot.
<code>max.strlen</code>	positive integer giving the length to which strings are truncated in banner plot labeling.
<code>xax.pretty</code>	logical or integer indicating if <code>pretty(*, n = xax.pretty)</code> should be used for the x axis. <code>xax.pretty = FALSE</code> is for back compatibility.
<code>...</code>	graphical parameters (see <code>par</code> ) may also be supplied and are passed to <code>bannerplot()</code> or <code>pltree()</code> (see <code>pltree.twins</code> ), respectively.

**Details**

When `ask = TRUE`, rather than producing each plot sequentially, `plot.agnes` displays a menu listing all the plots that can be produced. If the menu is not desired but a pause between plots is still wanted one must set `par(ask= TRUE)` before invoking the plot command.

The banner displays the hierarchy of clusters, and is equivalent to a tree. See Rousseeuw (1986) or chapter 5 of Kaufman and Rousseeuw (1990). The banner plots distances at which observations and clusters are merged. The observations are listed in the order found by the *agnes* algorithm, and the numbers in the `height` vector are represented as bars between the observations.

The leaves of the clustering tree are the original observations. Two branches come together at the distance between the two clusters being merged.

For more customization of the plots, rather call `bannerplot` and `pltree()`, i.e., its method `pltree.twins`, respectively.

directly with corresponding arguments, e.g., `xlab` or `ylab`.

**Side Effects**

Appropriate plots are produced on the current graphics device. This can be one or both of the following choices:

Banner  
Clustering tree

**Note**

In the banner plot, observation labels are only printed when the number of observations is limited less than `nmax.lab` (35, by default), for readability. Moreover, observation labels are truncated to maximally `max.strlen` (5) characters.

For the dendrogram, more flexibility than via `pltree()` is provided by `dg <- as.dendrogram(x)` and plotting `dg` via `plot.dendrogram`.

## References

- Kaufman, L. and Rousseeuw, P.J. (1990) *Finding Groups in Data: An Introduction to Cluster Analysis*. Wiley, New York.
- Rousseeuw, P.J. (1986). A visual display for hierarchical classification, in *Data Analysis and Informatics 4*; edited by E. Diday, Y. Escoufier, L. Lebart, J. Pages, Y. Schektman, and R. Tomassone. North-Holland, Amsterdam, 743–748.
- Struyf, A., Hubert, M. and Rousseeuw, P.J. (1997) Integrating Robust Clustering Techniques in S-PLUS, *Computational Statistics and Data Analysis*, **26**, 17-37.

## See Also

[agnes](#) and [agnes.object](#); [bannerplot](#), [pltree.twins](#), and [par](#).

## Examples

```
## Can also pass `labels` to pltree() and bannerplot():
data(iris)
cS <- as.character(Sp <- iris$Species)
cS[Sp == "setosa"] <- "S"
cS[Sp == "versicolor"] <- "V"
cS[Sp == "virginica"] <- "G"
ai <- agnes(iris[, 1:4])
plot(ai, labels = cS, nmax = 150) # bannerplot labels are mess
```

---

plot.diana

*Plots of a Divisive Hierarchical Clustering*

---

## Description

Creates plots for visualizing a diana object.

## Usage

```
## S3 method for class 'diana':
plot(x, ask = FALSE, which.plots = NULL, main = NULL,
      sub = paste("Divisive Coefficient = ", round(x$dc, digits = 2)),
      adj = 0, nmax.lab = 35, max.strlen = 5, xax.pretty = TRUE, ...)
```

## Arguments

- |             |   |
|-------------|---|
| x           | an object of class "diana", typically created by <a href="#">diana(.)</a> .   |
| ask         | logical; if true and which.plots is NULL, plot.diana operates in interactive mode, via <a href="#">menu</a> .   |
| which.plots | integer vector or NULL (default), the latter producing both plots. Otherwise, which.plots must contain integers of 1 for a <i>banner</i> plot or 2 for a dendrogram or “clustering tree”. |
| main, sub   | main and sub title for the plot, each with a convenient default. See documentation for these arguments in <a href="#">plot.default</a> .  |
| adj         | for label adjustment in <a href="#">bannerplot()</a> .  |

nmax.lab	integer indicating the number of labels which is considered too large for single-name labelling the banner plot.
max.strlen	positive integer giving the length to which strings are truncated in banner plot labeling.
xax.pretty	logical or integer indicating if <code>pretty(*, n = xax.pretty)</code> should be used for the x axis. <code>xax.pretty = FALSE</code> is for back compatibility.
...	graphical parameters (see <code>par</code> ) may also be supplied and are passed to <code>bannerplot()</code> or <code>pltree()</code> , respectively.

### Details

When `ask = TRUE`, rather than producing each plot sequentially, `plot.diana` displays a menu listing all the plots that can be produced. If the menu is not desired but a pause between plots is still wanted one must set `par(ask= TRUE)` before invoking the plot command.

The banner displays the hierarchy of clusters, and is equivalent to a tree. See Rousseeuw (1986) or chapter 6 of Kaufman and Rousseeuw (1990). The banner plots the diameter of each cluster being splitted. The observations are listed in the order found by the `diana` algorithm, and the numbers in the `height` vector are represented as bars between the observations.

The leaves of the clustering tree are the original observations. A branch splits up at the diameter of the cluster being splitted.

### Side Effects

An appropriate plot is produced on the current graphics device. This can be one or both of the following choices:

Banner  
Clustering tree

### Note

In the banner plot, observation labels are only printed when the number of observations is limited less than `nmax.lab` (35, by default), for readability. Moreover, observation labels are truncated to maximally `max.strlen` (5) characters.

### References

see those in `plot.agnes`.

### See Also

`diana`, `diana.object`, `twins.object`, `par`.

### Examples

```
example(diana)# -> dv <- diana(...)

plot(dv, which = 1, nmax.lab = 100)

## wider labels :
op <- par(mar = par("mar") + c(0, 2, 0, 0))
plot(dv, which = 1, nmax.lab = 100, max.strlen = 12)
par(op)
```



---

plot.mona

*Banner of Monothetic Divisive Hierarchical Clusterings*


---

### Description

Creates the banner of a `mona` object.

### Usage

```
## S3 method for class 'mona':
plot(x, main = paste("Banner of ", deparse(x$call)),
      sub = NULL, xlab = "Separation step",
      col = c(2,0), axes = TRUE, adj = 0,
      nmax.lab = 35, max.strlen = 5, ...)
```

### Arguments

<code>x</code>	an object of class "mona", typically created by <code>mona(.)</code> .
<code>main, sub</code>	main and sub titles for the plot, with convenient defaults. See documentation in <a href="#">plot.default</a> .
<code>xlab</code>	x axis label, see <a href="#">title</a> .
<code>col, adj</code>	graphical parameters passed to <code>bannerplot()</code> .
<code>axes</code>	logical, indicating if (labeled) axes should be drawn.
<code>nmax.lab</code>	integer indicating the number of labels which is considered too large for labeling.
<code>max.strlen</code>	positive integer giving the length to which strings are truncated in labeling.
<code>...</code>	further graphical arguments are passed to <code>bannerplot()</code> and <code>text</code> .

### Details

Plots the separation step at which clusters are splitted. The observations are given in the order found by the `mona` algorithm, the numbers in the `step` vector are represented as bars between the observations.

When a long bar is drawn between two observations, those observations have the same value for each variable. See chapter 7 of Kaufman and Rousseeuw (1990).

### Side Effects

A banner is plotted on the current graphics device.

### Note

In the banner plot, observation labels are only printed when the number of observations is limited less than `nmax.lab` (35, by default), for readability. Moreover, observation labels are truncated to maximally `max.strlen` (5) characters.

### References

see those in [plot.agnes](#).

**See Also**

[mona](#), [mona.object](#), [par](#).

---

plot.partition      *Plot of a Partition of the Data Set*

---

**Description**

Creates plots for visualizing a `partition` object.

**Usage**

```
## S3 method for class 'partition':
plot(x, ask = FALSE, which.plots = NULL,
     nmax.lab = 40, max.strlen = 5, data = x$data, dist = NULL,
     cor = TRUE, stand = FALSE, lines = 2,
     shade = FALSE, color = FALSE, labels = 0, plotchar = TRUE,
     span = TRUE, xlim = NULL, ylim = NULL, main = NULL, ...)
```

**Arguments**

<code>x</code>	an object of class "partition", typically created by the functions <a href="#">pam</a> , <a href="#">clara</a> , or <a href="#">fanny</a> .
<code>ask</code>	logical; if true and <code>which.plots</code> is NULL, <code>plot.partition</code> operates in interactive mode, via <a href="#">menu</a> .
<code>which.plots</code>	integer vector or NULL (default), the latter producing both plots. Otherwise, <code>which.plots</code> must contain integers of 1 for a <i>clusplot</i> or 2 for <i>silhouette</i> .
<code>nmax.lab</code>	integer indicating the number of labels which is considered too large for single-name labeling the silhouette plot.
<code>max.strlen</code>	positive integer giving the length to which strings are truncated in silhouette plot labeling.
<code>data</code>	numeric matrix with the scaled data; per default taken from the partition object <code>x</code> , but can be specified explicitly.
<code>dist</code>	when <code>x</code> does not have a <code>diss</code> component as for <a href="#">pam</a> (*, <code>keep.diss=FALSE</code> ), <code>dist</code> must be the dissimilarity if a <i>clusplot</i> is desired.
<code>cor, stand, lines, shade, color, labels, plotchar, span, xlim, ylim, main, ...</code>	All optional arguments available for the <a href="#">clusplot.default</a> function (except for the <code>diss</code> one) and graphical parameters (see <a href="#">par</a> ) may also be supplied as arguments to this function.

**Details**

When `ask= TRUE`, rather than producing each plot sequentially, `plot.partition` displays a menu listing all the plots that can be produced. If the menu is not desired but a pause between plots is still wanted, call `par(ask= TRUE)` before invoking the plot command.

The *clusplot* of a cluster partition consists of a two-dimensional representation of the observations, in which the clusters are indicated by ellipses (see [clusplot.partition](#) for more details).

The *silhouette plot* of a nonhierarchical clustering is fully described in Rousseeuw (1987) and in chapter 2 of Kaufman and Rousseeuw (1990). For each observation  $i$ , a bar is drawn, representing its silhouette width  $s(i)$ , see [silhouette](#) for details. Observations are grouped per cluster, starting with cluster 1 at the top. Observations with a large  $s(i)$  (almost 1) are very well clustered, a small  $s(i)$  (around 0) means that the observation lies between two clusters, and observations with a negative  $s(i)$  are probably placed in the wrong cluster.

A clustering can be performed for several values of  $k$  (the number of clusters). Finally, choose the value of  $k$  with the largest overall average silhouette width.

### Side Effects

An appropriate plot is produced on the current graphics device. This can be one or both of the following choices:

Clusplot  
Silhouette plot

### Note

In the silhouette plot, observation labels are only printed when the number of observations is less than `nmax.lab` (40, by default), for readability. Moreover, observation labels are truncated to maximally `max.strlen` (5) characters.

For more flexibility, use `plot(silhouette(x), ...)`, see [plot.silhouette](#).

### References

Rousseeuw, P.J. (1987) Silhouettes: A graphical aid to the interpretation and validation of cluster analysis. *J. Comput. Appl. Math.*, **20**, 53–65.

Further, the references in [plot.agnes](#).

### See Also

[partition.object](#), [clusplot.partition](#), [clusplot.default](#), [pam](#),  
[pam.object](#), [clara](#), [clara.object](#), [fanny](#), [fanny.object](#), [par](#).

### Examples

```
## generate 25 objects, divided into 2 clusters.
x <- rbind(cbind(rnorm(10,0,0.5), rnorm(10,0,0.5)),
           cbind(rnorm(15,5,0.5), rnorm(15,5,0.5)))
plot(pam(x, 2))

## Save space not keeping data in clus.object, and still clusplot() it:
data(xclara)
cx <- clara(xclara, 3, keep.data = FALSE)
cx$data # is NULL
plot(cx, data = xclara)
```

---

 pltree

*Clustering Trees - Generic Function*


---

**Description**

Generic function drawing a clustering tree (“dendrogram”) on the current graphics device. There is a `twins` method, see `pltree.twins` for usage and examples.

**Usage**

```
pltree(x, ...)
```

**Arguments**

`x` an R object (for which a `pltree` method is defined).

`...` methods may have additional arguments. Graphical parameters (see `par`) may also be supplied as arguments to this function.

**See Also**

`pltree.twins`, `twins.object`.

---

 pltree.twins

*Clustering Tree of a Hierarchical Clustering*


---

**Description**

Draws a clustering tree (dendrogram) of a `twins` object, i.e., hierarchical clustering, typically resulting from `agnes()` or `diana()`.

**Usage**

```
## S3 method for class 'twins':
pltree(x, main = paste("Dendrogram of ", deparse(x$call)),
       labels = NULL, ylab = "Height", ...)
```

**Arguments**

`x` an object of class "twins", typically created by either `agnes()` or `diana()`.

`main` main title with a sensible default.

`labels` labels to use; the default is constructed from `x`.

`ylab` label for y-axis.

`...` graphical parameters (see `par`) may also be supplied as arguments to this function.

**Details**

Creates a plot of a clustering tree given a `twins` object. The leaves of the tree are the original observations. In case of an agglomerative clustering, two branches come together at the distance between the two clusters being merged. For a divisive clustering, a branch splits up at the diameter of the cluster being splitted.

Note that currently the method function simply calls `plot(as.hclust(x), ...)`, which dispatches to `plot.hclust(...)`. If more flexible plots are needed, consider `xx <- as.dendrogram(as.hclust(x))` and plotting `xx`, see `plot.dendrogram`.

**Value**

a NULL value is returned.

**See Also**

`agnes`, `agnes.object`, `diana`, `diana.object`, `hclust`, `par`, `plot.agnes`, `plot.diana`.

**Examples**

```
data(votes.repub)
agn <- agnes(votes.repub)
pltree(agn)

dagn <- as.dendrogram(as.hclust(agn))
dagn2 <- as.dendrogram(as.hclust(agn), hang = 0.2)
op <- par(mar = par("mar") + c(0,0,0, 2)) # more space to the right
plot(dagn2, horiz = TRUE)
plot(dagn, horiz = TRUE, center = TRUE,
      nodePar = list(lab.cex = 0.6, lab.col = "forest green", pch = NA),
      main = deparse(agn$call))
par(op)
```

---

pluton

*Isotopic Composition Plutonium Batches*

---

**Description**

The `pluton` data frame has 45 rows and 4 columns, containing percentages of isotopic composition of 45 Plutonium batches.

**Usage**

```
data(pluton)
```

**Format**

This data frame contains the following columns:

**Pu238** the percentages of  $^{238}\text{Pu}$ , always less than 2 percent.

**Pu239** the percentages of  $^{239}\text{Pu}$ , typically between 60 and 80 percent (from neutron capture of Uranium,  $^{238}\text{U}$ ).

**Pu240** percentage of the plutonium 240 isotope.

**Pu241** percentage of the plutonium 241 isotope.

### Details

Note that the percentage of plutonium-242 can be computed from the other four percentages, see the examples.

In the reference below it is explained why it is very desirable to combine these plutonium patches in three groups of similar size.

### Source

Available as 'pluton.dat' from the archive

currently <http://www.agoras.ua.ac.be/datasets/clusplot-examples.tar.gz>.

### References

Rousseeuw, P.J. and Kaufman, L and Trauwaert, E. (1996) Fuzzy clustering using scatter matrices, *Computational Statistics and Data Analysis* **23**(1), 135–151.

### Examples

```
data(pluton)

hist(apply(pluton,1,sum), col = "gray") # between 94% and 100%
pu5 <- pluton
pu5$Pu242 <- 100 - apply(pluton,1,sum) # the remaining isotope.
pairs(pu5)
```

---

predict.ellipsoid *Predict Method for Ellipsoid Objects*

---

### Description

Compute points on the ellipsoid boundary, mostly for drawing.

### Usage

```
predict.ellipsoid(object, n.out=201, ...)
## S3 method for class 'ellipsoid':
predict(object, n.out=201, ...)
ellipsoidPoints(A, d2, loc, n.half = 201)
```

### Arguments

object	an object of class <code>ellipsoid</code> , typically from <code>ellipsoidhull()</code> ; alternatively any list-like object with proper components, see details below.
n.out, n.half	half the number of points to create.
A, d2, loc	arguments of the auxiliary <code>ellipsoidPoints</code> , see below.
...	passed to and from methods.

**Details**

Note `ellipsoidPoints` is the workhorse function of `predict.ellipsoid` a standalone function and method for `ellipsoid` objects, see [ellipsoidhull](#). The class of object is not checked; it must solely have valid components `loc` (length  $p$ ), the  $p \times p$  matrix `cov` (corresponding to  $A$ ) and `d2` for the center, the shape (“covariance”) matrix and the squared average radius (or distance) or `qchisq`(\*,  $p$ ) quantile.

Unfortunately, this is only implemented for  $p = 2$ , currently; contributions for  $p \geq 3$  are *very welcome*.

**Value**

a numeric matrix of dimension  $2 * n.out$  times  $p$ .

**See Also**

[ellipsoidhull](#), [volume.ellipsoid](#).

**Examples**

```
## see also example(ellipsoidhull)

## Robust vs. L.S. covariance matrix
set.seed(143)
x <- rt(200, df=3)
y <- 3*x + rt(200, df=2)
plot(x,y, main="non-normal data (N=200)")
mtext("with classical and robust cov.matrix ellipsoids")
X <- cbind(x,y)
C.ls <- cov(X) ; m.ls <- colMeans(X)
d2.99 <- qchisq(0.99, df = 2)
lines(ellipsoidPoints(C.ls, d2.99, loc=m.ls), col="green")
if(require(MASS)) {
  Cxy <- cov.rob(cbind(x,y))
  lines(ellipsoidPoints(Cxy$cov, d2 = d2.99, loc=Cxy$center), col="red")
}# MASS
```

---

print.agnes

*Print Method for AGNES Objects*

---

**Description**

Prints the call, agglomerative coefficient, ordering of objects and distances between merging clusters (‘Height’) of an `agnes` object.

This is a method for the generic `print()` function for objects inheriting from class `agnes`, see [agnes.object](#).

**Usage**

```
## S3 method for class 'agnes':
print(x, ...)
```

**Arguments**

x                    an agnes object.  
...                   potential further arguments (required by generic).

**See Also**

[summary.agnes](#) producing more output; [agnes](#), [agnes.object](#), [print](#),  
[print.default](#).

---

print.clara                    *Print Method for CLARA Objects*

---

**Description**

Prints the best sample, medoids, clustering vector and objective function of clara object.  
This is a method for the function [print \(\)](#) for objects inheriting from class [clara](#).

**Usage**

```
## S3 method for class 'clara':  
print(x, ...)
```

**Arguments**

x                    a clara object.  
...                   potential further arguments (require by generic).

**See Also**

[summary.clara](#) producing more output; [clara](#), [clara.object](#), [print](#),  
[print.default](#).

---

print.diana                    *Print Method for DIANA Objects*

---

**Description**

Prints the ordering of objects, diameters of splitted clusters, and divisive coefficient of a diana object.  
This is a method for the function [print \(\)](#) for objects inheriting from class [diana](#).

**Usage**

```
## S3 method for class 'diana':  
print(x, ...)
```



**Arguments**

`x` a diana object.  
`...` potential further arguments (require by generic).

**See Also**

[diana](#), [diana.object](#), [print](#), [print.default](#).

---

```
print.dissimilarity
```

*Print and Summary Methods for Dissimilarity Objects*

---

**Description**

Print or summarize the distances and the attributes of a dissimilarity object.

These are methods for the functions `print()` and `summary()` for dissimilarity objects.

See `print`, `print.default`, or `summary` for the general behavior of these.

**Usage**

```
## S3 method for class 'dissimilarity':
print(x, diag = NULL, upper = NULL,
      digits = getOption("digits"), justify = "none", right = TRUE, ...)
## S3 method for class 'dissimilarity':
summary(object,
        digits = max(3, getOption("digits") - 2), ...)
## S3 method for class 'summary.dissimilarity':
print(x, ...)
```

**Arguments**

`x`, `object` a dissimilarity object or a `summary.dissimilarity` one for `print.summary.dissimilarity()`.

`digits` the number of digits to use, see [print.default](#).

`diag`, `upper`, `justify`, `right` optional arguments specifying how the triangular dissimilarity matrix is printed; see [print.dist](#).

`...` potential further arguments (require by generic).

**See Also**

[daisy](#), [dissimilarity.object](#), [print](#), [print.default](#), [print.dist](#).

**Examples**

```
## See example(daisy)

sd <- summary(daisy(matrix(rnorm(100), 20, 5)))
sd # -> print.summary.dissimilarity(.)
str(sd)
```

---

`print.fanny`*Print and Summary Methods for FANNY Objects*

---

**Description**

Prints the objective function, membership coefficients and clustering vector of `fanny` object.

This is a method for the function `print ()` for objects inheriting from class `fanny`.

**Usage**

```
## S3 method for class 'fanny':
print(x, digits = getOption("digits"), ...)
## S3 method for class 'fanny':
summary(object, ...)
## S3 method for class 'summary.fanny':
print(x, digits = getOption("digits"), ...)
```

**Arguments**

`x`, `object`      a `fanny` object.  
`digits`            number of significant digits for printing, see `print.default`.  
`...`              potential further arguments (required by generic).

**See Also**

`fanny`, `fanny.object`, `print`, `print.default`.

---

`print.mona`*Print Method for MONA Objects*

---

**Description**

Prints the ordering of objects, separation steps, and used variables of a `mona` object.

This is a method for the function `print ()` for objects inheriting from class `mona`.

**Usage**

```
## S3 method for class 'mona':
print(x, ...)
```

**Arguments**

`x`                    a `mona` object.  
`...`                potential further arguments (require by generic).

**See Also**

`mona`, `mona.object`, `print`, `print.default`.

---

`print.pam`*Print Method for PAM Objects*

---

**Description**

Prints the medoids, clustering vector and objective function of `pam` object.

This is a method for the function `print()` for objects inheriting from class `pam`.

**Usage**

```
## S3 method for class 'pam':  
print(x, ...)
```

**Arguments**

`x` a `pam` object.  
`...` potential further arguments (require by generic).

**See Also**

`pam`, `pam.object`, `print`, `print.default`.

---

`ruspini`*Ruspini Data*

---

**Description**

The Ruspini data set, consisting of 75 points in four groups that is popular for illustrating clustering techniques.

**Usage**

```
data(ruspini)
```

**Format**

A data frame with 75 observations on 2 variables giving the x and y coordinates of the points, respectively.

**Source**

E. H. Ruspini (1970): Numerical methods for fuzzy clustering. *Inform. Sci.*, **2**, 319–350.

**References**

Anja Struyf, Mia Hubert & Peter J. Rousseeuw (1996): Clustering in an Object-Oriented Environment. *Journal of Statistical Software*, **1**. <http://www.stat.ucla.edu/journals/jss/>

**Examples**

```

data(ruspini)

## Plot similar to Figure 4 in Stryuf et al (1996)
## Not run: plot(pam(ruspini, 4), ask = TRUE)

## Plot similar to Figure 6 in Stryuf et al (1996)
plot(fanny(ruspini, 5))

```

silhouette

*Compute or Extract Silhouette Information from Clustering***Description**

Compute silhouette information according to a given clustering in  $k$  clusters.

**Usage**

```

silhouette(x, ...)
## Default S3 method:
silhouette(x, dist, dmatrix, ...)
## S3 method for class 'partition':
silhouette(x, ...)
## S3 method for class 'clara':
silhouette(x, full = FALSE, ...)

sortSilhouette(object, ...)
## S3 method for class 'silhouette':
summary(object, FUN = mean, ...)
## S3 method for class 'silhouette':
plot(x, nmax.lab = 40, max.strlen = 5,
     main = NULL, sub = NULL, xlab = expression("Silhouette width "* s[i]),
     col = "gray", do.col.sort = length(col) > 1, border = 0,
     cex.names = par("cex.axis"), do.n.k = TRUE, do.clus.stat = TRUE, ...)

```

**Arguments**

<code>x</code>	an object of appropriate class; for the default method an integer vector with $k$ different integer cluster codes or a list with such an <code>x\$clustering</code> component. Note that silhouette statistics are only defined if $2 \leq k \leq n - 1$ .
<code>dist</code>	a dissimilarity object inheriting from class <code>dist</code> or coercible to one. If not specified, <code>dmatrix</code> must be.
<code>dmatrix</code>	a symmetric dissimilarity matrix ( $n \times n$ ), specified instead of <code>dist</code> , which can be more efficient.
<code>full</code>	logical specifying if a <i>full</i> silhouette should be computed for <code>clara</code> object. Note that this requires $O(n^2)$ memory, since the full dissimilarity (see <code>daisy</code> ) is needed internally.
<code>object</code>	an object of class <code>silhouette</code> .
<code>...</code>	further arguments passed to and from methods.

<code>FUN</code>	function used to summarize silhouette widths.
<code>nmax.lab</code>	integer indicating the number of labels which is considered too large for single-name labeling the silhouette plot.
<code>max.strlen</code>	positive integer giving the length to which strings are truncated in silhouette plot labeling.
<code>main, sub, xlab</code>	arguments to <code>title</code> ; have a sensible non-NULL default here.
<code>col, border, cex.names</code>	arguments passed <code>barplot()</code> ; note that the default used to be <code>col = heat.colors(n)</code> , <code>border = par("fg")</code> instead. <code>col</code> can also be a color vector of length $k$ for clusterwise coloring, see also <code>do.col.sort</code> :
<code>do.col.sort</code>	logical indicating if the colors <code>col</code> should be sorted “along” the silhouette; this is useful for casewise or clusterwise coloring.
<code>do.n.k</code>	logical indicating if $n$ and $k$ “title text” should be written.
<code>do.clus.stat</code>	logical indicating if cluster size and averages should be written right to the silhouettes.

### Details

For each observation  $i$ , the *silhouette width*  $s(i)$  is defined as follows:

Put  $a(i)$  = average dissimilarity between  $i$  and all other points of the cluster to which  $i$  belongs (if  $i$  is the *only* observation in its cluster,  $s(i) := 0$  without further calculations). For all *other* clusters  $C$ , put  $d(i, C)$  = average dissimilarity of  $i$  to all observations of  $C$ . The smallest of these  $d(i, C)$  is  $b(i) := \min_C d(i, C)$ , and can be seen as the dissimilarity between  $i$  and its “neighbor” cluster, i.e., the nearest one to which it does *not* belong. Finally,

$$s(i) := \frac{b(i) - a(i)}{\max(a(i), b(i))}.$$

`silhouette.default()` is now based on C code donated by Romain Francois (the R version being still available as `cluster:::silhouette.default.R`).

Observations with a large  $s(i)$  (almost 1) are very well clustered, a small  $s(i)$  (around 0) means that the observation lies between two clusters, and observations with a negative  $s(i)$  are probably placed in the wrong cluster.

### Value

`silhouette()` returns an object, `sil`, of class `silhouette` which is an  $[n \times 3]$  matrix with attributes. For each observation  $i$ , `sil[i, ]` contains the cluster to which  $i$  belongs as well as the neighbor cluster of  $i$  (the cluster, not containing  $i$ , for which the average dissimilarity between its observations and  $i$  is minimal), and the silhouette width  $s(i)$  of the observation. The `colnames` correspondingly are `c("cluster", "neighbor", "sil_width")`.

`summary(sil)` returns an object of class `summary.silhouette`, a list with components

<code>si.summary</code>	numerical <a href="#">summary</a> of the individual silhouette widths $s(i)$ .
<code>clus.avg.widths</code>	numeric (rank 1) array of clusterwise <i>means</i> of silhouette widths where <code>mean = FUN</code> is used.
<code>avg.width</code>	the total mean <code>FUN(s)</code> where $s$ are the individual silhouette widths.

clus.sizes    [table](#) of the  $k$  cluster sizes.  
 call         if available, the call creating `sil`.  
 Ordered      logical identical to `attr(sil, "Ordered")`, see below.

`sortSilhouette(sil)` orders the rows of `sil` as in the silhouette plot, by cluster (increasingly) and decreasing silhouette width  $s(i)$ .

`attr(sil, "Ordered")` is a logical indicating if `sil` is ordered as by `sortSilhouette()`. In that case, `rownames(sil)` will contain case labels or numbers, and

`attr(sil, "iOrd")` the ordering index vector.

### Note

While `silhouette()` is *intrinsic* to the [partition](#) clusterings, and hence has a (trivial) method for these, it is straightforward to get silhouettes from hierarchical clusterings from `silhouette.default()` with `cutree()` and distance as input.

By default, for `clara()` partitions, the silhouette is just for the best random *subset* used. Use `full = TRUE` to compute (and later possibly plot) the full silhouette.

### References

Rousseeuw, P.J. (1987) Silhouettes: A graphical aid to the interpretation and validation of cluster analysis. *J. Comput. Appl. Math.*, **20**, 53–65.

chapter 2 of Kaufman, L. and Rousseeuw, P.J. (1990), see the references in [plot.agnes](#).

### See Also

[partition.object](#), [plot.partition](#).

### Examples

```
data(ruspini)
pr4 <- pam(ruspini, 4)
str(si <- silhouette(pr4))
(ssi <- summary(si))
plot(si) # silhouette plot
plot(si, col = c("red", "green", "blue", "purple"))# with cluster-wise coloring

si2 <- silhouette(pr4$clustering, dist(ruspini, "canberra"))
summary(si2) # has small values: "canberra"'s fault
plot(si2, nmax= 80, cex.names=0.6)

op <- par(mfrow= c(3,2), oma= c(0,0, 3, 0),
          mgp= c(1.6, .8, 0), mar= .1+c(4,2,2,2))
for(k in 2:6)
  plot(silhouette(pam(ruspini, k=k)), main = paste("k = ",k), do.n.k=FALSE)
mtext("PAM(Ruspini) as in Kaufman & Rousseeuw, p.101",
      outer = TRUE, font = par("font.main"), cex = par("cex.main"))
par(op)

## clara(): standard silhouette is just for the best random subset
data(xclara)
set.seed(7)
str(xclk <- xclara[sample(nrow(xclara), size = 1000) ,])
```

```

cl3 <- clara(xclk, 3)
plot(silhouette(cl3)) # only of the "best" subset of 46
## The full silhouette: internally needs large (36 MB) dist object:
sf <- silhouette(cl3, full = TRUE) ## this is the same as
s.full <- silhouette(cl3$clustering, daisy(xclk))
if(paste(R.version$major, R.version$minor, sep=".") >= "2.3.0")
  stopifnot(all.equal(sf, s.full, check.attributes = FALSE, tol = 0))
## color dependent on original "3 groups of each 1000":
plot(sf, col = 2+ as.integer(names(cl3$clustering) ) %% 1000,
      main ="plot(silhouette(clara(.), full = TRUE))")

## Silhouette for a hierarchical clustering:
ar <- agnes(ruspini)
si3 <- silhouette(cutree(ar, k = 5), # k = 4 gave the same as pam() above
                 daisy(ruspini))
plot(si3, nmax = 80, cex.names = 0.5)
## 2 groups: Agnes() wasn't too good:
si4 <- silhouette(cutree(ar, k = 2), daisy(ruspini))
plot(si4, nmax = 80, cex.names = 0.5)

```

sizeDiss

*Sample Size of Dissimilarity Like Object***Description**

Returns the number of observations (*sample size*) corresponding to a dissimilarity like object, or equivalently, the number of rows or columns of a matrix when only the lower or upper triangular part (without diagonal) is given.

It is nothing else but the inverse function of  $f(n) = n(n - 1)/2$ .

**Usage**

```
sizeDiss(d)
```

**Arguments**

**d** any R object with length (typically)  $n(n - 1)/2$ .

**Value**

a number;  $n$  if length(d) ==  $n(n-1)/2$ , NA otherwise.

**See Also**

[dissimilarity.object](#) and also [as.dist](#) for class dissimilarity and dist objects which have a Size attribute.

**Examples**

```

sizeDiss(1:10) # 5, since 10 == 5 * (5 - 1) / 2
sizeDiss(1:9) # NA

n <- 1:100
stopifnot(n == sapply( n*(n-1)/2, function(n) sizeDiss(logical(n))))

```

---

summary.agnes	<i>Summary Method for 'agnes' Objects</i>
---------------	---

---

### Description

Returns (and prints) a summary list for an `agnes` object. Printing gives more output than the corresponding `print.agnes` method.

### Usage

```
## S3 method for class 'agnes':
summary(object, ...)
## S3 method for class 'summary.agnes':
print(x, ...)
```

### Arguments

`x`, `object`     a `agnes` object.  
`...`             potential further arguments (require by generic).

### See Also

`agnes`, `agnes.object`.

### Examples

```
data(agriculture)
summary(agnes(agriculture))
```

---

summary.clara	<i>Summary Method for 'clara' Objects</i>
---------------	---

---

### Description

Returns (and prints) a summary list for a `clara` object. Printing gives more output than the corresponding `print.clara` method.

### Usage

```
## S3 method for class 'clara':
summary(object, ...)
## S3 method for class 'summary.clara':
print(x, ...)
```

### Arguments

`x`, `object`     a `clara` object.  
`...`             potential further arguments (require by generic).



**See Also**

[clara.object](#)

**Examples**

```
## generate 2000 objects, divided into 5 clusters.
set.seed(47)
x <- rbind(cbind(rnorm(400, 0,4), rnorm(400, 0,4)),
           cbind(rnorm(400,10,8), rnorm(400,40,6)),
           cbind(rnorm(400,30,4), rnorm(400, 0,4)),
           cbind(rnorm(400,40,4), rnorm(400,20,2)),
           cbind(rnorm(400,50,4), rnorm(400,50,4))
)
clx5 <- clara(x, 5)
## Mis`classification' table:

table(rep(1:5, rep(400,5)), clx5$clust) # -> 1 "error"
summary(clx5)

## Graphically:
par(mfrow = c(3,1), mgp = c(1.5, 0.6, 0), mar = par("mar") - c(0,0,2,0))

plot(x, col = rep(2:6, rep(400,5)))
plot(clx5)
```

---

summary.diana

*Summary Method for 'diana' Objects*


---

**Description**

Returns (and prints) a summary list for a diana object.

**Usage**

```
## S3 method for class 'diana':
summary(object, ...)
## S3 method for class 'summary.diana':
print(x, ...)
```

**Arguments**

`x`, `object`     a [diana](#) object.  
`...`             potential further arguments (require by generic).

**See Also**

[diana](#), [diana.object](#).

---

`summary.mona`*Summary Method for 'mona' Objects*

---

**Description**

Returns (and prints) a summary list for a mona object.

**Usage**

```
## S3 method for class 'mona':  
summary(object, ...)  
## S3 method for class 'summary.mona':  
print(x, ...)
```

**Arguments**

`x, object` a [mona](#) object.  
`...` potential further arguments (require by generic).

**See Also**

[mona](#), [mona.object](#).

---

`summary.pam`*Summary Method for PAM Objects*

---

**Description**

Summarize a [pam](#) object and return an object of class `summary.pam`. There's a [print](#) method for the latter.

**Usage**

```
## S3 method for class 'pam':  
summary(object, ...)  
## S3 method for class 'summary.pam':  
print(x, ...)
```

**Arguments**

`x, object` a [pam](#) object.  
`...` potential further arguments (require by generic).

**See Also**

[pam](#), [pam.object](#).

---

`twins.object`      *Hierarchical Clustering Object*

---

**Description**

The objects of class "twins" represent an agglomerative or divisive (polythetic) hierarchical clustering of a dataset.

**Value**

See [agnes.object](#) and [diana.object](#) for details.

**GENERATION**

This class of objects is returned from `agnes` or `diana`.

**METHODS**

The "twins" class has a method for the following generic function: `pltree`.

**INHERITANCE**

The following classes inherit from class "twins": "agnes" and "diana".

**See Also**

[agnes,diana](#).

---

`volume.ellipsoid`      *Compute the Volume of Planar Object*

---

**Description**

Compute the volume of a planar object. This is a generic function and a method for `ellipsoid` objects.

**Usage**

```
## S3 method for class 'ellipsoid':
volume(object)
```

**Arguments**

`object`      an R object the volume of which is wanted; for the `ellipsoid` method, an object of that class (see [ellipsoidhull](#) or the example below).

**Value**

a number, the volume of the given object.

**See Also**

`ellipsoidhull` for spanning ellipsoid computation.

**Examples**

```
## example(ellipsoidhull) # which defines `ellipsoid' object <namefoo>
myEl <- structure(list(cov = rbind(c(3,1),1:2), loc = c(0,0), d2 = 10),
                  class = "ellipsoid")
volume(myEl) # i.e. "area" here (d = 2)
myEl # also mentions the "volume"
```

---

votes.repub

*Votes for Republican Candidate in Presidential Elections*

---

**Description**

A data frame with the percents of votes given to the republican candidate in presidential elections from 1856 to 1976. Rows represent the 50 states, and columns the 31 elections.

**Usage**

```
data(votes.repub)
```

**Source**

S. Peterson (1973): *A Statistical History of the American Presidential Elections*. New York: Frederick Ungar Publishing Co.

Data from 1964 to 1976 is from R. M. Scammon, *American Votes 12*, Congressional Quarterly.

---

xclara

*Bivariate Data Set with 3 Clusters*

---

**Description**

An artificial data set consisting of 3000 points in 3 well-separated clusters of size 1000 each.

**Usage**

```
data(xclara)
```

**Format**

A data frame with 3000 observations on 2 numeric variables giving the  $x$  and  $y$  coordinates of the points, respectively.

**Source**

Sample data set accompanying the reference below, obtained from <http://www.stat.ucla.edu/journals/jss/v01/i04/data/>.

**References**

Anja Struyf, Mia Hubert & Peter J. Rousseeuw (1996): Clustering in an Object-Oriented Environment. *Journal of Statistical Software*, **1**. <http://www.stat.ucla.edu/journals/jss/>

## Chapter 16

# The foreign package

---

lookup.xport

*Lookup Information on a SAS XPORT Format Library*

---

### Description

Scans a file as a SAS XPORT format library and returns a list containing information about the SAS library.

### Usage

```
lookup.xport (file)
```

### Arguments

file	character variable with the name of the file to read. The file must be in SAS XPORT format.
------	---

### Value

A list with one component for each dataset in the XPORT format library.

### Author(s)

Saikat DebRoy

### References

SAS Technical Support document TS-140: “The Record Layout of a Data Set in SAS Transport (XPORT) Format” available as <http://ftp.sas.com/techsup/download/technote/ts140.html>.

### See Also

[read.xport](#)

**Examples**

```
## Not run:  
lookup.xport("transport")  
  
## End(Not run)
```

---

read.arff                      *Read Data from ARFF Files*

---

**Description**

Reads data from Weka Attribute-Relation File Format (ARFF) files.

**Usage**

```
read.arff(file)
```

**Arguments**

`file`                      a character string with the name of the ARFF file to read from, or a [connection](#) which will be opened if necessary, and if so closed at the end of the function call.

**Value**

A data frame containing the data from the ARFF file.

**References**

Attribute-Relation File Format <http://www.cs.waikato.ac.nz/~ml/weka/arff.html>  
[http://weka.sourceforge.net/wekadoc/index.php/en:ARFF\\_\(3.5.1\)](http://weka.sourceforge.net/wekadoc/index.php/en:ARFF_(3.5.1))

**See Also**

[write.arff](#)

---

read.dbf                      *Read a DBF File*

---

**Description**

The function reads a DBF file into a data frame, converting character fields to factors, and trying to respect NULL fields.

**Usage**

```
read.dbf(file, as.is = FALSE)
```

## Arguments

<code>file</code>	name of input file
<code>as.is</code>	should character vectors not be converted to factors?

## Details

DBF is the extension used for files written for the 'XBASE' family of database languages, 'covering the dBase, Clipper, FoxPro, and their Windows equivalents Visual dBase, Visual Objects, and Visual FoxPro, plus some older products' (<http://www.clicketyclick.dk/databases/xbase/format/>). Most of these follow the file structure used by Ashton-Tate's dBase II, III or 4 (later owned by Borland).

`read.dbf` is based on C code from <http://shapelib.maptools.org/> which implements the 'XBASE' specification. It can convert fields of type "L" (logical), "N" and "F" (numeric and float) and "D" (dates): all other field types are read as-is as character vectors. A numeric field is read as an R integer vector if it is encoded to have no decimals, otherwise as a numeric vector. However, if the numbers are too large to fit into an integer vector, it is changed to numeric. Note that it is possible to read integers that cannot be represented exactly even as doubles: this sometimes occurs if IDs are incorrectly coded as numeric.

## Value

A data frame of data from the DBF file; note that the field names are adjusted to use in R using `make.names(unique=TRUE)`.

There is an attribute `"data_type"` giving the single-character dBase types for each field.

## Author(s)

Nicholas Lewin-Koh and Roger Bivand; shapelib by Frank Warmerdam

## References

<http://shapelib.maptools.org/>.

The Borland file specification *via* <http://www.wotsit.org>, currently at <http://www.wotsit.org/list.asp?fc=6>.

## See Also

[write.dbf](#)

## Examples

```
x <- read.dbf(system.file("files/sids.dbf", package="foreign"))[1]
str(x)
summary(x)
```



read.dta

*Read Stata Binary Files***Description**

Reads a file in Stata version 5–11 binary format into a data frame.

**Usage**

```
read.dta(file, convert.dates = TRUE, convert.factors = TRUE,
         missing.type = FALSE,
         convert.underscore = FALSE, warn.missing.labels = TRUE)
```

**Arguments**

`file` a filename or URL as a character string.

`convert.dates` Convert Stata dates to Date class?

`convert.factors` Use Stata value labels to create factors? (version 6.0 or later).

`missing.type` For version 8 or later, store information about different types of missing data?

`convert.underscore` Convert "\_" in Stata variable names to "." in R names?

`warn.missing.labels` Warn if a variable is specified with value labels and those value labels are not present in the file.

**Details**

If the filename appears to be a URL (of schemes 'http:', 'ftp:' or 'https:') the URL is first downloaded to a temporary file and then read. ('https:' is only supported on some platforms.)

The variables in the Stata data set become the columns of the data frame. Missing values are correctly handled. The data label, variable labels, and timestamp are stored as attributes of the data frame. Nothing is done with variable characteristics.

By default Stata dates (%d and %td formats) are converted to R's Date class and variables with Stata value labels are converted to factors. Ordinarily, read.dta will not convert a variable to a factor unless a label is present for every level. Use convert.factors = NA to override this. In any case the value label and format information is stored as attributes on the returned data frame.

Stata 8.0 introduced a system of 27 different missing data values. If missing.type is TRUE a separate list is created with the same variable names as the loaded data. For string variables the list value is NULL. For other variables the value is NA where the observation is not missing and 0–26 when the observation is missing. This is attached as the "missing" attribute of the returned value.

**Value**

A data frame with attributes. These will include "datalabel", "time.stamp", "formats", "types", "val.labels", "var.labels" and "version" and may include "label.table". Possible versions are 5, 6, 7, -7 (Stata 7SE, 'format-111'), 8 (Stata 8 and 9, 'format-113') and 10 (Stata 10 and 11, 'format-114').

The value labels in attribute "val.labels" name a table for each variable, or are an empty string. The tables are elements of the named list attribute "label.table": each is an integer vector with names,

### Author(s)

Thomas Lumley and R-core members

### References

Stata Users Manual (versions 5 & 6), Programming manual (version 7), or online help (version 8 and later) describe the format of the files. Or at <http://www.stata.com/help.cgi?dta> and [http://www.stata.com/help.cgi?dta\\_113](http://www.stata.com/help.cgi?dta_113)

### See Also

[write.dta](#), [attributes](#) [Date factor](#)

### Examples

```
data(swiss)
write.dta(swiss,swissfile <- tempfile())
read.dta(swissfile)
```

---

read.epiinfo            *Read Epi Info Data Files*

---

### Description

Reads data files in the .REC format used by Epi Info versions 6 and earlier and by EpiData. Epi Info is a public domain database and statistics package produced by the US Centers for Disease Control and EpiData is a freely available data entry and validation system.

### Usage

```
read.epiinfo(file, read.deleted = FALSE, guess.broken.dates = FALSE,
             thisyear = NULL, lower.case.names = FALSE)
```

### Arguments

`file`            A filename, URL, or connection.

`read.deleted` Deleted records are read if TRUE, omitted if FALSE or replaced with NA if NA.

`guess.broken.dates` Attempt to convert dates with 0 or 2 digit year information (see 'Details').

`thisyear`        A 4-digit year to use for dates with no year. Defaults to the current year.

`lower.case.names` Convert variable names to lowercase?

## Details

Epi Info allows dates to be specified with no year or with a 2 or 4 digits. Dates with four-digit years are always converted to `Date` class. With the `guess.broken.dates` option the function will attempt to convert two-digit years using the operating system's default method (see [Date](#)) and will use the current year or the `thisyear` argument for dates with no year information.

If `read.deleted` is `TRUE` the "deleted" attribute of the data frame indicates the deleted records.

## Value

A data frame.

## Note

Epi Info 2000, the current version, uses the Microsoft Access file format to store data. This may be readable with the `RODBC` or `RDCOM` packages.

## References

<http://www.cdc.gov/epiinfo/>, <http://www.epidata.dk>

## See Also

[DateTimeClasses](#)

## Examples

```
## Not run:
data<-read.epiinfo("oswego.rec",guess.broken.dates=TRUE,thisyear="1972")

## End(Not run)
```

---

read.mtp

*Read a Minitab Portable Worksheet*

---

## Description

Return a list with the data stored in a file as a Minitab Portable Worksheet.

## Usage

```
read.mtp(file)
```

## Arguments

`file` character variable with the name of the file to read. The file must be in Minitab Portable Worksheet format.

## Value

A list with one component for each column, matrix, or constant stored in the Minitab worksheet.

**Author(s)**

Douglas M. Bates

**References**

<http://www.minitab.com/>

**Examples**

```
## Not run:
read.mtp("ex1-10.mtp")

## End(Not run)
```

---

read.octave

*Read Octave Text Data Files*

---

**Description**

Read a file in Octave text data format into a list.

**Usage**

```
read.octave(file)
```

**Arguments**

`file` a character string with the name of the file to read.

**Details**

This function is used to read in files in Octave text data format, as created by `save -ascii` in Octave. It knows about most of the common types of variables, including the standard atomic (real and complex scalars, matrices, and  $N$ -d arrays, strings, ranges, and boolean scalars and matrices) and recursive (structs, cells, and lists) ones, but has no guarantee to read all types. If a type is not recognized, a warning indicating the unknown type is issued, it is attempted to skip the unknown entry, and NULL is used as its value. Note that this will give incorrect results, and maybe even errors, in the case of unknown recursive data types.

As Octave can read MATLAB binary files, one can make the contents of such files available to R by using Octave's load and save (as text) facilities as an intermediary step.

**Value**

A list with one named component for each variable in the file.

**Author(s)**

Stephen Eglen <[stephen@gnu.org](mailto:stephen@gnu.org)> and Kurt Hornik

**References**

<http://www.octave.org/>

read.spss

*Read an SPSS Data File***Description**

read.spss reads a file stored by the SPSS save or export commands.

**Usage**

```
read.spss(file, use.value.labels = TRUE, to.data.frame = FALSE,
          max.value.labels = Inf, trim.factor.names = FALSE,
          trim_values = TRUE, reencode = NA, use.missings = to.data.frame)
```

**Arguments**

file	Character string: the name of the file or URL to read.
use.value.labels	Convert variables with value labels into R factors with those levels?
to.data.frame	return a data frame?
max.value.labels	Only variables with value labels and at most this many unique values will be converted to factors if use.value.labels = TRUE.
trim.factor.names	Logical: trim trailing spaces from factor levels?
trim_values	logical: should values and value labels have trailing spaces ignored when matching for use.value.labels = TRUE?
reencode	logical: should character strings be re-encoded to the current locale. The default, NA, means to do so in a UTF-8 locale, only. Alternatively character, specifying an encoding to assume.
use.missings	logical: should information on user-defined missing values be used to set the corresponding values to NA?

**Details**

This uses modified code from the PSPP project (<http://www.gnu.org/software/pspp/>) for reading the SPSS formats.

If the filename appears to be a URL (of schemes 'http:', 'ftp:' or 'https:') the URL is first downloaded to a temporary file and then read. ('https:' is only supported on some platforms.)

Occasionally in SPSS value labels will be added to some values of a continuous variable (e.g. to distinguish different types of missing data), and you will not want these variables converted to factors. By setting max.val.labels you can specify that variables with a large number of distinct values are not converted to factors even if they have value labels. In addition, variables will not be converted to factors if there are non-missing values that have no value label. The value labels are then returned in the "value.labels" attribute of the variable.

If SPSS variable labels are present, they are returned as the "variable.labels" attribute of the answer.

Fixed length strings (including value labels) are padded on the right with spaces by SPSS, and so are read that way by R. The default argument trim\_values=TRUE causes trailing spaces to be

ignored when matching to value labels, as examples have been seen where the strings and the value labels had different amounts of padding. See the examples for `sub` for ways to remove trailing spaces in character data.

URL [http://msdn.microsoft.com/en-us/library/ms776446\(VS.85\).aspx](http://msdn.microsoft.com/en-us/library/ms776446(VS.85).aspx) provides a list of translations from Windows codepage numbers to encoding names that `iconv` is likely to know about and so suitable values for `reencode`. Automatic re-encoding is attempted for apparent codepages of 200 or more in a UTF-8 locale: some other high-numbered codepages can be re-encoded on most systems, but the encoding names are platform-dependent (see `iconvlist`).

### Value

A list (or data frame) with one component for each variable in the saved data set.

If what looks like a Windows codepage was recorded in the SPSS file, it is attached (as a number) as attribute `"codepage"` to the result.

There may be attributes `"label.table"` and `"variable.labels"`. Attribute `"label.table"` is a named list of value labels with one element per variable, either `NULL` or a names character vector. Attribute `"variable.labels"` is a named character vector with names the short variable names and elements the long names.

If there are user-defined missing values, there will be a attribute `"Missings"`. This is a named list with one list element per variable. Each element has an element `type`, a length-one character vector giving the type of missingness, and may also have an element `value` with the values corresponding to missingness. This is a complex subject (where the `R` and `C` source code for `read.spss` is the main documentation), but the simplest cases are types `"one"`, `"two"` and `"three"` with a corresponding number of (real or string) values whose labels can be found from the `"label.table"` attribute. Other possibilities are a finite or semi-infinite range, possibly plus a single value. See also [http://www.gnu.org/software/pspp/manual/html\\_node/Missing-Observations.html#Missing-Observations](http://www.gnu.org/software/pspp/manual/html_node/Missing-Observations.html#Missing-Observations).

### Note

If SPSS value labels are converted to factors the underlying numerical codes will not in general be the same as the SPSS numerical values, since the numerical codes in `R` are always 1, 2, 3, ...

You may see warnings about the file encoding for SPSS `save` files: it is possible such files contain non-ASCII character data which need re-encoding. The most common occurrence is Windows codepage 1252, a superset of Latin-1. The encoding is recorded (as an integer) in attribute `"codepage"` of the result if it looks like a Windows codepage. Automatic re-encoding is done only in UTF-8 locales: see argument `reencode`.

### Author(s)

Saikat DebRoy and the R Core team

### Examples

```
## Not run:
read.spss("datafile")
## don't convert value labels to factor levels
read.spss("datafile", use.value.labels = FALSE)
## convert value labels to factors for variables with at most
## ten distinct values.
read.spss("datafile", max.val.labels = 10)

## End(Not run)
```

---

 read.ssd

*Obtain a Data Frame from a SAS Permanent Dataset, via read.xport*


---

### Description

Generates a SAS program to convert the `ssd` contents to SAS transport format and then uses `read.xport` to obtain a data frame.

### Usage

```
read.ssd(libname, sectionnames,
         tmpXport=tempfile(), tmpProgLoc=tempfile(), sascmd="sas")
```

### Arguments

<code>libname</code>	character string defining the SAS library (usually a directory reference)
<code>sectionnames</code>	character vector giving member names. These are files in the <code>libname</code> directory. They will usually have a <code>.ssd0x</code> or <code>.sas7bdat</code> extension, which should be omitted.
<code>tmpXport</code>	character string: location where temporary xport format archive should reside – defaults to a randomly named file in the session temporary directory, which will be removed.
<code>tmpProgLoc</code>	character string: location where temporary conversion SAS program should reside – defaults to a randomly named file in session temporary directory, which will be removed on successful operation.
<code>sascmd</code>	character string giving full path to SAS executable.

### Details

Creates a SAS program and runs it.

Error handling is primitive.

### Value

A data frame if all goes well, or `NULL` with warnings and some enduring side effects (log file for auditing)

### Note

**This requires SAS to be available.** If you have a SAS dataset without access to SAS you will need another product to convert it to a format such as `.csv`, for example ‘Stat/Transfer’ or ‘DBMS/Copy’ or the ‘SAS System Viewer’ (Windows only).

### Author(s)

For Unix: VJ Carey <stvjc@channing.harvard.edu>

### See Also

[read.xport](#)

**Examples**

```
## if there were some files on the web we could get a real
## runnable example
## Not run:
R> list.files("trialdata")
 [1] "baseline.sas7bdat" "form11.sas7bdat" "form12.sas7bdat"
 [4] "form13.sas7bdat" "form22.sas7bdat" "form23.sas7bdat"
 [7] "form3.sas7bdat"   "form4.sas7bdat"   "form48.sas7bdat"
[10] "form50.sas7bdat"  "form51.sas7bdat"  "form71.sas7bdat"
[13] "form72.sas7bdat"  "form8.sas7bdat"   "form9.sas7bdat"
[16] "form90.sas7bdat"  "form91.sas7bdat"

R> baseline <- read.ssd("trialdata","baseline")
R> form90 <- read.ssd("trialdata","form90")

## Or for a Windows example
sashome <- "/Program Files/SAS/SAS 9.1"
read.ssd(file.path(sashome, "core", "sashelp"), "retail",
         sascmd = file.path(sashome, "sas.exe"))

## End(Not run)
```

read.systat

*Obtain a Data Frame from a Systat File***Description**

read.systat reads a rectangular data file stored by the Systat SAVE command as (legacy) \*.sys or more recently \*.syd files.

**Usage**

```
read.systat(file, to.data.frame = TRUE)
```

**Arguments**

file                    character variable with the name of the file to read  
to.data.frame            return a data frame (otherwise a list)

**Details**

The function only reads those Systat files that are rectangular data files (`mtype = 1`), and warns when files have non-standard variable name codings. The files tested were produced on MS-DOS and Windows: files for the Mac version of Systat have a completely different format.

The C code was originally written for an add-on module for Systat described in Bivand (1992 paper). Variable names retain the trailing dollar in the list returned when `to.data.frame` is FALSE, and in that case character variables are returned as is and filled up to 12 characters with blanks on the right. The original function was limited to reading Systat files with up to 256 variables (a Systat limitation); it will now read up to 8192 variables.

If there is a user comment in the header this is returned as attribute "comment". Such comments are always a multiple of 72 characters (with a maximum of 720 chars returned), normally padded with trailing spaces.



**Value**

A data frame (or list) with one component for each variable in the saved data set.

**Author(s)**

Roger Bivand

**References**

Systat Manual, 1987, 1989

Bivand, R. S. (1992) SYSTAT-compatible software for modelling spatial dependence among observations. *Computers and Geosciences* **18**, 951–963.

**Examples**

```
summary(iris)
iris.s <- read.systat(system.file("files/Iris.syd", package="foreign")[1])
str(iris.s)
summary(iris.s)
```

---

read.xport

*Read a SAS XPORT Format Library*

---

**Description**

Reads a file as a SAS XPORT format library and returns a list of data.frames.

**Usage**

```
read.xport(file)
```

**Arguments**

`file` character variable with the name of the file to read. The file must be in SAS XPORT format.

**Value**

If there is a more than one dataset in the XPORT format library, a named list of data frames, otherwise a data frame. The columns of the data frames will be either numeric (corresponding to numeric in SAS) or factor (corresponding to character in SAS). All SAS numeric missing values (including special missing values represented by `._`, `.A` to `.Z` by SAS) are mapped to `R NA`.

Trailing blanks are removed from character columns before conversion to a factor. Some sources claim that character missing values in SAS are represented by `' '` or `" "`: these are not treated as R missing values.

**Author(s)**

Saikat DebRoy <saikat@stat.wisc.edu>

**References**

SAS Technical Support document TS-140: “The Record Layout of a Data Set in SAS Transport (XPORT) Format” available at <http://ftp.sas.com/techsup/download/technote/ts140.html>.

**See Also**

[lookup.xport](#)

**Examples**

```
## Not run:
read.xport("transport")

## End(Not run)
```

---

S3 read functions *Read an S3 Binary or data.dump File*

---

**Description**

Reads binary data files or `data.dump` files that were produced in S version 3.

**Usage**

```
data.restore(file, print = FALSE, verbose = FALSE, env = .GlobalEnv)
read.S(file)
```

**Arguments**

<code>file</code>	the filename of the S-PLUS <code>data.dump</code> or binary file.
<code>print</code>	whether to print the name of each object as read from the file.
<code>verbose</code>	whether to print the name of every subitem within each object.
<code>env</code>	environment within which to create the restored object(s).

**Details**

`read.S` can read the binary files produced in some older versions of S-PLUS on either Windows (versions 3.x, 4.x, 2000) or Unix (version 3.x with 4 byte integers). It automatically detects whether the file was produced on a big- or little-endian machine and adapts itself accordingly.

`data.restore` can read a similar range of files produced by `data.dump` and for newer versions of S-PLUS, those from `data.dump(....., oldStyle=TRUE)`.

Not all S3 objects can be handled in the current version. The most frequently encountered exceptions are functions and expressions; you will also have trouble with objects that contain model formulas. In particular, comments will be lost from function bodies, and the argument lists of functions will often be changed.

**Value**

For `read.S`, an R version of the S3 object.

For `data.restore`, the name of the file.

**Author(s)**

Duncan Murdoch

**Examples**

```
## Not run: read.S(file.path("_Data", "myobj"))
data.restore("dumpdata", print = TRUE)

## End(Not run)
```

---

`write.arff`*Write Data into ARFF Files*

---

**Description**

Writes data into Weka Attribute-Relation File Format (ARFF) files.

**Usage**

```
write.arff(x, file, eol = "\n", relation = deparse(substitute(x)))
```

**Arguments**

<code>x</code>	the data to be written, preferably a matrix or data frame. If not, coercion to a data frame is attempted.
<code>file</code>	either a character string naming a file, or a connection. "" indicates output to the standard output connection.
<code>eol</code>	the character(s) to print at the end of each line (row).
<code>relation</code>	The name of the relation to be written in the file.

**Details**

`relation` will be passed through `make.names` before writing to the file, in an attempt to it them acceptable to Weka, and column names what do not start with an alphabetic character will have `X` prepended.

However, the references say that ARFF files are ASCII files, and that encoding is not enforced.

**References**

Attribute-Relation File Format <http://www.cs.waikato.ac.nz/~ml/weka/arff.html>  
[http://weka.sourceforge.net/wekadoc/index.php/en:ARFF\\_\(3.5.1\)](http://weka.sourceforge.net/wekadoc/index.php/en:ARFF_(3.5.1))

**See Also**

[read.arff](#)

**Examples**

```
write.arff(iris, file = "")
```

---

write.dbf	<i>Write a DBF File</i>
-----------	-------------------------

---

### Description

The function tries to write a data frame to a DBF file.

### Usage

```
write.dbf(dataframe, file, factor2char = TRUE, max_nchar = 254)
```

### Arguments

dataframe	a data frame object.
file	a file name to be written to.
factor2char	logical, default TRUE, convert factor columns to character: otherwise they are written as the internal integer codes.
max_nchar	The maximum number of characters allowed in a character field. Strings which exceed this will be truncated with a warning. See Details.

### Details

Dots in column names are replaced by underlines in the DBF file, and names are truncated to 11 characters.

Only vector columns of classes "logical", "numeric", "integer", "character", "factor" and "Date" can be written. Other columns should be converted to one of these.

Maximum precision (number of digits including minus sign and decimal sign) for numeric is 19 - scale (digits after the decimal sign) which is calculated internally based on the number of digits before the decimal sign.

The original DBASE format limited character fields to 254 bytes. It is said that Clipper and FoxPro can read up to 32K, and it is possible to write a reader that could accept up to 65535 bytes. (The documentation suggests that only ASCII characters can be assumed to be supported.) Readers expecting the older standard (which includes Excel 2003, Access 2003 and OpenOffice 2.0) will truncate the field to the maximum width modulo 256, so increase `max_nchar` only if you are sure the intended reader supports wider character fields.

### Value

Invisible NULL.

### Note

Other applications have varying abilities to read the data types used here. Microsoft Access reads "numeric", "integer", "character" and "Date" fields, including recognizing missing values, but not "logical" (read as 0, -1). Microsoft Excel understood all possible types but did not interpret missing values in character fields correctly (showing them as character nuls).

### Author(s)

Nicholas J. Lewin-Koh, modified by Roger Bivand and Brian Ripley; shapelib by Frank Warmerdam.

**References**

<http://shapelib.maptools.org/>  
[http://www.clicketyclick.dk/databases/xbase/format/data\\_types.html](http://www.clicketyclick.dk/databases/xbase/format/data_types.html)

**See Also**

[read.dbf](#)

**Examples**

```
str(warpbreaks)
try1 <- paste(tempfile(), ".dbf", sep = "")
write.dbf(warpbreaks, try1, factor2char = FALSE)
in1 <- read.dbf(try1)
str(in1)
try2 <- paste(tempfile(), ".dbf", sep = "")
write.dbf(warpbreaks, try2, factor2char = TRUE)
in2 <- read.dbf(try2)
str(in2)
unlink(c(try1, try2))
```

---

write.dta

*Write Files in Stata Binary Format*

---

**Description**

Writes the data frame to file in the Stata binary format. Does not write array variables unless they can be [drop](#)-ed to a vector.

**Usage**

```
write.dta(dataframe, file, version = 7L,
          convert.dates = TRUE, tz = "GMT",
          convert.factors = c("labels", "string", "numeric", "codes"))
```

**Arguments**

dataframe	a data frame.
file	character string giving filename.
version	integer: Stata version: 6, 7, 8 and 10 are supported, and 9 is mapped to 8, 11 to 10.
convert.dates	Convert Date and POSIXt objects to Stata dates?
tz	timezone for date conversion
convert.factors	how to handle factors

## Details

The major differences between file formats in Stata versions is that version 7.0 and later allow 32-character variable names (5 and 6 were restricted to 8-character name). The `abbreviate` function is used to trim long variables to the permitted length. A warning is given if this is needed and it is an error for the abbreviated names not to be unique.

The columns in the data frame become variables in the Stata data set. Missing values are correctly handled.

Unless deselected, R date and date-time objects (`POSIXt` classes) are converted into the Stata format. For date-time objects this may lose information – Stata dates are in days since 1960-1-1. `POSIXct` objects can be written without conversion but will not be understood as dates by Stata; `POSIXlt` objects cannot be written without conversion.

There are four options for handling factors. The default is to use Stata `value labels` for the factor levels. With `convert.factors="string"`, the factor levels are written as strings. With `convert.factors="numeric"` the numeric values of the levels are written, or NA if they cannot be coerced to numeric. Finally, `convert.factors="codes"` writes the underlying integer codes of the factors. This last used to be the only available method and is provided largely for backwards compatibility.

For Stata 8 or later use the default `version=7` – the only advantage of Stata 8 format is that it can represent multiple different missing value types, and R doesn't have them. Stata 10/11 allows longer format lists, but R does not make use of them.

Note that the Stata formats are documented to be use ASCII strings – R does not enforce this, but use of non-ASCII character strings will not be portable as the encoding is not recorded. Up to 244 bytes are allowed in character data, and longer strings will be truncated with a warning.

Stata uses some large numerical values to represent missing values. This function does not currently check, and hence integers greater than 2147483620 and doubles greater than 8.988e+307 may be misinterpreted by Stata.

## Value

NULL

## Author(s)

Thomas Lumley and R-core members

## References

Stata 6.0 Users Manual, Stata 7.0 Programming manual, Stata online help (version 8 and later, also <http://www.stata.com/help.cgi?dta> and [http://www.stata.com/help.cgi?dta\\_113](http://www.stata.com/help.cgi?dta_113)) describe the file formats.

## See Also

[read.dta](#), [attributes](#), [DateTimeClasses](#), [abbreviate](#)

## Examples

```
write.dta(swiss, swissfile <- tempfile())
read.dta(swissfile)
```

---

write.foreign      *Write Text Files and Code to Read Them*

---

### Description

This function exports simple data frames to other statistical packages by writing the data as free-format text and writing a separate file of instructions for the other package to read the data.

### Usage

```
write.foreign(df, datafile, codefile,
              package = c("SPSS", "Stata", "SAS"), ...)
```

### Arguments

df	A data frame
datafile	Name of file for data output
codefile	Name of file for code output
package	Name of package
...	Other arguments for the individual writeForeign functions

### Details

The work for this function is done by `foreign::writeForeignStata`, `foreign::writeForeignSAS` and `foreign::writeForeignSPSS`. To add support for another package, eg Systat, create a function `writeForeignSystat` with the same first three arguments as `write.foreign`. This will be called from `write.foreign` when `package="Systat"`.

Numeric variables and factors are supported for all packages: dates and times (`Date`, `dates`, `date`, and `POSIXt` classes) are also supported for SAS and characters are supported for SPSS.

For `package="SAS"` there are optional arguments `dataname="rdata"` taking a string that will be the SAS data set name and `validvarname` taking either `"V6"` or `"V7"`.

### Value

None

### Author(s)

Thomas Lumley and Stephen Weigand

### Examples

```
## Not run:
datafile<-tempfile()
codefile<-tempfile()
write.foreign(esoph, datafile, codefile, package="SPSS")
file.show(datafile)
file.show(codefile)
unlink(datafile)
unlink(codefile)
```

```
## End(Not run)
```





# Chapter 17

## The `lattice` package

---

A\_01\_Lattice

*Lattice Graphics*

---

### Description

Trellis Graphics for R

### Details

Trellis Graphics is a framework for data visualization developed at the Bell Labs by Rick Becker, Bill Cleveland, et al, extending ideas presented in Bill Cleveland's 1993 book *Visualizing Data*. Lattice is an implementation of Trellis Graphics for R.

Type `help(package = lattice)` to see a list of (public) functions for which further documentation is available. The 'See Also' section below lists specific areas of interest with pointers to the help pages with respective details. Apart from the documentation accompanying this package, a book on lattice is also available as part of Springer's 'Use R' series.

Lattice is built upon the Grid graphics engine and requires the `grid` add-on package. It is not (readily) compatible with traditional R graphics tools. The public interface is based on the implementation in S-PLUS, but features several extensions, in addition to incompatibilities introduced through the use of `grid`. To the extent possible, care has been taken to ensure that existing Trellis code written for S-PLUS works unchanged (or with minimal change) in Lattice. If you are having problems porting S-PLUS code, read the entry for `panel` in the documentation for `xypplot`. Most high level Trellis functions in S-PLUS are implemented, with the exception of `piechart`.

The example section below shows how to bring up a brief history of changes to the lattice package, which provides a summary of new features.

### Note

High level Lattice functions (like `xypplot`) are different from conventional R graphics functions because they don't actually draw anything. Instead, they return an object of class "trellis" which has to be then `printed` or `plotted` to create the actual plot. This is normally done automatically, but not when the high level functions are called inside another function (most often `source`) or other contexts where automatic printing is suppressed (e.g. `for` or `while` loops). In such situations, an explicit call to `print` or `plot` is required.

Lattice plots are highly customizable via user-modifiable settings. However, these are completely unrelated to base graphics settings; in particular, changing `par()` settings usually have no effect on lattice plots.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### References

Sarkar, Deepayan (2008) “Lattice: Multivariate Data Visualization with R”, Springer. ISBN: 978-0-387-75968-5 <http://lmdvr.r-forge.r-project.org/>

Cleveland, W.S. (1993) *Visualizing Data*.

Becker, R.A., Cleveland, W.S. and Shyu, M. “The Visual Design and Control of Trellis Display”, *Journal of Computational and Graphical Statistics*

Bell Lab’s Trellis Page contains several documents outlining the use of Trellis graphics; these provide a holistic introduction to the Trellis paradigm: <http://cm.bell-labs.com/cm/ms/departments/sia/project/trellis/>

### See Also

The Lattice user interface primarily consists of several ‘high level’ generic functions (listed below), each designed to create a particular type of statistical display by default. While each function does different things, they share several common features, reflected in several common arguments that affect the resulting displays in similar ways. These arguments are extensively (sometimes only) documented in the help page for `xyplot`. This includes a discussion of *conditioning* and control of the Trellis layout.

Lattice employs an extensive system of user-controllable parameters to determine the look and feel of the displays it produces. To learn how to use and customise the Graphical parameters used by the Lattice functions, see `trellis.par.set`. For other settings, see `lattice.options`. The default graphical settings are different for different graphical devices. To learn how to initialise new devices with the desired settings or change the settings of the current device, see `trellis.device`.

To learn about sophisticated (non-default) printing capabilities, see `print.trellis`. See `update.trellis` to learn about manipulating a “trellis” object. Tools to augment lattice plots after they are drawn (including `locator`-like functionality) is described in the `trellis.focus` help page.

The following is a list of ‘high level’ functions in the Lattice package with a brief description of what they do. In all cases, the actual display is produced by the so-called `panel` function, which has a suitable default, but can be substituted by an user defined function to create custom displays. The user will most often be interested in the default panel functions, which have a separate help page, linked to from the help pages of the corresponding high level function. Although documented separately, arguments to these panel functions can be supplied directly to the high level functions, which will forward the arguments as appropriate.

#### Univariate:

`barchart` bar plots

`bwplot` box and whisker plots

`densityplot` kernel density plots

`dotplot` dot plots

[histogram](#) histograms

[qqmath](#) quantile plots against mathematical distributions

[stripplot](#) 1-dimensional scatterplot

**Bivariate:**

[qq](#) q-q plot for comparing two distributions

[xyplot](#) scatter plot (and possibly a lot more)

**Trivariate:**

[levelplot](#) level plots (similar to image plots in R)

[contourplot](#) contour plots

[cloud](#) 3-D scatter plots

[wireframe](#) 3-D surfaces (similar to persp plots in R)

**Hypervariate:**

[splom](#) scatterplot matrix

[parallel](#) parallel coordinate plots

**Miscellaneous:**

[rfs](#) residual and fitted value plot (also see [oneway](#))

[tmd](#) Tukey Mean-Difference plot

Additionally, there are several panel functions that do little by themselves, but can be useful components of custom panel functions. These are documented in [panel.functions](#). Lattice also has a collection of convenience functions that correspond to the base graphics primitives [lines](#), [points](#), etc. They are implemented using Grid graphics, but try to be as close to the base versions as possible in terms of their argument list. These functions have imaginative names like [llines](#) or [panel.lines](#) and are often useful when writing (or porting from S-PLUS code) nontrivial panel functions.

**Examples**

```
## Not run:
RShowDoc("NEWS", package = "lattice")

## End(Not run)
```

**Description**

These are the most commonly used high level Trellis functions to plot pairs of variables. By far the most common is `xyplot`, designed mainly for two continuous variates (though factors can be supplied as well, in which case they will simply be coerced to numeric), which produces Conditional Scatter plots. The others are useful when one of the variates is a factor or a shingle. Most of these arguments are also applicable to other high level functions in the lattice package, but are only documented here.

**Usage**

```

xyplot(x, data, ...)
dotplot(x, data, ...)
barchart(x, data, ...)
stripplot(x, data, ...)
bwplot(x, data, ...)

## S3 method for class 'formula':
xyplot(x,
      data,
      allow.multiple = is.null(groups) || outer,
      outer = !is.null(groups),
      auto.key = FALSE,
      aspect = "fill",
      panel = lattice.getOption("panel.xyplot"),
      prepanel = NULL,
      scales = list(),
      strip = TRUE,
      groups = NULL,
      xlab,
      xlim,
      ylab,
      ylim,
      drop.unused.levels = lattice.getOption("drop.unused.levels"),
      ...,
      lattice.options = NULL,
      default.scales,
      subscripts = !is.null(groups),
      subset = TRUE)

## S3 method for class 'formula':
dotplot(x,
      data,
      panel = lattice.getOption("panel.dotplot"),
      ...)

## S3 method for class 'formula':
barchart(x,
      data,
      panel = lattice.getOption("panel.barchart"),
      box.ratio = 2,
      ...)

## S3 method for class 'formula':
stripplot(x,
      data,
      panel = lattice.getOption("panel.stripplot"),
      ...)

## S3 method for class 'formula':
bwplot(x,

```

```

data,
allow.multiple = is.null(groups) || outer,
outer = FALSE,
auto.key = FALSE,
aspect = "fill",
panel = lattice.getOption("panel.bwplot"),
prepanel = NULL,
scales = list(),
strip = TRUE,
groups = NULL,
xlab,
xlim,
ylab,
ylim,
box.ratio = 1,
horizontal = NULL,
drop.unused.levels = lattice.getOption("drop.unused.levels"),
...,
lattice.options = NULL,
default.scales,
subscripts = !is.null(groups),
subset = TRUE)

```

## Arguments

x

The object on which method dispatch is carried out.

For the "formula" methods, a formula describing the form of conditioning plot. The formula is generally of the form  $y \sim x \mid g1 * g2 * \dots$ , indicating that plots of  $y$  (on the  $y$  axis) versus  $x$  (on the  $x$  axis) should be produced conditional on the variables  $g1, g2, \dots$ . However, the conditioning variables  $g1, g2, \dots$  may be omitted. The formula can also be supplied as  $y \sim x \mid g1 + g2 + \dots$ .

For all of these functions, with the exception of `xyplot`, a formula of the form  $\sim x \mid g1 * g2 * \dots$  is also allowed. In that case,  $y$  defaults to `names(x)` if  $x$  is named, and a factor with a single level otherwise.

Other usage of the form `dotplot(x)` is handled by method dispatch as appropriate. The numeric method is equivalent to a call with no left hand side and no conditioning variables in the formula. For `barchart` and `dotplot`, non-trivial methods exist for tables and arrays, documented under [barchart.table](#).

The conditioning variables  $g1, g2, \dots$  must be either factors or shingles. Shingles are a way of processing numeric variables for use in conditioning. See documentation of [shingle](#) for details. Like factors, they have a "levels" attribute, which is used in producing the conditional plots.

Numeric conditioning variables are converted to shingles by the function `shingle` (however, using `equal.count` might be more appropriate in many cases) and character vectors are coerced to factors.

The formula can involve expressions, e.g. `sqrt()`, `log()`.

A special case is when the left and/or right sides of the formula (before the conditioning variables) contain a '+' sign, e.g.,  $y1+y2 \sim x \mid a*b$ . This for-

mula would be taken to mean that the user wants to plot both  $y1 \sim x \mid a*b$  and  $y2 \sim x \mid a*b$ , but with the  $y1 \sim x$  and  $y2 \sim x$  superposed in each panel (this is slightly more complicated in `barchart`). The two parts would be distinguished by different graphical parameters. This is essentially what the `groups` argument would produce, if  $y1$  and  $y2$  were concatenated to produce a longer vector, with the `groups` argument being an indicator of which rows come from which variable. In fact, this is exactly what is done internally using the `reshape` function. This feature cannot be used in conjunction with the `groups` argument.

To interpret  $y1 + y2$  as a sum, one can either set `allow.multiple=FALSE` or use `I(y1+y2)`.

A variation on this feature is when the `outer` argument is set to `TRUE` as well as `allow.multiple`. In that case, the plots are not superposed in each panel, but instead separated into different panels (as if a new conditioning variable had been added).

The `x` and `y` variables should both be numeric in `xyplot`, and an attempt is made to coerce them if not. However, if either is a factor, the levels of that factor are used as axis labels. In the other four functions documented here, exactly one of `x` and `y` should be numeric, and the other a factor or shingle. Which of these will happen is determined by the `horizontal` argument — if `horizontal=TRUE`, then `y` will be coerced to be a factor or shingle, otherwise `x`. The default value of `horizontal` is `FALSE` if `x` is a factor or shingle, `TRUE` otherwise. (The functionality provided by `horizontal=FALSE` is not S-compatible.)

Note that this argument used to be called `formula` in earlier versions (when the high level functions were not generic and the `formula` method was essentially the only method). This is no longer allowed. It is recommended that this argument not be named in any case, but rather be the first (unnamed) argument.

`data` For the `formula` method, a data frame containing values (or more precisely, anything that is a valid `envir` argument in `eval`, e.g. a list or an environment) for any variables in the formula, as well as `groups` and `subset` if applicable. If not found in `data`, or if `data` is unspecified, the variables are looked for in the environment of the formula. For other methods (where `x` is not a formula), `data` is usually ignored, often with a warning.

`allow.multiple, outer` logical flags to control what happens with formulas like  $y1 + y2 \sim x$ . See the entry for `x` for details. `allow.multiple` defaults to `TRUE` whenever it makes sense, and `outer` defaults to `FALSE` except when `groups` is explicitly specified or grouping doesn't make sense for the default panel function

`box.ratio` applicable to `bwplot`, `barchart` and `stripplot`, specifies the ratio of the width of the rectangles to the inter rectangle space.

`horizontal` logical, applicable to `bwplot`, `dotplot`, `barchart` and `stripplot`. Determines which of `x` and `y` is to be a factor or shingle (`y` if `TRUE`, `x` otherwise). Defaults to `FALSE` if `x` is a factor or shingle, `TRUE` otherwise. This argument is used to process the arguments to these high level functions, but more importantly, it is passed as an argument to the panel function, which is supposed to use it as appropriate.

A potentially useful component of `scales` in this case might be `abbreviate = TRUE`, in which case long labels which would usually overlap will be abbreviated. `scales` could also contain a `minlength` argument in this case, which would be passed to the `abbreviate` function.

The following arguments are common to all the functions documented here, as well as most other high level Trellis functions. These are not documented elsewhere, except to override the usage given here.

panel

Once the subset of rows defined by each unique combination of the levels of the grouping variables are obtained (see details), the corresponding  $x$  and  $y$  variables (or other variables, as appropriate, in the case of other high level functions) are passed on to be plotted in each panel. The actual plotting is done by the function specified by the `panel` argument. Each high level function has its own default panel function, which could depend on whether the `groups` argument was supplied.

The panel function can be a function object or a character string giving the name of a predefined function.

Much of the power of Trellis Graphics comes from the ability to define customized panel functions. A panel function appropriate for the functions described here would usually expect arguments named  $x$  and  $y$ , which would be provided by the conditioning process. It can also have other arguments. It might be useful to know in this context that all arguments passed to a high level Trellis function (such as `xyplot`) that are not recognized by it are passed through to the panel function. It is thus generally good practice when defining panel functions to allow a `...` argument. Such extra arguments typically control graphical parameters, but other uses are also common. See documentation for individual panel functions for specifics.

Note that unlike in S-PLUS, it is not guaranteed that panel functions will be supplied only numeric vectors for the  $x$  and  $y$  arguments; they can be factors as well (but not shingles). Panel functions need to handle this case, which in most cases can be done by simply coercing them to numeric.

Technically speaking, panel functions must be written using Grid graphics functions. However, knowledge of Grid is usually not necessary to construct new custom panel functions, there are several predefined panel functions which can help; for example, `panel.grid`, `panel.loess`, etc. There are also some grid-compatible replacements of commonly used base R graphics functions useful for this purpose. For example, `lines` can be replaced by `llines` (or equivalently, `panel.lines`). Note that base R graphics functions like `lines` will not work in a lattice panel function.

One case where a bit more is required of the panel function is when the `groups` argument is not null. In that case, the panel function should also accept arguments named `groups` and `subscripts` (see below for details). A useful panel function predefined for use in such cases is `panel.superpose`, which can be combined with different `panel.groups` functions determining what is plotted for each group. See the examples section for an interaction plot constructed in this way. Several other panel functions can also handle the `groups` argument, including the default ones for `barchart`, `dotplot` and `stripplot`.

Even when `groups` is not present, the panel function can have `subscripts` as a formal argument. In either case, the `subscripts` argument passed to the panel function are the indices of the  $x$  and  $y$  data for that panel in the original data, BEFORE taking into account the effect of the `subset` argument. Note that `groups` remains unaffected by any subsetting operations, so `groups[subscripts]` gives the values of `groups` that correspond to the data in that panel.

This interpretation of `subscripts` does not hold when the extended formula



interface is in use (i.e., when `allow.multiple` is in effect). A comprehensive description would be too complicated (details can be found in the source code of the function `latticeParseFormula`), but in short, the extended interface works by creating an artificial grouping variable that is longer than the original data frame, and consequently, `subscripts` needs to refer to rows beyond those in the original data. To further complicate matters, the artificial grouping variable is created after any effect of `subset`, in which case `subscripts` has practically no relationship with corresponding rows in the original data frame.

One can also use functions called `panel.number` and `packet.number`, representing panel order and packet order respectively, inside the panel function (as well as the strip function or while interacting with a lattice display using `trellis.focus` etc). Both provide a simple integer index indicating which panel is currently being drawn, but differ in how the count is calculated. The panel number is a simple incremental counter that starts with 1 and is incremented each time a panel is drawn. The packet number on the other hand indexes the combination of levels of the conditioning variables that is represented by that panel. The two indices coincide unless the order of conditioning variables is permuted and/or the plotting order of levels within one or more conditioning variables is altered (using `perm.cond` and `index.cond` respectively), in which case `packet.number` gives the index corresponding to the ‘natural’ ordering of that combination of levels of the conditioning variables.

`panel.xyplot` has an argument called `type` which is worth mentioning here because it is quite frequently used (and as mentioned above, can be passed to `xyplot` directly). In the event that a `groups` variable is used, `panel.xyplot` calls `panel.superpose`, arguments of which can also be passed directly to `xyplot`. Panel functions for `bwplot` and friends should have an argument called `horizontal` to account for the cases when `x` is the factor or shingle.

`aspect` controls physical aspect ratio of the panels (same for all the panels). It can be specified as a ratio (vertical size/horizontal size) or as a character string. Legitimate values are `"fill"` (the default) which tries to make the panels as big as possible to fill the available space; `"xy"`, which **tries** to compute the aspect based on the 45 degree banking rule (see *Visualizing Data* by William S. Cleveland for details); and `"iso"` for isometric scales, where the relation between physical distance on the device and distance in the data scale are forced to be the same for both axes.

If a `prepanel` function is specified and it returns components `dx` and `dy`, these are used for banking calculations. Otherwise, values from the default `prepanel` function are used. Currently, only the default `prepanel` function for `xyplot` can be expected to produce sensible banking calculations. See [banking](#) for details on the implementation of banking .

`groups` a variable or expression to be evaluated in the data frame specified by `data`, expected to act as a grouping variable within each panel, typically used to distinguish different groups by varying graphical parameters like color and line type. Formally, if `groups` is specified, then `groups` along with `subscripts` is passed to the panel function, which is expected to handle these arguments. Not all pre-defined panel functions know how to, but for high level functions where grouping is appropriate, the default panel functions are chosen so that they do. It is very common to use a key (legend) when a grouping variable is specified. See entries for `key`, `auto.key` and [simpleKey](#) for how to draw a key.

- `auto.key` A logical, or a list containing components to be used as arguments to `simpleKey`. `auto.key=TRUE` is equivalent to `auto.key=list()`, in which case `simpleKey` is called with a set of default arguments (which may depend on the relevant high-level function). Most valid components to the `key` argument can be specified in this manner, as `simpleKey` will simply add unrecognized arguments to the list it produces.
- `auto.key` is typically used to automatically produce a suitable legend in conjunction with a grouping variable. If `auto.key=TRUE`, a suitable legend will be drawn if a `groups` argument is also provided, and not otherwise. In list form, `auto.key` will modify the default legend thus produced. For example, `auto.key=list(columns = 2)` will create a legend split into two columns (`columns` is documented in the entry for `key`).
- More precisely, if `auto.key` is not `FALSE`, `groups` is non-null, and there is no `key` or `legend` argument specified in the call, a key is created with `simpleKey` with `levels(groups)` as the first (`text`) argument. (Note: this may not work in all high level functions, but it does work for the ones where grouping makes sense with the default panel function). If `auto.key` is provided as a list and includes a `text` component, then that is used instead as the text labels in the key, and the key is drawn even if `groups` is not specified. Note that `simpleKey` uses the default settings (see `trellis.par.get`) to determine the graphical parameters in the key, so the resulting legend will be meaningful only if the same settings are used in the plot as well.
- One disadvantage to using `key` (or even `simpleKey`) directly is that the graphical parameters used in the key are absolutely determined at the time when the "trellis" object is created. Consequently, if a plot once created is re-plotted with different settings, the original parameter settings will be used for the key even though the new settings are used for the actual display. However, with `auto.key`, the key is actually created at plotting time, so the settings will match.
- `prepanel` function that takes the same arguments as the `panel` function and returns a list, possibly containing components named `xlim`, `ylim`, `dx` and `dy` (and less frequently, `xat` and `yat`).
- The `xlim` and `ylim` components are similar to the high level `xlim` and `ylim` arguments (i.e., they are usually a numeric vector of length 2 defining a range of values, or a character vector representing levels of a factor). If the `xlim` and `ylim` arguments are not explicitly specified (possibly as components in `scales`), then the actual limits of the panels are guaranteed to include the limits returned by the `prepanel` function. This happens globally if the `relation` component of `scales` is "same", and on a panel by panel basis otherwise. See `xlim` to see what forms of the components `xlim` and `ylim` are allowed.
- The `dx` and `dy` components are used for banking computations in case `aspect` is specified as "xy". See documentation for the function `banking` for details regarding how this is done.
- The return value of the `prepanel` function need not have all the components named above; in case some are missing, they are replaced by the usual component-wise defaults.
- If `xlim` or `ylim` is a character vector (which is appropriate when the corresponding variable is a factor), this implicitly indicates that the scale should include the first `n` integers, where `n` is the length of `xlim` or `ylim`, as the case may be. The elements of the character vector are used as the default labels for these `n` integers. Thus, to make this information consistent between panels, the

`xlim` or `ylim` values should represent all the levels of the corresponding factor, even if some are not used within that particular panel.

In such cases, an additional component `xat` or `yat` may be returned by the `prepanel` function, which should be a subset of `1:n`, indicating which of the `n` values (levels) are actually represented in the panel. This is useful when calculating the limits with `relation="free"` or `relation="sliced"` in `scales`.

The `prepanel` function is responsible for providing a meaningful return value when the `x`, `y` (etc.) variables are zero-length vectors. When nothing is appropriate, values of `NA` should be returned for the `xlim` and `ylim` components.

<code>strip</code>	logical flag or function. If <code>FALSE</code> , strips are not drawn. Otherwise, strips are drawn using the <code>strip</code> function, which defaults to <code>strip.default</code> . See documentation of <code>strip.default</code> to see the arguments that are available to the <code>strip</code> function. This description also applies to the <code>strip.left</code> argument (see . . . below), which can be used to draw strips on the left of each panel, which can be useful for wide short panels, e.g. in time series plots.
<code>xlab</code>	character string or expression (or a "grob") giving label for the x-axis. Defaults to the expression for <code>x</code> in <code>formula</code> . Can be specified as <code>NULL</code> to omit the label altogether. Finer control is possible, as described in the entry for <code>main</code> , with the additional feature that if the <code>label</code> component is omitted from the list, it is replaced by the default <code>xlab</code> .
<code>ylab</code>	character string or expression (or "grob") giving label for the y-axis. Defaults to the expression for <code>y</code> in <code>formula</code> . Fine control is possible, see entries for <code>main</code> and <code>xlab</code> .
<code>scales</code>	list determining how the x- and y-axes (tick marks and labels) are drawn. The list contains parameters in <code>name=value</code> form, and may also contain two other lists called <code>x</code> and <code>y</code> of the same form (described below). Components of <code>x</code> and <code>y</code> affect the respective axes only, while those in <code>scales</code> affect both. When parameters are specified in both lists, the values in <code>x</code> or <code>y</code> are used. Note that certain high-level functions have defaults that are specific to a particular axis (e.g., <code>bwplot</code> has <code>alternating=FALSE</code> for the y-axis only); these can be overridden only by an entry in the corresponding component of <code>scales</code> .

The possible components are :

`relation` character string that determines how axis limits are calculated for each panel. Possible values are "same" (default), "free" and "sliced". For `relation="same"`, the same limits, usually large enough to encompass all the data, are used for all the panels. For `relation="free"`, limits for each panel is determined by just the points in that panel. Behavior for `relation="sliced"` is similar, except that the length (max - min) of the scales are constrained to remain the same across panels.

The determination of what axis limits are suitable for each panel can be controlled by the `prepanel` function, which can be overridden by `xlim`, `ylim` or `scales$limits`. If `relation` is not "same", the value of `xlim` etc is normally ignored, except when it is a list, in which case it is treated as if its components were the limit values obtained from the `prepanel` calculations for each panel.

`tick.number` Suggested number of ticks (ignored for a factor, shingle or character vector, in which case there is no natural rule for leaving out some of the labels. But see `xlim`).

`draw` logical, defaults to TRUE, whether to draw the axis at all.

`alternating` logical specifying whether axis labels should alternate from one side of the group of panels to the other. For finer control, `alternating` can be a vector (replicated to be as long as the number of rows or columns per page) consisting of the following numbers

- 0: do not draw tick labels
- 1: bottom/left
- 2: top/right
- 3: both.

`alternating` applies only when `relation="same"`. The default is TRUE, or equivalently, `c(1, 2)`

`limits` same as `xlim` and `ylim`.

`at` location of tick marks along the axis (in native coordinates), or a list as long as the number of panels describing tick locations for each panel.

`labels` Labels (strings or expressions) to go along with `at`. Can be a list like `at` as well.

`cex` numeric multiplier to control character sizes for axis labels. Can be a vector of length 2, to control left/bottom and right/top separately.

`font`, `fontface`, `fontfamily` specifies font for axis labels.

`tck` numeric to control length of tick marks. Can be a vector of length 2, to control left/bottom and right/top separately.

`col` color of ticks and labels.

`rot` Angle by which the axis labels are to be rotated. Can be a vector of length 2, to control left/bottom and right/top separately.

`abbreviate` logical, whether to abbreviate the labels using `abbreviate`. Can be useful for long labels (e.g., in factors), especially on the x-axis.

`minlength` argument passed to `abbreviate` if `abbreviate=TRUE`.

`log` Controls whether the corresponding variable (`x` or `y`) will be log transformed before being passed to the panel function. Defaults to FALSE, in which case the data are not transformed. Other possible values are any number that works as a base for taking logarithm, TRUE (which is equivalent to 10), and "e" (for the natural logarithm). As a side effect, the corresponding axis is labeled differently. Note that this is a transformation of the data, not the axes. Other than the axis labeling, using this feature is no different than transforming the data in the formula; e.g., `scales=list(x = list(log = 2))` is equivalent to  $y \sim \log_2(x)$ .

`format` the format to use for POSIXct variables. See `strptime` for description of valid values.

`axs` character, "r" or "i". In the latter case, the axis limits are calculated as the exact data range, instead of being padded on either side. (May not always work as expected.)

Note that much of the function of `scales` is accomplished by `pcales` in `splom`.

`subscripts` logical specifying whether or not a vector named `subscripts` should be passed to the panel function. Defaults to FALSE, unless `groups` is specified, or if the panel function accepts an argument named `subscripts`. (One should be careful when defining the panel function on-the-fly.)

`subset` logical or integer indexing vector (can be specified in terms of variables in data). Only these rows of data will be used for the plot. If `subscripts` is

- TRUE, the subscripts will provide indices to the rows of data before the subsetting is done. Whether levels of factors in the data frame that are unused after the subsetting will be dropped depends on the `drop.unused.levels` argument.
- `xlim` Normally a numeric vector of length 2 (possibly a `DateTime` object) giving minimum and maximum for the x-axis, or, a character vector, expected to denote the levels of `x`. The latter form is interpreted as a range containing `c(1, length(xlim))`, with the character vector determining labels at tick positions `1:length(xlim)`
- `xlim` could also be a list, with as many components as the number of panels (recycled if necessary), with each component as described above. This is meaningful only when `scales$x$relation` is "free" or "sliced", in which case these are treated as if they were the corresponding limit components returned by `prepanel` calculations.
- `ylim` similar to `xlim`, applied to the y-axis.
- `drop.unused.levels` logical indicating whether the unused levels of factors will be dropped, usually relevant with a subsetting operation is performed or an [interaction](#) is created. Unused levels are usually dropped, but it is sometimes appropriate to suppress dropping to preserve a useful layout. For finer control, this argument could also be list containing components `cond` and `data`, both logical, indicating desired behavior for conditioning variables and data variables respectively. The default is given by `lattice.getOption("drop.unused.levels")`, which is initially set to TRUE for both components. Note that this argument does not control dropping of levels of the `groups` argument.
- `default.scales` list giving the default values of `scales` for a particular high level function. This should not be of any interest to the normal user, but may be helpful when defining other functions that act as a wrapper to one of the high level lattice functions.
- `lattice.options` a list that could be supplied to `lattice.options`. These options are temporarily in effect for the duration of the call, after which the settings revert back to whatever they were before. The settings are also retained along with the object and reused during plotting. This enables the user to attach options settings to the trellis object itself rather than change the settings globally. See also the `par.settings` argument described below for a similar treatment of graphical settings.
- ... further arguments, usually not directly processed by the high level functions documented here, but rather passed on to other functions. Such arguments can be broadly categorized into two types: those that affect all high level Trellis functions in a similar manner, and those that are meant for the specific panel function used, which may differ across high level functions.
- The first group of arguments are processed by a common, unexported function called `trellis.skeleton`. These arguments affect all high level functions, but are only documented here, except to override the behaviour described here. All other arguments specified in a high level call, specifically those neither described here nor in the help page of the relevant high level function, are passed unchanged to the panel function used. By convention, the default panel function used for any high level function is named as "panel." followed by the name of the high level function; for example, the default panel function for `bwplot` is `panel.bwplot`. In practical terms, this means that in addition to the help

page of the high level function being used, the user should also consult the help page of the corresponding panel function for arguments that may be specified in the high level call.

The effect of the first group of common arguments are as follows:

`as.table`: logical that controls the order in which panels should be plotted: if `FALSE` (the default), panels are drawn left to right, bottom to top (as in a graph); if `TRUE`, left to right, top to bottom.

`between`: a list with components `x` and `y` (both usually 0 by default), numeric vectors specifying the space between the panels (units are character heights). `x` and `y` are repeated to account for all panels in a page and any extra components are ignored. The result is used for all pages in a multi page display. (In other words, it is not possible to use different `between` values for different pages).

`key`: A list of arguments that define a legend to be drawn on the plot. This list is used as an argument to the `draw.key` function, which produces a grid object eventually plotted by the print method for "trellis" objects.

There is also a less flexible but usually sufficient shortcut function `simpleKey` that can generate such a list, as well as the argument `auto.key` that can be convenient in the most common situation where legends are used, namely when there is a grouping variable. To use more than one legend, or to have arbitrary legends not constrained by the structure imposed by `key`, use the `legend` argument.

The position of the key can be controlled in either of two possible ways. If a component called `space` is present, the key is positioned outside the plot region, in one of the four sides, determined by the value of `space`, which can be one of "top", "bottom", "left" and "right". Alternatively, the key can be positioned inside the plot region by specifying components `x`, `y` and `corner`. `x` and `y` determine the location of the corner of the key given by `corner`, which is usually one of `c(0, 0)`, `c(1, 0)`, `c(1, 1)` and `c(0, 1)`, which denote the corners of the unit square. Fractional values are also allowed, in which case `x` and `y` determine the position of an arbitrary point inside (or outside for values outside the unit interval) the key.

`x` and `y` should be numbers between 0 and 1, giving coordinates with respect to the "display area". Depending on the value of `lattice.getOption("legend.bbox")`, this can be either the full figure region ("full"), or just the region that bounds the panels and strips ("panel").

The key essentially consists of a number of columns, possibly divided into blocks, each containing some rows. The contents of the key are determined by (possibly repeated) components named "rectangles", "lines", "points" or "text". Each of these must be lists with relevant graphical parameters (see later) controlling their appearance. The `key` list itself can contain graphical parameters, these would be used if relevant graphical components are omitted from the other components.

The length (number of rows) of each such column (except "text"s) is taken to be the largest of the lengths of the graphical components, including the ones specified outside (see the entry for `rep` below for details on this). The "text" component has to have a character or expression vector as its first component, and the length of this vector determines the number of rows.

The graphical components that can be included in `key` (and also in the com-

ponents named "text", "lines", "points" and "rectangles" as appropriate) are:

- `cex=1`
- `col="black"`
- `alpha=1`
- `lty=1`
- `lwd=1`
- `font=1`
- `fontface`
- `fontfamily`
- `pch=8`
- `adj=0`
- `type="l"`
- `size=5`
- `angle=0`
- `density=-1`

In addition, the component `border` can be included inside the "rect" component to control the border color of the rectangles; when specified at the top level, `border` controls the border of the entire key (see below).

`angle` and `density` are unimplemented. `size` determines the width of columns of rectangles and lines in character widths. `type` is relevant for lines; "l" denotes a line, "p" denotes a point, and "b" and "o" both denote both together.

Other possible components of `key` are:

`reverse.rows` logical, defaulting to `FALSE`. If `TRUE`, all components are reversed *after* being replicated (the details of which may depend on the value of `rep`). This is useful in certain situations, e.g. with a grouped `barchart` with `stack = FALSE` with the categorical variable on the vertical axis, where the bars in the plot will usually be ordered from bottom to top, but the corresponding legend will have the levels from top to bottom (unless, of course, `reverse.rows = TRUE`). Note that in this case, unless all columns have the same number of rows, they will no longer be aligned.

`between` numeric vector giving the amount of space (character widths) surrounding each column (split equally on both sides)

`title` string or expression giving a title for the key

`rep` logical, defaults to `TRUE`. By default, it's assumed that all columns in the key (except the "text"s) will have the same number of rows, and all components are replicated to be as long as the longest. This can be suppressed by specifying `rep=FALSE`, in which case the length of each column will be determined by components of that column alone.

`cex.title` `cex` for the title

`lines.title` how many lines the title should occupy (in multiples of itself). Defaults to 2.

`padding.text` how much space (padding) should be used above and below each row containing text, in multiples of the default, which is currently  $0.2 * \text{"lines"}$ . This padding is in addition to the normal height of any row that contains text, which is the minimum amount necessary to contain all the text entries.

- `background` background color, defaults to default background
- `alpha.background` An alpha transparency value between 0 and 1
- `border` either a color for the border, or a logical. In the latter case, the border color is black if `border` is TRUE, and no border is drawn if it is FALSE (the default)
- `transparent=FALSE` logical, whether key area should have a transparent background
- `columns` the number of columns column-blocks the key is to be divided into, which are drawn side by side.
- `between.columns` Space between column blocks, in addition to `between`.
- `divide` Number of point symbols to divide each line when `type` is "b" or "o" in lines.
- legend:** the legend argument can be useful if one wants to place more than one key. It also allows one to use arbitrary "grob"s (grid objects) as legends. If used, `legend` must be a list, with an arbitrary number of components. Each component must be named one of "left", "right", "top", "bottom" or "inside". The name "inside" can be repeated, but not the others. This name will be used to determine the location for that component, and is similar to the `space` component of `key`. If `key` (or `colorkey` for `levelplot` and `wireframe`) is specified, their `space` component must not conflict with the name of any component of `legend`. Each component of `legend` must have a component called `fun`. This can be a "grob", or a function or the name of a function that produces a "grob" when called. If this function expects any arguments, they must be supplied as a list in another component called `args`. For components named "inside", there can be additional components called `x`, `y` and `corner`, which work in the same way as it does for `key`.
- page:** a function of one argument (page number) to be called after drawing each page. The function must be 'grid-compliant', and is called with the whole display area as the default viewport.
- main:** typically a character string or expression describing the main title to be placed on top of each page. Defaults to NULL. `main` (as well as `xlab`, `ylab` and `sub`) is usually a character string or an expression that gets used as the label, but can also be a list that controls further details. Expressions are treated as specification of LaTeX-like markup as described in `plotmath`. The label can be a vector, in which case the components will be spaced out horizontally (or vertically for `ylab`). This feature can be used to provide column or row labels rather than a single axis label. When `main` (etc.) is a list, the actual label should be specified as the `label` component (which may be unnamed if it is the first component). The label can be missing, in which case the default will be used (`xlab` and `ylab` usually have defaults, but `main` and `sub` do not). Further named arguments are passed on to `textGrob`; this can include arguments controlling positioning like `just` and `rot` as well as graphical parameters such as `col` and `font` (see `gpar` for a full list). `main`, `xlab`, `ylab` and `sub` can also be an arbitrary "grob" (grid graphical object).
- sub:** character string or expression (or a list or "grob") for a subtitle to be placed at the bottom of each page. See entry for `main` for finer control options.



- `par.strip.text`: list of parameters to control the appearance of strip text. Notable components are `col`, `cex`, `font` and `lines`. The first three control graphical parameters while the last is a means of altering the height of the strips. This can be useful, for example, if the strip labels (derived from factor levels, say) are double height (i.e., contains "`\n`"-s) or if the default height seems too small or too large. The `lineheight` component can control the space between multiple lines. Also, the labels can be abbreviated when shown by specifying `abbreviate = TRUE`, in which case the components `minlength` and `dot` (passed along to the `abbreviate` function) can be specified to control the details of how this is done.
- `layout`: In general, a Trellis conditioning plot consists of several panels arranged in a rectangular array, possibly spanning multiple pages. `layout` determines this arrangement. `layout` is a numeric vector giving the number of columns, rows and pages in a multi panel display. By default, the number of columns is the number of levels of the first conditioning variable and the number of rows is the number of levels of the second conditioning variable. If there is only one conditioning variable, the default layout vector is `c(0, n)`, where `n` is the number of levels of the given vector. Any time the first value in the layout vector is 0, the second value is used as the desired number of panels per page and the actual layout is computed from this, taking into account the aspect ratio of the panels and the device dimensions (via `par("din")`). The number of pages is by default set to as many as is required to plot all the panels. In general, giving a high value of `layout[3]` is not wasteful because blank pages are never created. If `NA` is specified for the number of rows or columns (not both), that dimension will be filled out according to the number of panels.
- `skip`: logical vector (default `FALSE`), replicated to be as long as the number of panels (spanning all pages). For elements that are `TRUE`, the corresponding panel position is skipped; i.e., nothing is plotted in that position. The panel that was supposed to be drawn there is now drawn in the next available panel position, and the positions of all the subsequent panels are bumped up accordingly. This is often useful for arranging plots in an informative manner.
- `strip.left`: `strip.left` can be used to draw strips on the left of each panel, which can be useful for wide short panels, as in time series (or similar) plots. It is a function similar to `strip`.
- `xlab.default`, `ylab.default`: fallback default for `xlab` and `ylab` when they are not specified. If `NULL`, the defaults are parsed from the Trellis formula. This is rarely useful for the end-user, but can be helpful when developing new Trellis functions.
- `xscale.components`, `yscale.components`: functions that determine axis annotation for the x and y axes respectively. See documentation for `xscale.components.default`, the default values of these arguments, to learn more.
- `axis`: function that draws axis annotation. See documentation for `axis.default`, the default value of this argument, to learn more.
- `perm.cond`: numeric vector, a permutation of `1:n`, where `n` is the number of conditioning variables. By default, the order in which panels are drawn depends on the order of the conditioning variables specified in the formula. `perm.cond` can modify this order. If the trellis display is thought of as

an n-dimensional array, then during printing, its dimensions are permuted using `perm.cond` as the `perm` argument to `aperm`.

`index.cond`: While `perm.cond` permutes the dimensions of the multidimensional array of panels, `index.cond` can be used to subset (or reorder) margins of that array. `index.cond` can be a list or a function, with behavior in each case described below.

The panel display order within each conditioning variable depends on the order of their levels. `index.cond` can be used to choose a ‘subset’ (in the R sense) of these levels, which is then used as the display order for that variable. If `index.cond` is a list, it has to be as long as the number of conditioning variables, and the *i*-th component has to be a valid indexing vector for `levels(g_i)`, where `g_i` is the *i*-th conditioning variable in the plot (note that these levels may not contain all levels of the original variable, depending on the effects of the `subset` and `drop.unused.levels` arguments). In particular, this indexing may repeat levels, or drop some altogether. The result of this indexing determines the order of panels within that conditioning variable. To keep the order of a particular variable unchanged, the corresponding component must be set to `TRUE`.

Note that the components of `index.cond` are in the order of the conditioning variables in the original call, and is not affected by `perm.cond`.

Another possibility is to specify `index.cond` as a function. In this case, this function is called once for each panel, potentially with all arguments that are passed to the panel function for that panel. (More specifically, if this function has a `...` argument, then all panel arguments are passed, otherwise, only named arguments that match are passed.) For a single conditioning variable, the levels of that variable are then sorted so that these values are in ascending order. For multiple conditioning variables, the order for each variable is determined by first taking the average over all other conditioning variables.

Although they can be supplied in high level function calls directly, it is more typical to use `perm.cond` and `index.cond` to update an existing "trellis" object, thus allowing it to be displayed in a different arrangement without re-calculating the data subsets that go into each panel. In the `update` method, both can be set to `NULL`, which reverts these back to their defaults.

`par.settings`: a list that could be supplied to `trellis.par.set`. This enables the user to attach some display settings to the trellis object itself rather than change the settings globally. When the object is plotted, these settings are temporarily in effect for the duration of the plot, after which the settings revert back to whatever they were before.

`plot.args`: a list of possible arguments to `plot.trellis`, which will be used by the `plot` or `print` methods when drawing the object, unless overridden explicitly. This enables the user to attach such arguments to the trellis object itself. Partial matching is not performed.

## Details

All the functions documented here are generic, with the `formula` method usually doing the actual work. The structure of the plot that is produced is mostly controlled by the formula. For each unique combination of the levels of the conditioning variables `g1`, `g2`, `...`, a separate panel is produced using the points  $(x, y)$  for the subset of the data (also called packet) defined by that combination. The display can be thought of as a 3-dimensional array of panels, consisting of

one 2-dimensional matrix per page. The dimensions of this array are determined by the `layout` argument. If there are no conditioning variables, the plot produced consists of a single panel.

The coordinate system used by `lattice` by default is like a graph, with the origin at the bottom left, with axes increasing right and up. In particular, panels are by default drawn starting from the bottom left corner, going right and then up; unless `as.table = TRUE`, in which case panels are drawn from the top left corner, going right and then down. One might wish to set a global preference for a table-like arrangement by changing the default to `as.table=TRUE`; this can be done by setting `lattice.options(default.args = list(as.table = TRUE))`. In fact, default values can be set in this manner for the following arguments: `as.table`, `aspect`, `between`, `page`, `main`, `sub`, `par.strip.text`, `layout`, `skip` and `strip`. Note that these global defaults are sometimes overridden by individual functions.

The order of the panels depends on the order in which the conditioning variables are specified, with `g1` varying fastest. Within a conditioning variable, the order depends on the order of the levels (which for factors is usually in alphabetical order). Both of these orders can be modified using the `index.cond` and `perm.cond` arguments, possibly using the `update` (and other related) method(s).

### Value

An object of class `"trellis"`. The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

### Note

Most of the arguments documented here are also applicable for the other high level functions in the `lattice` package. These are not described in any detail elsewhere unless relevant, and this should be considered the canonical documentation for such arguments.

Any arguments passed to these functions and not recognized by them will be passed to the panel function. Most predefined panel functions have arguments that customize its output. These arguments are described only in the help pages for these panel functions, but can usually be supplied as arguments to the high level plot.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### References

Sarkar, Deepayan (2008) "Lattice: Multivariate Data Visualization with R", Springer. <http://lmdvr.r-forge.r-project.org/>

### See Also

`Lattice` for an overview of the package, as well as `barchart.table`, `print.trellis`, `shingle`, `banking`, `reshape`, `panel.xyplot`, `panel.bwplot`, `panel.barchart`, `panel.dotplot`, `panel.stripplot`, `panel.superpose`, `panel.loess`, `panel.linejoin`, `strip.default`, `simpleKey` `trellis.par.set`

**Examples**

```

## Not run:
## wait for user input before each new page (like 'par(ask = TRUE)')
old.prompt <- grid::grid.prompt(TRUE)

## End(Not run)

require(stats)

## Tonga Trench Earthquakes

Depth <- equal.count(quakes$depth, number=8, overlap=.1)
xyplot(lat ~ long | Depth, data = quakes)
update(trellis.last.object(),
       strip = strip.custom(strip.names = TRUE, strip.levels = TRUE),
       par.strip.text = list(cex = 0.75),
       aspect = "iso")

## Examples with data from `Visualizing Data' (Cleveland)
## (obtained from Bill Cleveland's Homepage :
## http://cm.bell-labs.com/cm/ms/departments/sia/wsc/, also
## available at statlib)

EE <- equal.count(ethanol$E, number=9, overlap=1/4)
## Constructing panel functions on the fly; prepanel
xyplot(NOx ~ C | EE, data = ethanol,
       prepanel = function(x, y) prepanel.loess(x, y, span = 1),
       xlab = "Compression Ratio", ylab = "NOx (micrograms/J)",
       panel = function(x, y) {
         panel.grid(h=-1, v= 2)
         panel.xyplot(x, y)
         panel.loess(x,y, span=1)
       },
       aspect = "xy")

## with and without banking

plot <- xyplot(sunspot.year ~ 1700:1988, xlab = "", type = "l",
              scales = list(x = list(alternating = 2)),
              main = "Yearly Sunspots")
print(plot, position = c(0, .3, 1, .9), more = TRUE)
print(update(plot, aspect = "xy", main = "", xlab = "Year"),
      position = c(0, 0, 1, .3))

## Multiple variables in formula for grouped displays

xyplot(Sepal.Length + Sepal.Width ~ Petal.Length + Petal.Width | Species,
       data = iris, scales = "free", layout = c(2, 2),
       auto.key = list(x = .6, y = .7, corner = c(0, 0)))

```

```

## user defined panel functions

states <- data.frame(state.x77,
                     state.name = dimnames(state.x77)[[1]],
                     state.region = state.region)
xyplot(Murder ~ Population | state.region, data = states,
       groups = state.name,
       panel = function(x, y, subscripts, groups)
         ltext(x = x, y = y, labels = groups[subscripts], cex=1,
              fontfamily = "HersheySans"))

barchart(yield ~ variety | site, data = barley,
         groups = year, layout = c(1,6),
         ylab = "Barley Yield (bushels/acre)",
         scales = list(x = list(abbreviate = TRUE,
                               minlength = 5)))
barchart(yield ~ variety | site, data = barley,
         groups = year, layout = c(1,6), stack = TRUE,
         auto.key = list(points = FALSE, rectangles = TRUE, space = "right"),
         ylab = "Barley Yield (bushels/acre)",
         scales = list(x = list(rot = 45)))

bwplot(voice.part ~ height, data=singer, xlab="Height (inches)")
dotplot(variety ~ yield | year * site, data=barley)

dotplot(variety ~ yield | site, data = barley, groups = year,
       key = simpleKey(levels(barley$year), space = "right"),
       xlab = "Barley Yield (bushels/acre) ",
       aspect=0.5, layout = c(1,6), ylab=NULL)

stripplot(voice.part ~ jitter(height), data = singer, aspect = 1,
          jitter.data = TRUE, xlab = "Height (inches)")
## Interaction Plot

xyplot(decrease ~ treatment, OrchardSprays, groups = rowpos,
       type = "a",
       auto.key =
         list(space = "right", points = FALSE, lines = TRUE))

## longer version with no x-ticks

## Not run:
bwplot(decrease ~ treatment, OrchardSprays, groups = rowpos,
       panel = "panel.superpose",
       panel.groups = "panel.linejoin",
       xlab = "treatment",
       key = list(lines = Rows(trellis.par.get("superpose.line"),
                              c(1:7, 1)),
                 text = list(lab = as.character(unique(OrchardSprays$rowpos))),
                              columns = 4, title = "Row position"))

## End(Not run)

## Not run:
grid::grid.prompt(old.prompt)

## End(Not run)

```

---

 B\_01\_xyplot.ts      *Time series plotting methods*


---

### Description

This function handles time series plotting, including cut-and-stack plots. Examples are given of superposing, juxtaposing and styling different time series.

### Usage

```
## S3 method for class 'ts':
xyplot(x, data = NULL,
       screens = if (superpose) 1 else colnames(x),
       ...,
       superpose = FALSE,
       cut = FALSE,
       type = "l",
       col = NULL,
       lty = NULL,
       lwd = NULL,
       pch = NULL,
       cex = NULL,
       fill = NULL,
       auto.key = superpose,
       panel = if (superpose) "panel.superpose"
               else "panel.superpose.plain",
       par.settings = list(),
       layout = NULL, as.table = TRUE,
       xlab = "Time", ylab = NULL,
       default.scales = list(y = list(relation =
                                     if (missing(cut)) "free" else "same")))
```

### Arguments

x	an object of class <code>ts</code> , which may be multi-variate, i.e. have a matrix structure with multiple columns.
data	not used, and must be left as <code>NULL</code> .
...	additional arguments passed to <code>xyplot</code> , which may pass them on to <code>panel.xyplot</code> .
screens	factor (or coerced to factor) whose levels specify which panel each series is to be plotted in. <code>screens = c(1, 2, 1)</code> would plot series 1, 2 and 3 in panels 1, 2 and 1. May also be a named list, see Details below.
superpose	overlays all series in one panel (via <code>screens = 1</code> ) and uses grouped style settings (from <code>trellis.par.get("superpose.line")</code> , etc). Note that this is just a convenience argument: its only action is to change the default values of other arguments.

<code>cut</code>	defines a cut-and-stack plot. <code>cut</code> can be a list of arguments to the function <code>equal.count</code> , i.e. <code>number</code> (number of intervals to divide into) and <code>overlap</code> (the fraction of overlap between cuts, default 0.5). If <code>cut</code> is numeric this is passed as the <code>number</code> argument.  <code>cut = TRUE</code> tries to choose an appropriate number of cuts (up to a maximum of 6), using <code>banking</code> , and assuming a square plot region. This should have the effect of minimising wasted space when <code>aspect = "xy"</code> .
<code>type, col, lty, lwd, pch, cex, fill</code>	graphical arguments, which are processed and eventually passed to <code>panel.xyplot</code> . These arguments can also be vectors or (named) lists, see <code>Details</code> for more information.
<code>auto.key</code>	a logical, or a list describing how to draw a key. See the <code>auto.key</code> entry in <code>xyplot</code> . The default here is to draw lines, not points, and any specified style arguments should show up automatically.
<code>panel</code>	the panel function. It is recommended to leave this alone, but one can pass a <code>panel.groups</code> argument which is handled by <code>panel.superpose</code> for each series.
<code>par.settings</code>	style settings beyond the standard <code>col, lty, lwd, etc</code> ; see <code>trellis.par.set</code> and <code>simpleTheme</code> .
<code>layout</code>	numeric vector of length 2 specifying number of columns and rows in the plot. The default is to fill columns with up to 6 rows.
<code>as.table</code>	to draw panels from top to bottom. The order is determined by the order of columns in <code>x</code> .
<code>xlab, ylab</code>	X axis and Y axis labels; see <code>xyplot</code> . Note in particular that <code>ylab</code> may be a character vector, in which case the labels are spaced out equally, to correspond to the panels; but <i>NOTE</i> in this case the vector should be reversed OR the argument <code>as.table</code> set to <code>FALSE</code> .
<code>default.scales</code>	scales specification. The default is set to have "free" Y axis scales unless <code>cut</code> is given. Note, users should pass the <code>scales</code> argument rather than <code>default.scales</code> .

## Details

The handling of several graphical parameters is more flexible for multivariate series. These parameters can be vectors of the same length as the number of series plotted or are recycled if shorter. They can also be (partially) named list, e.g., `list(A = c(1, 2), c(3, 4))` in which `c(3, 4)` is the default value and `c(1, 2)` the value only for series A. The `screens` argument can be specified in a similar way.

Some examples are given below.

## Value

An object of class "trellis". The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

## Author(s)

Gabor Grothendieck, Achim Zeileis, Deepayan Sarkar and Felix Andrews  
<felix@nfrac.org>.

The first two authors developed `xyplot.ts` in their **zoo** package, including the screens approach. The third author developed a different `xyplot.ts` for cut-and-stack plots in the **lattice-Extra** package. The final author fused these together.

## References

Sarkar, Deepayan (2008) “Lattice: Multivariate Data Visualization with R”, Springer. ISBN: 978-0-387-75968-5 <http://lmdvr.r-forge.r-project.org/> (cut-and-stack plots)

## See Also

`xyplot`, `panel.xyplot`, `plot.ts`, `ts`, `xyplot.zoo` in the **zoo** package.

## Examples

```
xyplot(ts(c(1:10,10:1)))

### Figure 14.1 from Sarkar (2008)
xyplot(sunspot.year, aspect = "xy",
       strip = FALSE, strip.left = TRUE,
       cut = list(number = 4, overlap = 0.05))

### A multivariate example; first juxtaposed, then superposed
xyplot(EuStockMarkets, scales = list(y = "same"))
xyplot(EuStockMarkets, superpose = TRUE, aspect = "xy", lwd = 2,
       type = c("l", "g"), ylim = c(0, max(EuStockMarkets)))

### Examples using screens (these two are identical)
xyplot(EuStockMarkets, screens = c(rep("Continental", 3), "UK"))
xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"))

### Automatic group styles
xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"),
       superpose = TRUE)

xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"),
       superpose = TRUE, xlim = extendrange(1996:1998),
       par.settings = standard.theme(color = FALSE))

### Specifying styles for series by name
xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"),
       col = list(DAX = "red", FTSE = "blue", "black"), auto.key = TRUE)

xyplot(EuStockMarkets, screens = list(FTSE = "UK", "Continental"),
       col = list(DAX = "red"), lty = list(SMI = 2), lwd = 1:2,
       auto.key = TRUE)

### Example with simpler data, few data points
set.seed(1)
z <- ts(cbind(a = 1:5, b = 11:15, c = 21:25) + rnorm(5))
xyplot(z, screens = 1)
xyplot(z, screens = list(a = "primary (a)", "other (b & c)"),
       type = list(a = c("p", "h"), b = c("p", "s"), "o"),
       pch = list(a = 2, c = 3), auto.key = list(type = "o"))
```



---

 B\_02\_barchart.table

*table methods for barchart and dotplot*


---

### Description

Contingency tables are often displayed using barcharts and dotplots. These methods are provided for convenience and operate directly on tables. Arrays and matrices are simply coerced to be a table.

### Usage

```
## S3 method for class 'table':
barchart(x, data, groups = TRUE,
         origin = 0, stack = TRUE, ..., horizontal = TRUE)

## S3 method for class 'array':
barchart(x, data, ...)

## S3 method for class 'matrix':
barchart(x, data, ...)

## S3 method for class 'table':
dotplot(x, data, groups = TRUE, ..., horizontal = TRUE)

## S3 method for class 'array':
dotplot(x, data, ...)

## S3 method for class 'matrix':
dotplot(x, data, ...)
```

### Arguments

x	a table, array or matrix object.
data	should not be specified. If specified, will be ignored with a warning.
groups	logical, whether to use the last dimension as the grouping variable in the display.
origin, stack	arguments to <code>panel.barchart</code> controlling the display. The defaults for the table method are different.
horizontal	logical, indicating whether the plot should be horizontal (with the categorical variable on the y-axis) or vertical.
...	other arguments, passed to the underlying <code>formula</code> method.

### Details

The first dimension is used as the variable on the vertical axis. The last dimension is optionally used as a grouping variable (to produce stacked barcharts by default). All other dimensions are used as conditioning variables. The order of these variables cannot be altered (except by permuting the original argument using `t` or `aperm`). For more flexibility, use the `formula` method after converting the table to a data frame using the relevant `as.data.frame` method.

**Value**

An object of class "trellis". The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

`barchart`, `t`, `aperm`, `table`, `panel.barchart`, `Lattice`

**Examples**

```
barchart(Titanic, scales = list(x = "free"),
         auto.key = list(title = "Survived"))
```

---

B\_03\_histogram

*Histograms and Kernel Density Plots*

---

**Description**

Draw Histograms and Kernel Density Plots, possibly conditioned on other variables.

**Usage**

```
histogram(x, data, ...)
densityplot(x, data, ...)
## S3 method for class 'formula':
histogram(x,
          data,
          allow.multiple, outer = TRUE,
          auto.key = FALSE,
          aspect = "fill",
          panel = lattice.getOption("panel.histogram"),
          prepanel, scales, strip, groups,
          xlab, xlim, ylab, ylim,
          type = c("percent", "count", "density"),
          nint = if (is.factor(x)) nlevels(x)
                  else round(log2(length(x)) + 1),
          endpoints = extend.limits(range(as.numeric(x), finite = TRUE), prop =
          breaks,
          equal.widths = TRUE,
          drop.unused.levels = lattice.getOption("drop.unused.levels"),
          ...,
          lattice.options = NULL,
          default.scales = list(),
          subscripts,
          subset)
```

```

## S3 method for class 'numeric':
histogram(x, data = NULL, xlab, ...)
## S3 method for class 'factor':
histogram(x, data = NULL, xlab, ...)

## S3 method for class 'formula':
densityplot(x,
            data,
            allow.multiple = is.null(groups) || outer,
            outer = !is.null(groups),
            auto.key = FALSE,
            aspect = "fill",
            panel = lattice.getOption("panel.densityplot"),
            prepanel, scales, strip, groups, weights,
            xlab, xlim, ylab, ylim,
            bw, adjust, kernel, window, width, give.Rkern,
            n = 50, from, to, cut, na.rm,
            drop.unused.levels = lattice.getOption("drop.unused.levels"),
            ...,
            lattice.options = NULL,
            default.scales = list(),
            subscripts,
            subset)
## S3 method for class 'numeric':
densityplot(x, data = NULL, xlab, ...)

do.breaks(endpoints, nint)

```

## Arguments

<code>x</code>	<p>The object on which method dispatch is carried out.</p> <p>For the <code>formula</code> method, a formula of the form <code>~ x   g1 * g2 * ...</code> indicates that histograms or Kernel Density estimates of <code>x</code> should be produced conditioned on the levels of the (optional) variables <code>g1</code>, <code>g2</code>, <code>...</code>. <code>x</code> can be numeric (or factor for histogram), and each of <code>g1</code>, <code>g2</code>, <code>...</code> must be either factors or shingles.</p> <p>As a special case, the right hand side of the formula can contain more than one variable separated by a <code>+</code> sign. What happens in this case is described in details in the documentation for <a href="#">xyplot</a>. Note that in either form, all the variables involved in the formula have to have same length.</p> <p>For the <code>numeric</code> and <code>factor</code> methods, <code>x</code> replaces the <code>x</code> vector described above. Conditioning is not allowed in these cases.</p>
<code>data</code>	<p>For the <code>formula</code> method, an optional data frame in which variables are to be evaluated. Ignored with a warning in other cases.</p>
<code>type</code>	<p>Character string indicating type of histogram to be drawn. <code>"percent"</code> and <code>"count"</code> give relative frequency and frequency histograms, and can be misleading when breakpoints are not equally spaced. <code>"density"</code> produces a density scale histogram.</p> <p><code>type</code> defaults to <code>"percent"</code>, except when the breakpoints are unequally spaced or <code>breaks = NULL</code>, when it defaults to <code>"density"</code>.</p>

nint	Number of bins. Applies only when <code>breaks</code> is unspecified or <code>NULL</code> in the call. Not applicable when the variable being plotted is a factor.
endpoints	vector of length 2 indicating the range of x-values that is to be covered by the histogram. This applies only when <code>breaks</code> is unspecified and the variable being plotted is not a factor. In <code>do.breaks</code> , this specifies the interval that is to be divided up.
breaks	usually a numeric vector of length (number of bins + 1) defining the breakpoints of the bins. Note that when breakpoints are not equally spaced, the only value of type that makes sense is density. When unspecified, the default is to use <pre>breaks = seq_len(1 + nlevels(x)) - 0.5</pre> <p>when <code>x</code> is a factor, and</p> <pre>breaks = do.breaks(endpoints, nint)</pre> <p>otherwise. Breakpoints calculated in such a manner are used in all panels. Other values of <code>breaks</code> are possible, in which case they affect the display in each panel differently. A special value of <code>breaks</code> is <code>NULL</code>, in which case the number of bins is determined by <code>nint</code> and then breakpoints are chosen according to the value of <code>equal.widths</code>. Other valid values of <code>breaks</code> are those of the <code>breaks</code> argument in <code>hist</code>. This allows specification of <code>breaks</code> as an integer giving the number of bins (similar to <code>nint</code>), as a character string denoting a method, and as a function.</p>
equal.widths	logical, relevant only when <code>breaks=NULL</code> . If <code>TRUE</code> , equally spaced bins will be selected, otherwise, approximately equal area bins will be selected (this would mean that the breakpoints will <b>not</b> be equally spaced).
n	number of points at which density is to be evaluated
panel	The function that uses the packet (subset of display variables) corresponding to a panel to create a display. Default panel functions are documented separately, and often have arguments that can be used to customize its display in various ways. Such arguments can usually be directly supplied to the high level function.
allow.multiple, outer, auto.key, aspect, prepanel, scales, strip, groups, xlab,	See <a href="#">xyplot</a>
weights	numeric vector of weights for the density calculations, evaluated in the non-standard manner used for <code>groups</code> and terms in the formula, if any. If this is specified, it is subsetted using <code>subscripts</code> inside the panel function to match it to the corresponding <code>x</code> values. At the time of writing, <code>weights</code> do not work in conjunction with an extended formula specification (this is not too hard to fix, so just bug the maintainer if you need this feature).
bw, adjust, kernel, window, width, give.Rkern, from, to, cut, na.rm	arguments to <code>density</code> , passed on as appropriate
...	Further arguments. See corresponding entry in <a href="#">xyplot</a> for non-trivial details.

### Details

`histogram` draws Conditional Histograms, while `densityplot` draws Conditional Kernel Density Plots. The density estimate in `densityplot` is actually calculated using the function `density`, and all arguments accepted by it can be passed (as `...`) in the call to `densityplot`

to control the output. See documentation of `density` for details. (Note: The default value of the argument `n` of `density` is changed to 50.)

These and all other high level Trellis functions have several arguments in common. These are extensively documented only in the help page for `xyplot`, which should be consulted to learn more detailed usage.

`do.breaks` is an utility function that calculates breakpoints given an interval and the number of pieces to break it into.

### Value

An object of class "trellis". The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

### Note

The form of the arguments accepted by the default panel function `panel.histogram` is different from that in S-PLUS. Whereas S-PLUS calculates the heights inside `histogram` and passes only the breakpoints and the heights to the panel function, here the original variable `x` is passed along with the breakpoints. This allows plots as in the second example below.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### References

Sarkar, Deepayan (2008) "Lattice: Multivariate Data Visualization with R", Springer. <http://lmdvr.r-forge.r-project.org/>

### See Also

`xyplot`, `panel.histogram`, `density`, `panel.densityplot`, `panel.mathdensity`, `Lattice`

### Examples

```
require(stats)
histogram( ~ height | voice.part, data = singer, nint = 17,
           endpoints = c(59.5, 76.5), layout = c(2,4), aspect = 1,
           xlab = "Height (inches)")

histogram( ~ height | voice.part, data = singer,
           xlab = "Height (inches)", type = "density",
           panel = function(x, ...) {
             panel.histogram(x, ...)
             panel.mathdensity(dmath = dnorm, col = "black",
                               args = list(mean=mean(x), sd=sd(x)))
           } )

densityplot( ~ height | voice.part, data = singer, layout = c(2, 4),
             xlab = "Height (inches)", bw = 5)
```

**Description**

Quantile-Quantile plot of a sample and a theoretical distribution

**Usage**

```
qqmath(x, data, ...)

## S3 method for class 'formula':
qqmath(x,
       data,
       allow.multiple = is.null(groups) || outer,
       outer = !is.null(groups),
       distribution = qnorm,
       f.value = NULL,
       auto.key = FALSE,
       aspect = "fill",
       panel = lattice.getOption("panel.qqmath"),
       prepanel = NULL,
       scales, strip, groups,
       xlab, xlim, ylab, ylim,
       drop.unused.levels = lattice.getOption("drop.unused.levels"),
       ...,
       lattice.options = NULL,
       default.scales = list(),
       subscripts,
       subset)
## S3 method for class 'numeric':
qqmath(x, data = NULL, ylab, ...)
```

**Arguments**

<code>x</code>	The object on which method dispatch is carried out. For the "formula" method, a formula of the form $\sim x \mid g1 * g2 * \dots$ , where <code>x</code> must be a numeric. For the "numeric" method, a numeric vector.
<code>data</code>	For the <code>formula</code> method, an optional data frame in which variables in the formula (as well as <code>groups</code> and <code>subset</code> , if any) are to be evaluated. Usually ignored with a warning in other methods.
<code>distribution</code>	a quantile function that takes a vector of probabilities as argument and produces the corresponding quantiles. Possible values are <code>qnorm</code> , <code>qunif</code> etc. Distributions with other required arguments need to be passed in as user defined functions.
<code>f.value</code>	optional numeric vector of probabilities, quantiles corresponding to which should be plotted. Can also be a function of a single integer (representing sample size) that returns such a numeric vector. The typical value for this argument is the function <code>ppoints</code> , which is also the S-PLUS default. If specified, the

probabilities generated by this function is used for the plotted quantiles, using the `quantile` function for the sample, and the function specified as the `distribution` argument for the theoretical distribution.

`f.value` defaults to `NULL`, which has the effect of using `ppoints` for the quantiles of the theoretical distribution, but the exact data values for the sample. This is similar to what happens for `qqnorm`, but different from the S-PLUS default of `f.value=ppoints`.

For large `x`, this argument can be useful in plotting a smaller set of quantiles, which is usually enough to capture the pattern.

`panel` The panel function to be used. Unlike in older versions, the default panel function does most of the actual computations and has support for grouping. See [panel.qqmath](#) for details.

`allow.multiple`, `outer`, `auto.key`, `aspect`, `prepanel`, `scales`, `strip`, `groups`, `xlab`,  
See [xyplot](#)

`...` Further arguments. See corresponding entry in [xyplot](#) for non-trivial details.

### Details

`qqmath` produces a Q-Q plot of the given sample and a theoretical distribution. The default behaviour of `qqmath` is different from the corresponding S-PLUS function, but is similar to `qqnorm`. See the entry for `f.value` for specifics.

The implementation details are also different from S-PLUS. In particular, all the important calculations are done by the `panel` (and `prepanel` function) and not `qqmath` itself. In fact, both the arguments `distribution` and `f.value` are passed unchanged to the `panel` and `prepanel` function. This allows, among other things, display of grouped Q-Q plots, which are often useful. See the help page for [panel.qqmath](#) for further details.

This and all other high level Trellis functions have several arguments in common. These are extensively documented only in the help page for `xyplot`, which should be consulted to learn more detailed usage.

### Value

An object of class `"trellis"`. The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### See Also

[xyplot](#), [panel.qqmath](#), [panel.qqmathline](#), [prepanel.qqmathline](#), [Lattice](#), [quantile](#)

### Examples

```
qqmath(~ rnorm(100), distribution = function(p) qt(p, df = 10))
qqmath(~ height | voice.part, aspect = "xy", data = singer,
       prepanel = prepanel.qqmathline,
       panel = function(x, ...) {
         panel.qqmathline(x, ...)
       })
```

```

        panel.qqmath(x, ...)
    })
vp.comb <-
  factor(sapply(strsplit(as.character(singer$voice.part), split = " "),
                "[", 1),
        levels = c("Bass", "Tenor", "Alto", "Soprano"))
vp.group <-
  factor(sapply(strsplit(as.character(singer$voice.part), split = " "),
                "[", 2))
qqmath(~ height | vp.comb, data = singer,
       groups = vp.group, auto.key = list(space = "right"),
       aspect = "xy",
       prepanel = prepanel.qqmathline,
       panel = function(x, ...) {
         panel.qqmathline(x, ...)
         panel.qqmath(x, ...)
       })

```

B\_05\_qq

*Quantile-Quantile Plots of Two Samples***Description**

Quantile-Quantile plots for comparing two Distributions

**Usage**

```

qq(x, data, ...)

## S3 method for class 'formula':
qq(x, data, aspect = "fill",
   panel = lattice.getOption("panel.qq"),
   prepanel, scales, strip,
   groups, xlab, xlim, ylab, ylim, f.value = NULL,
   drop.unused.levels = lattice.getOption("drop.unused.levels"),
   ...,
   lattice.options = NULL,
   qtype = 7,
   default.scales = list(),
   subscripts,
   subset)

```

**Arguments**

- |      |   |
|------|---|
| x    | The object on which method dispatch is carried out.<br>For the formula method, a formula of the form $y \sim x \mid g_1 * g_2 * \dots$ , where $x$ must be a numeric, and $y$ can be a factor, shingle, character or numeric vector, with the restriction that there must be exactly two levels of $y$ , which divide the values of $x$ into two groups. Quantiles for these groups will be plotted along the two axes. |
| data | For the formula methods, an optional data frame in which variables in the formula (as well as groups and subset, if any) are to be evaluated.   |



<code>f.value</code>	optional numeric vector of probabilities, quantiles corresponding to which should be plotted. Can also be a function of a single integer (representing sample size) that returns such a numeric vector. The typical value for this argument is the function <code>ppoints</code> , which is also the S-PLUS default. If specified, the probabilities generated by this function is used for the plotted quantiles, using the <code>quantile</code> function.  <code>f.value</code> defaults to <code>NULL</code> , which is equivalent to using <code>function(n) ppoints(n, a = 1)</code> . This has the effect of including the minimum and maximum data values in the computed quantiles. This is similar to what happens for <code>qqplot</code> but different from the default <code>qq</code> behaviour in S-PLUS.  For large data, this argument can be useful in plotting a smaller set of quantiles, which is usually enough to capture the pattern.
<code>panel</code>	The function that uses the packet (subset of display variables) corresponding to a panel to create a display. Default panel functions are documented separately, and often have arguments that can be used to customize its display in various ways. Such arguments can usually be directly supplied to the high level function.
<code>qtype</code>	type argument for the <a href="#">quantile</a>
<code>aspect, prepanel, scales, strip, groups, xlab, xlim, ylab, ylim, drop.unused.levels</code>	See <a href="#">xyplot</a>
<code>...</code>	Further arguments. See corresponding entry in <a href="#">xyplot</a> for non-trivial details.

### Details

`qq` produces a Q-Q plot of two samples. The default behaviour of `qq` is different from the corresponding S-PLUS function. See the entry for `f.value` for specifics.

This and all other high level Trellis functions have several arguments in common. These are extensively documented only in the help page for `xyplot`, which should be consulted to learn more detailed usage.

### Value

An object of class `"trellis"`. The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### See Also

[xyplot](#), [panel.qq](#), [qqmath](#), [Lattice](#)

### Examples

```
qq(voice.part ~ height, aspect = 1, data = singer,
   subset = (voice.part == "Bass 2" | voice.part == "Tenor 1"))
```

---

B\_06\_levelplot      *Level plots and contour plots*

---

## Description

Draw Level Plots and Contour plots.

## Usage

```
levelplot(x, data, ...)
contourplot(x, data, ...)

## S3 method for class 'formula':
levelplot(x,
          data,
          allow.multiple = is.null(groups) || outer,
          outer = TRUE,
          aspect = "fill",
          panel = lattice.getOption("panel.levelplot"),
          prepanel = NULL,
          scales = list(),
          strip = TRUE,
          groups = NULL,
          xlab,
          xlim,
          ylab,
          ylim,
          at,
          cuts = 15,
          pretty = FALSE,
          region = TRUE,
          drop.unused.levels = lattice.getOption("drop.unused.levels"),
          ...,
          lattice.options = NULL,
          default.scales = list(),
          colorkey = region,
          col.regions,
          alpha.regions,
          subset = TRUE)

## S3 method for class 'formula':
contourplot(x,
            data,
            panel = lattice.getOption("panel.contourplot"),
            cuts = 7,
            labels = TRUE,
            contour = TRUE,
            pretty = TRUE,
            region = FALSE,
            ...)
```

```

## S3 method for class 'table':
levelplot(x, data = NULL, aspect = "iso", ..., xlim, ylim)

## S3 method for class 'table':
contourplot(x, data = NULL, aspect = "iso", ..., xlim, ylim)

## S3 method for class 'matrix':
levelplot(x, data = NULL, aspect = "iso",
          ..., xlim, ylim,
          row.values = seq_len(nrow(x)),
          column.values = seq_len(ncol(x)))

## S3 method for class 'matrix':
contourplot(x, data = NULL, aspect = "iso",
            ..., xlim, ylim,
            row.values = seq_len(nrow(x)),
            column.values = seq_len(ncol(x)))

## S3 method for class 'array':
levelplot(x, data = NULL, ...)

## S3 method for class 'array':
contourplot(x, data = NULL, ...)

```

## Arguments

- x** for the `formula` method, a formula of the form  $z \sim x * y | g1 * g2 * \dots$ , where  $z$  is a numeric response, and  $x, y$  are numeric values evaluated on a rectangular grid.  $g1, g2, \dots$  are optional conditional variables, and must be either factors or shingles if present. Calculations are based on the assumption that all  $x$  and  $y$  values are evaluated on a grid (defined by their unique values). The function will not return an error if this is not true, but the display might not be meaningful. However, the  $x$  and  $y$  values need not be equally spaced. Both `levelplot` and `wireframe` have methods for `matrix`, `array`, and `table` objects, in which case  $x$  provides the  $z$  vector described above, while its rows and columns are interpreted as the  $x$  and  $y$  vectors respectively. This is similar to the form used in `filled.contour` and `image`. For higher-dimensional arrays and tables, further dimensions are used as conditioning variables. Note that the `dimnames` may be duplicated; this is handled by calling `make.unique` to make the names unique (although the original labels are used for the  $x$ - and  $y$ -axes).
- data** For the `formula` methods, an optional data frame in which variables in the formula (as well as `groups` and `subset`, if any) are to be evaluated. Usually ignored with a warning in other cases.
- row.values, column.values** Optional vectors of values that define the grid when  $x$  is a matrix. `row.values` and `column.values` must have the same lengths as `nrow(x)` and `ncol(x)` respectively. By default, row and column numbers.

panel	panel function used to create the display, as described in <a href="#">xyplot</a>
aspect	For the <code>matrix</code> methods, the default aspect ratio is chosen to make each cell square. The usual default is <code>aspect="fill"</code> , as described in <a href="#">xyplot</a> .
at	numeric vector giving breakpoints along the range of <code>z</code> . Contours (if any) will be drawn at these heights, and the regions in between would be colored using <code>col.regions</code> . In the latter case, values outside the range of <code>at</code> will not be drawn at all. This serves as a way to limit the range of the data shown, similar to what a <code>zlim</code> argument might have been used for. However, this also means that when supplying <code>at</code> explicitly, one has to be careful to include values outside the range of <code>z</code> to ensure that all the data are shown.
col.regions	color vector to be used if <code>regions</code> is <code>TRUE</code> . The general idea is that this should be a color vector of moderately large length (longer than the number of regions. By default this is 100). It is expected that this vector would be gradually varying in color (so that nearby colors would be similar). When the colors are actually chosen, they are chosen to be equally spaced along this vector. When there are more regions than colors in <code>col.regions</code> , the colors are recycled. The actual color assignment is performed by <code>level.colors</code> , which is documented separately.
alpha.regions	numeric, specifying alpha transparency (works only on some devices)
colorkey	logical specifying whether a color key is to be drawn alongside the plot, or a list describing the color key. The list may contain the following components: <code>space</code> : location of the colorkey, can be one of "left", "right", "top" and "bottom". Defaults to "right". <code>x, y</code> : location, currently unused <code>col</code> : vector of colors <code>at</code> : numeric vector specifying where the colors change. must be of length 1 more than the <code>col</code> vector. <code>labels</code> : a character vector for labelling the <code>at</code> values, or more commonly, a list describing characteristics of the labels. This list may include components <code>labels</code> , <code>at</code> , <code>cex</code> , <code>col</code> , <code>rot</code> , <code>font</code> , <code>fontface</code> and <code>fontfamily</code> . <code>tick.number</code> : approximate number of ticks. <code>corner</code> : interacts with <code>x, y</code> ; unimplemented <code>width</code> : width of the key <code>height</code> : length of key w.r.t side of plot.
contour	logical, whether to draw contour lines.
cuts	number of levels the range of <code>z</code> would be divided into
labels	typically a logical indicating whether contour lines should be labelled, but other possibilities for more sophisticated control exists. Details are documented in the help page for <a href="#">panel.levelplot</a> , to which this argument is passed on unchanged. That help page also documents the <code>label.style</code> argument, which affects how the labels are rendered.
pretty	logical, whether to use pretty cut locations and labels
region	logical, whether regions between contour lines should be filled
allow.multiple, outer, prepanel, scales, strip, groups, xlab, xlim, ylab, ylim,	these arguments are described in the help page for <a href="#">xyplot</a> .
...	other arguments. Some are processed by <code>levelplot</code> or <code>contourplot</code> , and those unrecognized are passed on to the panel function.

## Details

These and all other high level Trellis functions have several arguments in common. These are extensively documented only in the help page for `xyplot`, which should be consulted to learn more detailed usage.

Other useful arguments are mentioned in the help page for the default panel function `panel.levelplot` (these are formally arguments to the panel function, but can be specified in the high level calls directly).

## Value

An object of class "trellis". The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

## Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

## References

Sarkar, Deepayan (2008) "Lattice: Multivariate Data Visualization with R", Springer. <http://lmdvr.r-forge.r-project.org/>

## See Also

`xyplot`, `Lattice`, `panel.levelplot`

## Examples

```
x <- seq(pi/4, 5 * pi, length.out = 100)
y <- seq(pi/4, 5 * pi, length.out = 100)
r <- as.vector(sqrt(outer(x^2, y^2, "+")))
grid <- expand.grid(x=x, y=y)
grid$z <- cos(r^2) * exp(-r/(pi^3))
levelplot(z~x*y, grid, cuts = 50, scales=list(log="e"), xlab="",
          ylab="", main="Weird Function", sub="with log scales",
          colorkey = FALSE, region = TRUE)

#S-PLUS example
require(stats)
attach(environmental)
ozo.m <- loess((ozone^(1/3)) ~ wind * temperature * radiation,
              parametric = c("radiation", "wind"), span = 1, degree = 2)
w.marginal <- seq(min(wind), max(wind), length.out = 50)
t.marginal <- seq(min(temperature), max(temperature), length.out = 50)
r.marginal <- seq(min(radiation), max(radiation), length.out = 4)
wtr.marginal <- list(wind = w.marginal, temperature = t.marginal,
                    radiation = r.marginal)
grid <- expand.grid(wtr.marginal)
grid[, "fit"] <- c(predict(ozo.m, grid))
contourplot(fit ~ wind * temperature | radiation, data = grid,
            cuts = 10, region = TRUE,
            xlab = "Wind Speed (mph)",
            ylab = "Temperature (F)",
```

```

        main = "Cube Root Ozone (cube root ppb)")
detach()

```

---

B\_07\_cloud

3d Scatter Plot and Wireframe Surface Plot

---

## Description

Generic functions to draw 3d scatter plots and surfaces. The "formula" methods do most of the actual work.

## Usage

```

cloud(x, data, ...)
wireframe(x, data, ...)

## S3 method for class 'formula':
cloud(x,
      data,
      allow.multiple = is.null(groups) || outer,
      outer = FALSE,
      auto.key = FALSE,
      aspect = c(1,1),
      panel.aspect = 1,
      panel = lattice.getOption("panel.cloud"),
      prepanel = NULL,
      scales = list(),
      strip = TRUE,
      groups = NULL,
      xlab,
      ylab,
      zlab,
      xlim = if (is.factor(x)) levels(x) else range(x, finite = TRUE),
      ylim = if (is.factor(y)) levels(y) else range(y, finite = TRUE),
      zlim = if (is.factor(z)) levels(z) else range(z, finite = TRUE),
      at,
      drape = FALSE,
      pretty = FALSE,
      drop.unused.levels,
      ...,
      lattice.options = NULL,
      default.scales =
      list(distance = c(1, 1, 1),
           arrows = TRUE,
           axs = axs.default),
      colorkey,
      col.regions,
      alpha.regions,
      cuts = 70,
      subset = TRUE,
      axs.default = "r")

```

```

## S3 method for class 'formula':
wireframe(x,
          data,
          panel = lattice.getOption("panel.wireframe"),
          ...)

## S3 method for class 'matrix':
cloud(x, data = NULL, type = "h",
      zlab = deparse(substitute(x)), aspect, ...,
      xlim, ylim, row.values, column.values)

## S3 method for class 'table':
cloud(x, data = NULL, groups = FALSE,
      zlab = deparse(substitute(x)),
      type = "h", ...)

## S3 method for class 'matrix':
wireframe(x, data = NULL,
          zlab = deparse(substitute(x)), aspect, ...,
          xlim, ylim, row.values, column.values)

```

## Arguments

**x** The object on which method dispatch is carried out. For the "formula" methods, a formula of the form  $z \sim x * y | g1 * g2 * \dots$ , where  $z$  is a numeric response, and  $x, y$  are numeric values.  $g1, g2, \dots$ , if present, are conditioning variables used for conditioning, and must be either factors or shingles. In the case of `wireframe`, calculations are based on the assumption that the  $x$  and  $y$  values are evaluated on a rectangular grid defined by their unique values. The grid points need not be equally spaced. For `wireframe`,  $x, y$  and  $z$  may also be matrices (of the same dimension), in which case they are taken to represent a 3-D surface parametrized on a 2-D grid (e.g., a sphere). Conditioning is not possible with this feature. See details below. Missing values are allowed, either as NA values in the  $z$  vector, or missing rows in the data frame (note however that in that case the X and Y grids will be determined only by the available values). For a grouped display (producing multiple surfaces), missing rows are not allowed, but NA-s in  $z$  are. Both `wireframe` and `cloud` have methods for `matrix` objects, in which case  $x$  provides the  $z$  vector described above, while its rows and columns are interpreted as the  $x$  and  $y$  vectors respectively. This is similar to the form used in `persp`.

**data** for the "formula" methods, an optional data frame in which variables in the formula (as well as `groups` and `subset`, if any) are to be evaluated. `data` should not be specified except when using the "formula" method.

**row.values, column.values** Optional vectors of values that define the grid when  $x$  is a matrix. `row.values` and `column.values` must have the same lengths as `nrow(x)` and `ncol(x)` respectively. By default, row and column numbers.

**allow.multiple, outer, auto.key, prepanel, strip, groups, xlab, xlim, ylab, ylim** These arguments are documented in the help page for `xyplot`. For the

	<code>cloud.table</code> method, <code>groups</code> must be a logical indicating whether the last dimension should be used as a grouping variable as opposed to a conditioning variable. This is only relevant if the table has more than 2 dimensions.
<code>type</code>	type of display in <code>cloud</code> (see <a href="#">panel.3dscatter</a> for details). Defaults to "h" for the <code>matrix</code> method.
<code>aspect, panel.aspect</code>	unlike other high level functions, <code>aspect</code> is taken to be a numeric vector of length 2, giving the relative aspects of the y-size/x-size and z-size/x-size of the enclosing cube. The usual role of the <code>aspect</code> argument in determining the aspect ratio of the panel (see <a href="#">xyplot</a> for details) is played by <code>panel.aspect</code> , except that it can only be a numeric value. For the <code>matrix</code> methods, the default y/x aspect is <code>ncol(x) / nrow(x)</code> and the z/x aspect is the smaller of the y/x aspect and 1.
<code>panel</code>	panel function used to create the display. See <a href="#">panel.cloud</a> for (non-trivial) details.
<code>scales</code>	a list describing the scales. As with other high level functions (see <a href="#">xyplot</a> for details), this list can contain parameters in <code>name=value</code> form. It can also contain components with the special names <code>x</code> , <code>y</code> and <code>z</code> , which can be similar lists with axis-specific values overriding the ones specified in <code>scales</code> . The most common use for this argument is to set <code>arrows=FALSE</code> , which causes tick marks and labels to be used instead of arrows being drawn (the default). Both can be suppressed by <code>draw=FALSE</code> . Another special component is <code>distance</code> , which specifies the relative distance of the axis label from the bounding box. If specified as a component of <code>scales</code> (as opposed to one of <code>scales\$z</code> etc), this can be (and is recycled if not) a vector of length 3, specifying distances for the x, y and z labels respectively. Other components that work in the <code>scales</code> argument of <code>xyplot</code> etc. should also work here (as long as they make sense), including explicit specification of tick mark locations and labels. (Not everything is implemented yet, but if you find something that should work but does not, feel free to bug the maintainer.) Note, however, that for these functions <code>scales</code> cannot contain information that is specific to particular panels. If you really need that, consider using the <code>scales.3d</code> argument of <code>panel.cloud</code> .
<code>axs.default</code>	Unlike 2-D display functions, <code>cloud</code> does not expand the bounding box to slightly beyond the range of the data, even though it should. This is primarily because this is the natural behaviour in <code>wireframe</code> , which uses the same code. <code>axs.default</code> is intended to provide a different default for <code>cloud</code> . However, this feature has not yet been implemented.
<code>zlab</code>	Specifies a label describing the z variable in ways similar to <code>xlab</code> and <code>ylab</code> (i.e. "grob", character string, expression or list) in other high level functions. Additionally, if <code>zlab</code> (and <code>xlab</code> and <code>ylab</code> ) is a list, it can contain a component called <code>rot</code> , controlling the rotation for the label
<code>zlim</code>	limits for the z-axis. Similar to <code>xlim</code> and <code>ylim</code> in other high level functions
<code>drape</code>	logical, whether the wireframe is to be draped in color. If <code>TRUE</code> , the height of a facet is used to determine its color in a manner similar to the coloring scheme used in <a href="#">levelplot</a> . Otherwise, the background color is used to color the facets. This argument is ignored if <code>shade = TRUE</code> (see <a href="#">panel.3dwire</a> ).
<code>at, col.regions, alpha.regions</code>	these arguments are analogous to those in <a href="#">levelplot</a> . if <code>drape=TRUE</code> , <code>at</code> gives the vector of cutpoints where the colors change, and <code>col.regions</code>



the vector of colors to be used in that case. `alpha.regions` determines the alpha-transparency on supporting devices. These are passed down to the panel function, and also used in the colorkey if appropriate. The default for `col.regions` and `alpha.regions` is derived from the Trellis setting "regions"

`cuts` if `at` is unspecified, the approximate number of cutpoints if `drape=TRUE`

`pretty` whether automatic choice of cutpoints should be prettified

`colorkey` logical indicating whether a color key should be drawn alongside, or a list describing such a key. See [levelplot](#) for details.

... Any number of other arguments can be specified, and are passed to the panel function. In particular, the arguments `distance`, `perspective`, `screen` and `R.mat` are very important in determining the 3-D display. The argument `shade` can be useful for `wireframe` calls, and controls shading of the rendered surface. These arguments are described in detail in the help page for [panel.cloud](#).

Additionally, an argument called `zoom` may be specified, which should be a numeric scalar to be interpreted as a scale factor by which the projection is magnified. This can be useful to get the variable names into the plot. This argument is actually only used by the default `prepanel` function.

## Details

These functions produce three dimensional plots in each panel (as long as the default panel functions are used). The orientation is obtained as follows: the data are scaled to fall within a bounding box that is contained in the  $[-0.5, 0.5]$  cube (even smaller for non-default values of `aspect`). The viewing direction is given by a sequence of rotations specified by the `screen` argument, starting from the positive Z-axis. The viewing point (camera) is located at a distance of  $1/\text{distance}$  from the origin. If `perspective=FALSE`, `distance` is set to 0 (i.e., the viewing point is at an infinite distance).

`cloud` draws a 3-D Scatter Plot, while `wireframe` draws a 3-D surface (usually evaluated on a grid). Multiple surfaces can be drawn by `wireframe` using the `groups` argument (although this is of limited use because the display is incorrect when the surfaces intersect). Specifying `groups` with `cloud` results in a `panel.superpose`-like effect (via [panel.3dscatter](#)).

`wireframe` can optionally render the surface as being illuminated by a light source (no shadows though). Details can be found in the help page for [panel.3dwire](#). Note that although arguments controlling these are actually arguments for the panel function, they can be supplied to `cloud` and `wireframe` directly.

For single panel plots, `wireframe` can also plot parametrized 3-D surfaces (i.e., functions of the form  $f(u,v) = (x(u,v), y(u,v), z(u,v))$ , where values of  $(u,v)$  lie on a rectangle. The simplest example of this sort of surface is a sphere parametrized by latitude and longitude. This can be achieved by calling `wireframe` with a formula `x` of the form  $z \sim x * y$ , where `x`, `y` and `z` are all matrices of the same dimension, representing the values of  $x(u,v)$ ,  $y(u,v)$  and  $z(u,v)$  evaluated on a discrete rectangular grid (the actual values of  $(u,v)$  are irrelevant).

When this feature is used, the heights used to calculate `drape` colors or shading colors are no longer the `z` values, but the distances of  $(x, y, z)$  from the origin.

Note that this feature does not work with `groups`, `subscripts`, `subset`, etc. Conditioning variables are also not supported in this case.

The algorithm for identifying which edges of the bounding box are 'behind' the points doesn't work in some extreme situations. Also, [panel.cloud](#) tries to figure out the optimal location of

the arrows and axis labels automatically, but can fail on occasion (especially when the view is from 'below' the data). This can be manually controlled by the `scpos` argument in `panel.cloud`.

These and all other high level Trellis functions have several other arguments in common. These are extensively documented only in the help page for `xypplot`, which should be consulted to learn more detailed usage.

### Value

An object of class "trellis". The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

### Note

There is a known problem with grouped `wireframe` displays when the (x, y) coordinates represented in the data do not represent the full evaluation grid. The problem occurs whether the grouping is specified through the `groups` argument or through the formula interface, and currently causes memory access violations. Depending on the circumstances, this is manifested either as a meaningless plot or a crash. To work around the problem, it should be enough to have a row in the data frame for each grid point, with an NA response (z) in rows that were previously missing.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### References

Sarkar, Deepayan (2008) "Lattice: Multivariate Data Visualization with R", Springer. <http://lmdvr.r-forge.r-project.org/>

### See Also

`Lattice` for an overview of the package, as well as `xypplot`, `levelplot`, `panel.cloud`.  
For interaction, see `panel.identify.cloud`.

### Examples

```
## volcano  ## 87 x 61 matrix
wireframe(volcano, shade = TRUE,
          aspect = c(61/87, 0.4),
          light.source = c(10,0,10))

g <- expand.grid(x = 1:10, y = 5:15, gr = 1:2)
g$z <- log((g$x^g$g + g$y^2) * g$gr)
wireframe(z ~ x * y, data = g, groups = gr,
          scales = list(arrows = FALSE),
          drape = TRUE, colorkey = TRUE,
          screen = list(z = 30, x = -60))

cloud(Sepal.Length ~ Petal.Length * Petal.Width | Species, data = iris,
      screen = list(x = -90, y = 70), distance = .4, zoom = .6)

## cloud.table

cloud(prop.table(Titanic, margin = 1:3),
```

```

type = c("p", "h"), strip = strip.custom(strip.names = TRUE),
scales = list(arrows = FALSE, distance = 2), panel.aspect = 0.7,
zlab = "Proportion")[, 1]

## transparent axes

par.set <-
  list(axis.line = list(col = "transparent"),
       clip = list(panel = "off"))
print(cloud(Sepal.Length ~ Petal.Length * Petal.Width,
           data = iris, cex = .8,
           groups = Species,
           main = "Stereo",
           screen = list(z = 20, x = -70, y = 3),
           par.settings = par.set,
           scales = list(col = "black")),
      split = c(1,1,2,1), more = TRUE)
print(cloud(Sepal.Length ~ Petal.Length * Petal.Width,
           data = iris, cex = .8,
           groups = Species,
           main = "Stereo",
           screen = list(z = 20, x = -70, y = 0),
           par.settings = par.set,
           scales = list(col = "black")),
      split = c(2,1,2,1))

```

---

## Description

Draw Conditional Scatter Plot Matrices and Parallel Coordinate Plots

## Usage

```

splom(x, data, ...)
parallel(x, data, ...)

## S3 method for class 'formula':
splom(x,
      data,
      auto.key = FALSE,
      aspect = 1,
      between = list(x = 0.5, y = 0.5),
      panel = lattice.getOption("panel.splom"),
      prepanel,
      scales,
      strip,
      groups,
      xlab,
      xlim,

```

```

    ylab = NULL,
    ylim,
    superpanel = lattice.getOption("panel.pairs"),
    pscales = 5,
    varnames,
    drop.unused.levels,
    ...,
    lattice.options = NULL,
    default.scales,
    subset = TRUE)
## S3 method for class 'formula':
parallel(x,
        data,
        auto.key = FALSE,
        aspect = "fill",
        between = list(x = 0.5, y = 0.5),
        panel = lattice.getOption("panel.parallel"),
        prepanel,
        scales,
        strip,
        groups,
        xlab = NULL,
        xlim,
        ylab = NULL,
        ylim,
        varnames,
        horizontal.axis = TRUE,
        drop.unused.levels,
        ...,
        lattice.options = NULL,
        default.scales,
        subset = TRUE)

## S3 method for class 'data.frame':
splom(x, data = NULL, ..., groups = NULL, subset = TRUE)
## S3 method for class 'matrix':
splom(x, data = NULL, ..., groups = NULL, subset = TRUE)

## S3 method for class 'matrix':
parallel(x, data = NULL, ..., groups = NULL, subset = TRUE)
## S3 method for class 'data.frame':
parallel(x, data = NULL, ..., groups = NULL, subset = TRUE)

```

### Arguments

- |      |  |
|------|--|
| x    | The object on which method dispatch is carried out.<br>For the "formula" method, a formula describing the structure of the plot, which should be of the form $\sim x \mid g1 * g2 * \dots$ , where $x$ is a data frame or matrix. Each of $g1, g2, \dots$ must be either factors or shingles. The conditioning variables $g1, g2, \dots$ may be omitted.<br>For the <code>data.frame</code> methods, a data frame. |
| data | For the formula methods, an optional data frame in which variables in the  |

	formula (as well as <code>groups</code> and <code>subset</code> , if any) are to be evaluated.
<code>aspect</code>	aspect ratio of each panel (and subpanel), square by default for <code>splom</code> .
<code>between</code>	to avoid confusion between panels and subpanels, the default is to show the panels of a <code>splom</code> plot with space between them.
<code>panel</code>	Usual interpretation for <code>parallel</code> , namely the function that creates the display within each panel. For <code>splom</code> , the terminology is slightly complicated. The role played by the <code>panel</code> function in most other high-level functions is played here by the <code>superpanel</code> function, which is responsible for the display for each conditional data subset. <code>panel</code> is simply an argument to the default <code>superpanel</code> function <code>panel.pairs</code> , and is passed on to it unchanged. It is used there to create each pairwise display. See <a href="#">panel.pairs</a> for more useful options.
<code>superpanel</code>	function that sets up the <code>splom</code> display, by default as a scatterplot matrix.
<code>pscales</code>	a numeric value or a list, meant to be a less functional substitute for the <code>scales</code> argument in <code>xyplot</code> etc. This argument is passed to the <code>superpanel</code> function, and is handled by the default <code>superpanel</code> function <code>panel.pairs</code> . The help page for the latter documents this argument in more detail.
<code>varnames</code>	character vector giving the names of the <code>p</code> variables in <code>x</code> . By default, the column names of <code>x</code> .
<code>horizontal.axis</code>	logical indicating whether the parallel axes should be laid out horizontally (TRUE) or vertically (FALSE).
<code>auto.key</code> , <code>prepanel</code> , <code>scales</code> , <code>strip</code> , <code>groups</code> , <code>xlab</code> , <code>xlim</code> , <code>ylab</code> , <code>ylim</code> , <code>drop.unused.l</code>	See <a href="#">xyplot</a>
<code>...</code>	Further arguments. See corresponding entry in <a href="#">xyplot</a> for non-trivial details.

### Details

`splom` produces Scatter Plot Matrices. The role usually played by `panel` is taken over by `superpanel`, which takes a data frame subset and is responsible for plotting it. It is called with the coordinate system set up to have both `x`- and `y`-limits from 0.5 to `ncol(z) + 0.5`. The only built-in option currently available is [panel.pairs](#), which calls a further panel function for each pair  $(i, j)$  of variables in `z` inside a rectangle of unit width and height centered at  $c(i, j)$  (see [panel.pairs](#) for details).

Many of the finer customizations usually done via arguments to high level function like `xyplot` are instead done by `panel.pairs` for `splom`. These include control of axis limits, tick locations and `prepanel` calculations. If you are trying to fine-tune your `splom` plot, definitely look at the [panel.pairs](#) help page. The `scales` argument is usually not very useful in `splom`, and trying to change it may have undesired effects.

[parallel](#) draws Parallel Coordinate Plots. (Difficult to describe, see example.)

These and all other high level Trellis functions have several arguments in common. These are extensively documented only in the help page for `xyplot`, which should be consulted to learn more detailed usage.

### Value

An object of class "trellis". The [update](#) method can be used to update components of the object and the [print](#) method (usually called by default) will plot it on an appropriate plotting device.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[xyplot](#), [Lattice](#), [panel.pairs](#), [panel.parallel](#).

**Examples**

```
super.sym <- trellis.par.get("superpose.symbol")
splom(~iris[1:4], groups = Species, data = iris,
      panel = panel.superpose,
      key = list(title = "Three Varieties of Iris",
                 columns = 3,
                 points = list(pch = super.sym$pch[1:3],
                               col = super.sym$col[1:3]),
                 text = list(c("Setosa", "Versicolor", "Virginica"))))
splom(~iris[1:3] | Species, data = iris,
      layout=c(2,2), pscales = 0,
      varnames = c("Sepal\nLength", "Sepal\nWidth", "Petal\nLength"),
      page = function(...) {
        ltext(x = seq(.6, .8, length.out = 4),
              y = seq(.9, .6, length.out = 4),
              labels = c("Three", "Varieties", "of", "Iris"),
              cex = 2)
      })
parallel(~iris[1:4] | Species, iris)
parallel(~iris[1:4], iris, groups = Species,
        horizontal.axis = FALSE, scales = list(x = list(rot = 90)))
```

**Description**

tmd Creates Tukey Mean-Difference Plots from a trellis object returned by `xyplot`, `qq` or `qqmath`. The `prepanel` and `panel` functions are used as appropriate. The formula method for `tmd` is provided for convenience, and simply calls `tmd` on the object created by calling `xyplot` on that formula.

**Usage**

```
tmd(object, ...)
```

```
## S3 method for class 'trellis':
tmd(object,
     xlab = "mean",
     ylab = "difference",
     panel,
     prepanel,
     ...)
```

```

prepanel.tmd.qqmath(x,
                    f.value = NULL,
                    distribution = qnorm,
                    qtype = 7,
                    groups = NULL,
                    subscripts, ...)
panel.tmd.qqmath(x,
                 f.value = NULL,
                 distribution = qnorm,
                 qtype = 7,
                 groups = NULL,
                 subscripts, ...)
panel.tmd.default(x, y, groups = NULL, ...)
prepanel.tmd.default(x, y, ...)

```

### Arguments

<code>object</code>	An object of class "trellis" returned by <code>xyplot</code> , <code>qq</code> or <code>qqmath</code> .
<code>xlab</code>	x label
<code>ylab</code>	y label
<code>panel</code>	panel function to be used. See details below.
<code>prepanel</code>	prepanel function. See details below.
<code>f.value</code> , <code>distribution</code> , <code>qtype</code>	see <a href="#">panel.qqmath</a> .
<code>groups</code> , <code>subscripts</code>	see <a href="#">xyplot</a> .
<code>x</code> , <code>y</code>	data as passed to panel functions in original call.
<code>...</code>	other arguments

### Details

The Tukey Mean-difference plot is produced by modifying the (x,y) values of each panel as follows: the new coordinates are given by  $x = (x+y) / 2$  and  $y = y - x$ , which are then plotted. The default panel function(s) add a reference line at  $y=0$  as well.

`tmd` acts on the a "trellis" object, not on the actual plot this object would have produced. As such, it only uses the arguments supplied to the panel function in the original call, and completely ignores what the original panel function might have done with this data. `tmd` uses these panel arguments to set up its own scales (using its `prepanel` argument) and display (using `panel`). It is thus important to provide suitable `prepanel` and `panel` functions to `tmd` depending on the original call.

Such functions currently exist for `xyplot`, `qq` (the ones with `default` in their name) and `qqmath`, as listed in the usage section above. These assume the default displays for the corresponding high-level call. If unspecified, the `prepanel` and `panel` arguments default to suitable choices.

`tmd` uses the `update` method for "trellis" objects, which processes all extra arguments supplied to `tmd`.

**Value**

An object of class "trellis". The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

`qq`, `qqmath`, `xyplot`, `Lattice`

**Examples**

```
tmd(qqmath(~height | voice.part, data = singer))
```

---

B\_10\_rfs

*Residual and Fit Spread Plots*

---

**Description**

Plots fitted values and residuals (via `qqmath`) on a common scale for any object that has methods for fitted values and residuals.

**Usage**

```
rfs(model, layout=c(2, 1), xlab="f-value", ylab=NULL,
     distribution = qunif,
     panel, prepanel, strip, ...)
```

**Arguments**

<code>model</code>	a fitted model object with methods <code>fitted.values</code> and <code>residuals</code> . Can be the value returned by <code>oneway</code>
<code>layout</code>	default layout is <code>c(2,1)</code>
<code>xlab</code>	defaults to <code>"f.value"</code>
<code>distribution</code>	the distribution function to be used for <code>qqmath</code>
<code>ylab</code> , <code>panel</code> , <code>prepanel</code> , <code>strip</code>	See <code>xyplot</code>
<code>...</code>	other arguments, passed on to <code>qqmath</code> .

**Value**

An object of class "trellis". The `update` method can be used to update components of the object and the `print` method (usually called by default) will plot it on an appropriate plotting device.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>



**See Also**

[oneway](#), [qqmath](#), [xyplot](#), [Lattice](#)

**Examples**

```
rfs(oneway(height ~ voice.part, data = singer, spread = 1), aspect = 1)
```

---

B\_11\_oneway

*Fit One-way Model*

---

**Description**

Fits a One-way model to univariate data grouped by a factor, the result often being displayed using `rfs`

**Usage**

```
oneway(formula, data, location=mean, spread=function(x) sqrt(var(x)))
```

**Arguments**

<code>formula</code>	formula of the form $y \sim x$ where $y$ is the numeric response and $x$ is the grouping factor
<code>data</code>	data frame in which the model is to be evaluated
<code>location</code>	function or numeric giving the location statistic to be used for centering the observations, e.g. <code>median</code> , 0 (to avoid centering).
<code>spread</code>	function or numeric giving the spread statistic to be used for scaling the observations, e.g. <code>sd</code> , 1 (to avoid scaling).

**Value**

A list with components

<code>location</code>	vector of locations for each group.
<code>spread</code>	vector of spreads for each group.
<code>fitted.values</code>	vector of locations for each observation.
<code>residuals</code>	residuals ( $y - \text{fitted.values}$ ).
<code>scaled.residuals</code>	residuals scaled by spread for their group

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[rfs](#), [Lattice](#)

---

`C_01_trellis.device`*Initializing Trellis Displays*

---

**Description**

Initialization of a display device with appropriate graphical parameters.

**Usage**

```
trellis.device(device = getOption("device"),
              color = !(dev.name == "postscript"),
              theme = lattice.getOption("default.theme"),
              new = TRUE,
              retain = FALSE,
              ...)

standard.theme(name, color)
canonical.theme(name, color)
col.whitebg()
```

**Arguments**

- |                     |   |
|---------------------|---|
| <code>device</code> | function (or the name of one as a character string) that starts a device. Admissible values depend on the platform and how R was compiled (see <a href="#">Devices</a> ), but usually "pdf", "postscript", "png", "jpeg" and at least one of "X11", "windows" and "quartz" will be available.   |
| <code>color</code>  | logical, whether the initial settings should be color or black and white. Defaults to FALSE for postscript devices, TRUE otherwise. Note that this only applies to the initial choice of colors, which can be overridden using <code>theme</code> or subsequent calls to <code>trellis.par.set</code> (and by arguments supplied directly in high level calls for some settings).   |
| <code>theme</code>  | list of components that changes the settings of the device opened, or, a function that when called produces such a list. The function name can be supplied as a quoted string. These settings are only used to modify the default settings (determined by other arguments), and need not contain all possible parameters. A possible use of this argument is to change the default settings by specifying <code>lattice.options(default.theme = "col.whitebg")</code> . For back-compatibility, this is initially (when <code>lattice</code> is loaded) set to <code>options(lattice.theme)</code> .<br>If <code>theme</code> is a function, it will not be supplied any arguments, however, it is guaranteed that a device will already be open when it is called, so one may use <code>.Device</code> inside the function to ascertain what device has been opened. |
| <code>new</code>    | logical flag indicating whether a new device should be started. If FALSE, the options for the current device are changed to the defaults determined by the other arguments.   |
| <code>retain</code> | logical. If TRUE and a setting for this device already exists, then that is used instead of the defaults for this device. By default, pre-existing settings are overwritten (and lost).   |

name name of the device for which the setting is required, as returned by `.Device`  
 ... additional parameters to be passed to the `device` function, most commonly `file` for non-screen devices, as well as `height`, `width`, etc. See the help file for individual devices for admissible arguments.

### Details

Trellis Graphics functions obtain the default values of various graphical parameters (colors, line types, fonts, etc.) from a customizable “settings” list. This functionality is analogous to `par` for standard R graphics and, together with `lattice.options`, mostly supplants it (`par` settings are mostly ignored by Lattice). Unlike `par`, Trellis settings can be controlled separately for each different device type (but not concurrently for different instances of the same device). `standard.theme` and `col.whitebg` produce predefined settings (a.k.a. themes), while `trellis.device` provides a high level interface to control which “theme” will be in effect when a new device is opened. `trellis.device` is called automatically when a “trellis” object is plotted, and the defaults can be used to provide sufficient control, so in a properly configured system it is rarely necessary for the user to call `trellis.device` explicitly.

The `standard.theme` function is intended to provide device specific settings (e.g. light colors on a grey background for screen devices, dark colors or black and white for print devices) which were used as defaults prior to R 2.3.0. However, these defaults are not always appropriate, due to the variety of platforms and hardware settings on which R is used, as well as the fact that a plot created on a particular device may be subsequently used in many different ways. For this reason, a “safe” default is used for all devices from R 2.3.0 onwards. The old behaviour can be reinstated by setting `standard.theme` as the default `theme` argument, e.g. by putting `options(lattice.theme = "standard.theme")` in a startup script (see the entry for `theme` above for details).

### Value

`standard.theme` returns a list of components defining graphical parameter settings for Lattice displays. It is used internally in `trellis.device`, and can also be used as the `theme` argument to `trellis.par.set`, or even as `theme` in `trellis.device` to use the defaults for another device. `canonical.theme` is an alias for `standard.theme`.

`col.whitebg` returns a similar (but smaller) list that is suitable as the `theme` argument to `trellis.device` and `trellis.par.set`. It contains settings values which provide colors suitable for plotting on a white background. Note that the name `col.whitebg` is somewhat of a misnomer, since it actually sets the background to transparent rather than white.

### Note

Earlier versions of `trellis.device` had a `bg` argument to set the background color, but this is no longer supported. If supplied, the `bg` argument will be passed on to the device function; however, this will have no effect on the Trellis settings. It is rarely meaningful to change the background alone; if you feel the need to change the background, consider using the `theme` argument instead.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### References

Sarkar, Deepayan (2008) "Lattice: Multivariate Data Visualization with R", Springer. <http://lmdvr.r-forge.r-project.org/>

**See Also**

[Lattice](#) for an overview of the `lattice` package.

[Devices](#) for valid choices of device on your platform.

[trellis.par.get](#) and [trellis.par.set](#) can be used to query and modify the settings *after* a device has been initialized. The `par.settings` argument to high level functions, described in [xyplot](#), can be used to attach transient settings to a "trellis" object.

C\_02\_trellis.par.get

*Graphical Parameters for Trellis Displays*

**Description**

Functions used to query, display and modify graphical parameters for fine control of Trellis displays. Modifications are made to the settings for the currently active device only.

**Usage**

```
trellis.par.set(name, value, ..., theme, warn = TRUE, strict = FALSE)
trellis.par.get(name = NULL)
```

```
show.settings(x = NULL)
```

**Arguments**

<code>name</code>	character giving the name of a component. If unspecified, <code>names(trellis.par.get())</code> returns a list containing all the current settings (this can be used to get the valid values for <code>name</code> )
<code>value</code>	a list giving the desired value of the component. Components that are already defined as part of the current settings but are not mentioned in <code>value</code> will remain unchanged.
<code>theme</code>	a list describing how to change the settings, similar to what is returned by <code>trellis.par.get()</code> . This is purely for convenience, allowing multiple calls to <code>trellis.par.set</code> to be condensed into one. The name of each component must be a valid name as described above, with the corresponding value a valid value as described above. As in <a href="#">trellis.device</a> , <code>theme</code> can also be a function that produces such a list when called. The function name can be supplied as a quoted string.
<code>...</code>	Multiple settings can be specified in <code>name = value</code> form. Equivalent to calling with <code>theme = list(...)</code>
<code>warn</code>	logical, indicating whether a warning should be issued when <code>trellis.par.get</code> is called when no graphics device is open
<code>strict</code>	logical, indicating whether the <code>value</code> should be interpreted strictly. Usually, assignment of <code>value</code> to the corresponding named component is fuzzy in the sense that sub-components that are absent from <code>value</code> but not currently <code>NULL</code> are retained. By specifying <code>strict = TRUE</code> , the assignment will be exact.

- x optional list of components that change the settings (any valid value of theme). These are used to modify the current settings (obtained by `trellis.par.get`) before they are displayed.

## Details

The various graphical parameters (color, line type, background etc) that control the look and feel of Trellis displays are highly customizable. Also, R can produce graphics on a number of devices, and it is expected that a different set of parameters would be more suited to different devices. These parameters are stored internally in a variable named `lattice.theme`, which is a list whose components define settings for particular devices. The components are identified by the name of the device they represent (as obtained by `.Device`), and are created as and when new devices are opened for the first time using `trellis.device` (or Lattice plots are drawn on a device for the first time in that session).

The initial settings for each device defaults to values appropriate for that device. In practice, this boils down to three distinct settings, one for screen devices like `x11` and `windows`, one for black and white plots (mostly useful for `postscript`) and one for color printers (`color postscript`, `pdf`).

Once a device is open, its settings can be modified. When another instance of the same device is opened later using `trellis.device`, the settings for that device are reset to its defaults, unless otherwise specified in the call to `trellis.device`. But settings for different devices are treated separately, i.e., opening a `postscript` device will not alter the `x11` settings, which will remain in effect whenever an `x11` device is active.

The functions `trellis.par.*` are meant to be interfaces to the global settings. They always apply on the settings for the currently ACTIVE device.

`trellis.par.get`, called without any arguments, returns the full list of settings for the active device. With the `name` argument present, it returns that component only. `trellis.par.get` sets the value of the `name` component of the current active device settings to `value`.

`trellis.par.get` is usually used inside `trellis` functions to get graphical parameters before plotting. Modifications by users via `trellis.par.set` is traditionally done as follows:

```
add.line <- trellis.par.get("add.line")
add.line$col <- "red"
trellis.par.set("add.line", add.line)
```

More convenient (but not S compatible) ways to do this are

```
trellis.par.set(list(add.line = list(col = "red")))
```

and

```
trellis.par.set(add.line = list(col = "red"))
```

The actual list of the components in `trellis.settings` has not been finalized, so I'm not attempting to list them here. The current value can be obtained by `print(trellis.par.get())`. Most names should be self-explanatory.

`show.settings` provides a graphical display summarizing some of the values in the current settings.

## Value

`trellis.par.get` returns a list giving parameters for that component. If `name` is missing, it returns the full list.

**Note**

In some ways, `trellis.par.get` and `trellis.par.set` together are a replacement for the `par` function used in traditional R graphics. In particular, changing `par` settings has little (if any) effect on lattice output. Since lattice plots are implemented using Grid graphics, its parameter system *does* have an effect unless overridden by a suitable lattice parameter setting. Such parameters can be specified as part of a lattice theme by including them in the `grid.pars` component (see `gpar` for a list of valid parameter names).

One of the uses of `par` is to set `par(ask = TRUE)` making R wait for user input before starting a new graphics page. For Grid graphics, this is done using `grid.prompt`. Lattice has no separate interface for this, and the user must call `grid.prompt` directly. If the grid package is not attached (lattice itself only loads the grid namespace), this may be done using `grid::grid.prompt(TRUE)`.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

`trellis.device`, `Lattice`, `grid.prompt`, `gpar`

**Examples**

```
show.settings()
```

---

C\_03\_simpleTheme     *Function to generate a simple theme*

---

**Description**

Simple interface to generate a list appropriate as a theme, typically used as the `par.settings` argument in a high level call

**Usage**

```
simpleTheme(col, alpha,
           cex, pch, lty, lwd, font, fill, border,
           col.points, col.line,
           alpha.points, alpha.line)
```

**Arguments**

`col`, `col.points`, `col.line`

A color specification. `col` is used for components `plot.symbol`, `plot.line`, `plot.polygon`, `superpose.symbol`, `superpose.line`, and `superpose.polygon`. `col.points` overrides `col`, and is used only for `plot.symbol` and `superpose.symbol`. Similarly, `col.lines` overrides `col` for `plot.line` and `superpose.line`. The arguments can be vectors, but only the first component is used for scalar targets (i.e., the ones without "superpose" in their name).

<code>alpha</code> , <code>alpha.points</code> , <code>alpha.line</code>	A numeric alpha transparency specification. The same rules as <code>col</code> , etc., apply.
<code>cex</code> , <code>pch</code> , <code>font</code>	Parameters for points. Applicable for components <code>plot.symbol</code> (for which only the first component is used) and <code>superpose.symbol</code> (for which the arguments can be vectors).
<code>lty</code> , <code>lwd</code>	Parameters for lines. Applicable for components <code>plot.line</code> (for which only the first component is used) and <code>superpose.line</code> (for which the arguments can be vectors).
<code>fill</code>	fill color, applicable for components <code>plot.symbol</code> , <code>plot.polygon</code> , <code>superpose.symbol</code> , and <code>superpose.polygon</code> .
<code>border</code>	border color, applicable for components <code>plot.polygon</code> and <code>superpose.polygon</code> .

### Details

The appearance of a lattice display depends partly on the “theme” active when the display is plotted (see `trellis.device` for details). This theme is used to obtain defaults for various graphical parameters, and in particular, the `auto.key` argument works on the premise that the same source is used for both the actual graphical encoding and the legend. The easiest way to specify custom settings for a particular display is to use the `par.settings` argument, which is usually tedious to construct as it is a nested list. The `simpleTheme` function can be used in such situations as a wrapper that generates a suitable list given parameters in simple `name=value` form, with the nesting made implicit. This is less flexible, but straightforward and sufficient in most situations.

### Value

A list that would work as the `theme` argument to `trellis.device` and `trellis.par.set`, or as the `par.settings` argument to any high level lattice function such as `xyplot`.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>, based on a suggestion from John Maindonald.

### See Also

`trellis.device`, `xyplot`, `Lattice`

### Examples

```
str(simpleTheme(pch = 16))

dotplot(variety ~ yield | site, data = barley, groups = year,
        auto.key = list(space = "right"),
        par.settings = simpleTheme(pch = 16),
        xlab = "Barley Yield (bushels/acre) ",
        aspect=0.5, layout = c(1,6))
```

---

`C_04_lattice.options`*Low-level Options Controlling Behaviour of Lattice*

---

### Description

Functions to handle settings used by lattice. Their main purpose is to make code maintenance easier, and users normally should not need to use these functions. However, fine control at this level maybe useful in certain cases.

### Usage

```
lattice.options(...)  
lattice.getOption(name)
```

### Arguments

<code>name</code>	character giving the name of a setting
<code>...</code>	new options can be defined, or existing ones modified, using one or more arguments of the form <code>name = value</code> or by passing a list of such tagged values. Existing values can be retrieved by supplying the names (as character strings) of the components as unnamed arguments.

### Details

These functions are modeled on `options` and `getOption`, and behave similarly for the most part. The components currently used are not documented here, but are fairly self-explanatory.

### Value

`lattice.getOption` returns the value of a single component, whereas `lattice.options` always returns a list with one or more named components. When changing the values of components, the old values of the modified components are returned by `lattice.options`. If called without any arguments, the full list is returned.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### See Also

[options](#), [trellis.device](#), [trellis.par.get](#), [Lattice](#)

### Examples

```
str(lattice.options())  
lattice.getOption("save.object")
```



---

C\_05\_print.trellis *Plot and Summarize Trellis Objects*


---

**Description**

The `print` and `plot` methods produce a graph from a "trellis" object. The `print` method is necessary for automatic plotting. `plot` method is essentially an alias, provided for convenience. The `summary` method gives a textual summary of the object. `dim` and `dimnames` describe the cross-tabulation induced by conditioning. `panel.error` is the default handler used when an error occurs while executing the panel function.

**Usage**

```
## S3 method for class 'trellis':
plot(x, position, split,
     more = FALSE, newpage = TRUE,
     packet.panel = packet.panel.default,
     draw.in = NULL,
     panel.height = lattice.getOption("layout.heights")$panel,
     panel.width = lattice.getOption("layout.widths")$panel,
     save.object = lattice.getOption("save.object"),
     panel.error = lattice.getOption("panel.error"),
     prefix,
     ...)

## S3 method for class 'trellis':
print(x, ...)

## S3 method for class 'trellis':
summary(object, ...)

## S3 method for class 'trellis':
dim(x)
## S3 method for class 'trellis':
dimnames(x)

panel.error(e)
```

**Arguments**

<code>x, object</code>	an object of class "trellis"
<code>position</code>	a vector of 4 numbers, typically <code>c(xmin, ymin, xmax, ymax)</code> that give the lower-left and upper-right corners of a rectangle in which the Trellis plot of <code>x</code> is to be positioned. The coordinate system for this rectangle is [0-1] in both the <code>x</code> and <code>y</code> directions.
<code>split</code>	a vector of 4 integers, <code>c(x,y,nx,ny)</code> , that says to position the current plot at the <code>x,y</code> position in a regular array of <code>nx</code> by <code>ny</code> plots. (Note: this has origin at top left)
<code>more</code>	A logical specifying whether more plots will follow on this page.

<code>newpage</code>	A logical specifying whether the plot should be on a new page. This option is specific to lattice, and is useful for including lattice plots in an arbitrary grid viewport (see the details section).
<code>packet.panel</code>	a function that determines which packet (data subset) is plotted in which panel. Panels are always drawn in an order such that columns vary the fastest, then rows and then pages. This function determines, given the column, row and page and other relevant information, the packet (if any) which should be used in that panel. By default, the association is determined by matching panel order with packet order, which is determined by varying the first conditioning variable the fastest, then the second, and so on. This association rule is encoded in the default, namely the function <code>packet.panel.default</code> , whose help page details the arguments supplied to whichever function is specified as the <code>packet.panel</code> argument.
<code>draw.in</code>	An optional (grid) viewport (used as the <code>name</code> argument in <code>downViewport</code> ) in which the plot is to be drawn. If specified, the <code>newpage</code> argument is ignored. This feature is not well-tested.
<code>panel.width,</code> <code>panel.height</code>	<code>panel.height</code> lists with 2 components, that should be valid <code>x</code> and <code>units</code> arguments to <code>unit()</code> (the <code>data</code> argument cannot be specified currently, but can be considered for addition if needed). The resulting <code>unit</code> object will be the width/height of each panel in the Lattice plot. These arguments can be used to explicitly control the dimensions of the panel, rather than letting them expand to maximize available space. Vector widths are allowed, and can specify unequal lengths across rows or columns.  Note that this option should not be used in conjunction with non-default values of the <code>aspect</code> argument in the original high level call (no error will be produced, but the resulting behaviour is undefined).
<code>save.object</code>	logical, specifying whether the object being printed is to be saved. The last object thus saved can be subsequently retrieved. This is an experimental feature that should allow access to a panel's data after the plot is done, making it possible to enhance the plot after the fact. This also allows the user to invoke the <code>update</code> method on the current plot, even if it was not assigned to a variable explicitly. For more details, see <code>trellis.focus</code> .
<code>panel.error</code>	a function, or a character string naming a function, that is to be executed when an error occurs during the execution of the panel function. The error is caught (using <code>tryCatch</code> ) and supplied as the only argument to <code>panel.error</code> . The default behaviour (implemented as the <code>panel.error</code> function) is to print the corresponding error message in the panel and continue. To stop execution on error, use <code>panel.error = stop</code> .  Normal error recovery and debugging tools are unhelpful when <code>tryCatch</code> is used. <code>tryCatch</code> can be completely bypassed by setting <code>panel.error</code> to <code>NULL</code> .
<code>prefix</code>	character string used as a prefix in viewport and grob names, used to distinguish similar viewports if a page contains multiple plots. The default is based on the serial number of the current plot on the current page (which is one more than the number of plots that have been drawn on the page before the current plot). If supplied explicitly, this has to be a valid R symbol name (briefly, it must start with a letter or a period followed by a letter) and must not contain the grid path separator (currently <code>" : "</code> ).
<code>e</code>	an error condition caught by <code>tryCatch</code>

... extra arguments, ignored by the `print` method. All arguments to the plot method are passed on to the `print` method.

### Details

This is the default print method for objects of class "trellis", produced by calls to functions like `xyplot`, `bwplot` etc. It is usually called automatically when a trellis object is produced. It can also be called explicitly to control plot positioning by means of the arguments `split` and `position`.

When `newpage = FALSE`, the current grid viewport is treated as the plotting area, making it possible to embed a Lattice plot inside an arbitrary grid viewport. The `draw.in` argument provides an alternative mechanism that may be simpler to use.

The print method uses the information in `x` (the object to be printed) to produce a display using the Grid graphics engine. At the heart of the plot is a grid layout, of which the entries of most interest to the user are the ones containing the display panels.

Unlike in older versions of Lattice (and Grid), the grid display tree is retained after the plot is produced, making it possible to access individual viewport locations and make additions to the plot. For more details and a lattice level interface to these viewports, see `trellis.focus`.

### Note

Unlike S-PLUS, trying to position a multipage display (using `position` and/or `split`) will mess things up.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### See Also

[Lattice](#), [unit](#), [update.trellis](#), [trellis.focus](#), [packet.panel.default](#)

### Examples

```
p11 <- histogram( ~ height | voice.part, data = singer, xlab="Height")
p12 <- densityplot( ~ height | voice.part, data = singer, xlab = "Height")
p2 <- histogram( ~ height, data = singer, xlab = "Height")

## simple positioning by split
print(p11, split=c(1,1,1,2), more=TRUE)
print(p2, split=c(1,2,1,2))

## Combining split and position:
print(p11, position = c(0,0,.75,.75), split=c(1,1,1,2), more=TRUE)
print(p12, position = c(0,0,.75,.75), split=c(1,2,1,2), more=TRUE)
print(p2, position = c(.5,.75,1,1), more=FALSE)

## Using seekViewport

## repeat same plot, with different polynomial fits in each panel
xyplot(Armed.Forces ~ Year, longley, index.cond = list(rep(1, 6)),
       layout = c(3, 2),
       panel = function(x, y, ...)
```

```

    {
      panel.xyplot(x, y, ...)
      fm <- lm(y ~ poly(x, panel.number()))
      llines(x, predict(fm))
    })

## Not run:
grid::seekViewport(trellis.vpname("panel", 1, 1))
cat("Click somewhere inside the first panel:\n")
ltext(grid::grid.locator(), lab = "linear")

## End(Not run)

grid::seekViewport(trellis.vpname("panel", 1, 1))
grid::grid.text("linear")

grid::seekViewport(trellis.vpname("panel", 2, 1))
grid::grid.text("quadratic")

grid::seekViewport(trellis.vpname("panel", 3, 1))
grid::grid.text("cubic")

grid::seekViewport(trellis.vpname("panel", 1, 2))
grid::grid.text("degree 4")

grid::seekViewport(trellis.vpname("panel", 2, 2))
grid::grid.text("degree 5")

grid::seekViewport(trellis.vpname("panel", 3, 2))
grid::grid.text("degree 6")

```

---

C\_06\_update.trellis

*Retrieve and Update Trellis Object*

---

## Description

Update method for objects of class "trellis", and a way to retrieve the last printed trellis object (that was saved).

## Usage

```

## S3 method for class 'trellis':
update(object,
       panel,
       aspect,
       as.table,
       between,
       key,
       auto.key,
       legend,
       layout,
       main,

```

```

    page,
    par.strip.text,
    prepanel,
    scales,
    skip,
    strip,
    strip.left,
    sub,
    xlab,
    xlim,
    ylab,
    ylim,
    par.settings,
    plot.args,
    lattice.options,
    index.cond,
    perm.cond,
    ...)

## S3 method for class 'trellis':
t(x)

## S3 method for class 'trellis':
x[i, j, ..., drop = FALSE]

trellis.last.object(warn = TRUE, ...)

```

### Arguments

<code>object, x</code>	The object to be updated, of class "trellis".
<code>i, j</code>	indices to be used. Names are not currently allowed.
<code>drop</code>	logical, whether dimensions with only one level are to be dropped. Currently ignored, behaves as if it were FALSE.
<code>warn</code>	logical, whether to warn when no plot is saved.
<code>panel, aspect, as.table, between, key, auto.key, legend, layout, main, page, par</code>	arguments that will be used to update <code>object</code> . See details below.

### Details

All high level lattice functions such as `xyplot` produce an object of (S3) class "trellis", which is usually displayed by its `print` method. However, the object itself can be manipulated and modified to a large extent using the `update` method, and then re-displayed as needed.

Most arguments to high level functions can also be supplied to the `update` method as well, with some exceptions. Generally speaking, anything that would need to change the data within each panel is a no-no (this includes the `formula`, `data`, `groups`, `subscripts` and `subset`). Everything else is technically game, though might not be implemented yet. If you find something missing that you wish to have, feel free to make a request.

Not all arguments accepted by a Lattice function are processed by `update`, but the ones listed above should work. The purpose of these arguments are described in the help page for `xyplot`. Any other argument is added to the list of arguments to be passed to the `panel` function. Because

of their somewhat special nature, updates to objects produced by `cloud` and `wireframe` do not work very well yet.

The `"["` method is a convenient shortcut for updating `index.cond`. The `t` method is a convenient shortcut for updating `perm.cond` in the special (but frequent) case where there are exactly two conditioning variables, when it has the effect of switching ('transposing') their order.

The print method for "trellis" objects optionally saves the object after printing it. If this feature is enabled, `trellis.last.object` can retrieve it. Note that at most one object can be saved at a time. If `trellis.last.object` is called with arguments, these are used to update the retrieved object before returning it.

### Value

An object of class `trellis`, by default plotted by `print.trellis`. `trellis.last.object` returns `NULL` if no saved object is available.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### See Also

`trellis.object`, `Lattice`, `xyplot`

### Examples

```
spots <- by(sunspots, gl(235, 12, labels = 1749:1983), mean)
old.options <- lattice.options(save.object = TRUE)
xyplot(spots ~ 1749:1983, xlab = "", type = "l",
       scales = list(x = list(alternating = 2)),
       main = "Average Yearly Sunspots")
update(trellis.last.object(), aspect = "xy")
trellis.last.object(xlab = "Year")
lattice.options(old.options)
```

---

C\_07\_shingles

*shingles*

---

### Description

Functions to handle shingles

### Usage

```
shingle(x, intervals=sort(unique(x)))
equal.count(x, ...)
as.shingle(x)
is.shingle(x)

## S3 method for class 'shingle':
plot(x, panel, xlab, ylab, ...)

## S3 method for class 'shingle':
```

```

print(x, showValues = TRUE, ...)

## S3 method for class 'shingleLevel':
as.character(x, ...)

## S3 method for class 'shingleLevel':
print(x, ...)

## S3 method for class 'shingle':
summary(object, showValues = FALSE, ...)

## S3 method for class 'shingle':
x[subset, drop = FALSE]
as.factorOrShingle(x, subset, drop)

```

### Arguments

<code>x</code>	numeric variable or R object, shingle in <code>plot.shingle</code> and <code>x[]</code> . An object (list of intervals) of class "shingleLevel" in <code>print.shingleLevel</code>
<code>object</code>	shingle object to be summarized
<code>showValues</code>	logical, whether to print the numeric part. If FALSE, only the intervals are printed
<code>intervals</code>	numeric vector or matrix with 2 columns
<code>subset</code>	logical vector
<code>drop</code>	whether redundant shingle levels are to be dropped
<code>panel, xlab, ylab</code>	standard Trellis arguments (see <code>xyplot</code> )
<code>...</code>	other arguments, passed down as appropriate. For example, extra arguments to <code>equal.count</code> are passed on to <code>co.intervals</code> . graphical parameters can be passed as arguments to the <code>plot</code> method.

### Details

A shingle is a data structure used in Trellis, and is a generalization of factors to ‘continuous’ variables. It consists of a numeric vector along with some possibly overlapping intervals. These intervals are the ‘levels’ of the shingle. The `levels` and `nlevels` functions, usually applicable to factors, also work on shingles. The implementation of shingles is slightly different from S.

There are print methods for shingles, as well as for printing the result of `levels()` applied to a shingle. For use in labelling, the `as.character` method can be used to convert levels of a shingle to character strings.

`equal.count` converts `x` to a shingle using the equal count algorithm. This is essentially a wrapper around `co.intervals`. All arguments are passed to `co.intervals`.

`shingle` creates a shingle using the given intervals. If `intervals` is a vector, these are used to form 0 length intervals.

`as.shingle` returns `shingle(x)` if `x` is not a shingle.

`is.shingle` tests whether `x` is a shingle.

`plot.shingle` displays the ranges of shingles via rectangles. `print.shingle` and `summary.shingle` describe the shingle object.

**Value**

x\$intervals for `levels.shingle(x)`, logical for `is.shingle`, an object of class "trellis" for `plot` (printed by default by `print.trellis`), and an object of class "shingle" for the others.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[xyplot](#), [co.intervals](#), [Lattice](#)

**Examples**

```
z <- equal.count(rnorm(50))
plot(z)
print(z)
print(levels(z))
```

---

D\_draw.colorkey      *Produce a Colorkey for levelplot*

---

**Description**

Produces (and possibly draws) a Grid frame grob which is a colorkey that can be placed in other Grid plots. Used in `levelplot`

**Usage**

```
draw.colorkey(key, draw=FALSE, vp=NULL)
```

**Arguments**

key	A list determining the key. See documentation for <code>levelplot</code> , in particular the section describing the <code>colorkey</code> argument, for details.
draw	logical, whether the grob is to be drawn.
vp	viewport

**Value**

A Grid frame object (that inherits from "grob")

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[xyplot](#)



---

D\_draw.key                    *Produce a Legend or Key*

---

**Description**

Produces (and possibly draws) a Grid frame grob which is a legend (aka key) that can be placed in other Grid plots.

**Usage**

```
draw.key(key, draw=FALSE, vp=NULL, ...)
```

**Arguments**

key	A list determining the key. See documentation for <code>xyplot</code> , in particular the section describing the <code>key</code> argument, for details.
draw	logical, whether the grob is to be drawn.
vp	viewport
...	ignored

**Value**

A Grid frame object (that inherits from 'grob').

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[xyplot](#)

---

D\_level.colors                    *A function to compute false colors representing a numeric or categorical variable*

---

**Description**

Calculates false colors from a numeric variable (including factors, using their numeric codes) given a color scheme and breakpoints.

**Usage**

```
level.colors(x, at, col.regions, colors = TRUE, ...)
```

**Arguments**

<code>x</code>	A numeric or <code>factor</code> variable.
<code>at</code>	A numeric variable of breakpoints defining intervals along the range of <code>x</code> .
<code>col.regions</code>	A specification of the colors to be assigned to each interval defined by <code>at</code> . This could be either a vector of colors, or a function that produces a vector of colors when called with a single argument giving the number of colors. See details below.
<code>colors</code>	logical indicating whether colors should be computed and returned. If <code>FALSE</code> , only the indices representing which interval (among those defined by <code>at</code> ) each value in <code>x</code> falls into is returned.
<code>...</code>	Extra arguments, ignored.

**Details**

If `at` has length `n`, then it defines `n-1` intervals. Values of `x` outside the range of `at` are not assigned to an interval, and the return value is `NA` for such values.

Colors are chosen by assigning a color to each of the `n-1` intervals. If `col.regions` is a palette function (such as `topo.colors`, or the result of calling `colorRampPalette`), it is called with `n-1` as an argument to obtain the colors. Otherwise, if there are exactly `n-1` colors in `col.regions`, these get assigned to the intervals. If there are fewer than `n-1` colors, `col.regions` gets recycled. If there are more, a more or less equally spaced (along the length of `col.regions`) subset is chosen.

**Value**

A vector of the same length as `x`. Depending on the `colors` argument, this could be either a vector of colors (in a form usable by `R`), or a vector of integer indices representing which interval the values of `x` fall in.

**Author(s)**

Deepayan Sarkar <deepayan.sarkar@r-project.org>

**See Also**

[levelplot](#), [colorRampPalette](#).

**Examples**

```
depth.col <-
  with(quakes,
       level.colors(depth, at = do.breaks(range(depth), 30),
                   col.regions = terrain.colors))

xyplot(lat ~ long | equal.count(stations), quakes,
       strip = strip.custom(var.name = "Stations"),
       colours = depth.col,
       panel = function(x, y, colours, subscripts, ...) {
         panel.xyplot(x, y, pch = 21, col = "transparent",
                     fill = colours[subscripts], ...)
       })
```

---

`D_make.groups`*Grouped data from multiple vectors*

---

**Description**

Combines two or more vectors, possibly of different lengths, producing a data frame with a second column indicating which of these vectors that row came from. This is mostly useful for getting data into a form suitable for use in high level Lattice functions.

**Usage**

```
make.groups(...)
```

**Arguments**

`...` one or more vectors of the same type (coercion is attempted if not), or one or more data frames with similar columns, with possibly differing number of rows.

**Value**

When all the input arguments are vectors, a data frame with two columns

`data` all the vectors supplied, concatenated

`which` factor indicating which vector the corresponding data value came from

When all the input arguments are data frames, the result of `rbind` applied to them, along with an additional `which` column as described above.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[Lattice](#)

**Examples**

```
sim.dat <-
  make.groups(uniform = runif(200),
             exponential = rexp(175),
             lognormal = rlnorm(150),
             normal = rnorm(125))
qqmath(~ data | which, sim.dat, scales = list(y = "free"))
```

---

D\_simpleKey                      *Function to generate a simple key*


---

### Description

Simple interface to generate a list appropriate for `draw.key`

### Usage

```
simpleKey(text, points = TRUE,
         rectangles = FALSE,
         lines = FALSE,
         col, cex, alpha, font,
         fontface, fontfamily,
         lineheight, ...)
```

### Arguments

<code>text</code>	character or expression vector, to be used as labels for levels of the grouping variable
<code>points</code>	logical
<code>rectangles</code>	logical
<code>lines</code>	logical
<code>col, cex, alpha, font, fontface, fontfamily, lineheight</code>	Used as top-level components of the list produced, to be used for the text labels. Defaults to the values in <code>trellis.par.get("add.text")</code>
<code>...</code>	further arguments added to the list, eventually passed to <code>draw.key</code>

### Details

A lattice plot can include a legend (key) if an appropriate list is specified as the `key` argument to a high level Lattice function such as `xyplot`. This key can be very flexible, but that flexibility comes at a cost: this list needs to be fairly complicated even in simple situations. `simpleKey` is designed as a useful shortcut in the common case of a key drawn in conjunction with a grouping variable, using the default graphical settings.

The `simpleKey` function produces a suitable `key` argument using a simpler interface. The resulting list will use the `text` argument as a text component, along with at most one set each of points, rectangles, and lines. The number of entries (rows) in the key will be the length of the `text` component. The graphical parameters for the additional components will be derived from the default graphical settings (wherein lies the simplification, as otherwise these would have to be provided explicitly).

Calling `simpleKey` directly is usually unnecessary. It is most commonly invoked (during the plotting of the "trellis" object) when the `auto.key` argument is supplied in a high-level plot with a `groups` argument. In that case, the `text` argument of `simpleKey` defaults to `levels(groups)`, and the defaults for the other arguments depend on the relevant high-level function. Note that these defaults can be overridden by supplying `auto.key` as a list containing the replacement values.

**Value**

A list that would work as the `key` argument to `xyplot`, etc.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

`Lattice`, `draw.key`, `trellis.par.get`, and `xyplot`, specifically the entry for `auto.key`.

---

D\_strip.default      *Default Trellis Strip Function*

---

**Description**

`strip.default` is the function that draws the strips by default in Trellis plots. Users can write their own strip functions, but most commonly this involves calling `strip.default` with a slightly different arguments. `strip.custom` provides a convenient way to obtain new strip functions that differ from `strip.default` only in the default values of certain arguments.

**Usage**

```
strip.default(which.given,
             which.panel,

             var.name,
             factor.levels,
             shingle.intervals,
             strip.names = c(FALSE, TRUE),
             strip.levels = c(TRUE, FALSE),
             sep = " : ",
             style = 1,
             horizontal = TRUE,
             bg = trellis.par.get("strip.background")$col[which.given],
             fg = trellis.par.get("strip.shingle")$col[which.given],
             par.strip.text = trellis.par.get("add.text"))
strip.custom(...)
```

**Arguments**

`which.given` integer index specifying which of the conditioning variables this strip corresponds to.

`which.panel` vector of integers as long as the number of conditioning variables. The contents are indices specifying the current levels of each of the conditioning variables (thus, this would be unique for each distinct packet). This is identical to the return value of `which.packet`, which is a more accurate name.

<code>var.name</code>	vector of character strings or expressions as long as the number of conditioning variables. The contents are interpreted as names for the conditioning variables. Whether they are shown on the strip depends on the values of <code>strip.names</code> and <code>style</code> (see below). By default, the names are shown for shingles, but not for factors.
<code>factor.levels</code>	vector of character strings or expressions giving the levels of the conditioning variable currently being drawn. For more than one conditioning variable, this will vary with <code>which.given</code> . Whether these levels are shown on the strip depends on the values of <code>strip.levels</code> and <code>style</code> (see below). <code>factor.levels</code> may be specified for both factors and shingles (despite the name), but by default they are shown only for factors. If shown, the labels may optionally be abbreviated by specifying suitable components in <code>par.strip.text</code> (see <a href="#">xyplot</a> )
<code>shingle.intervals</code>	if the current strip corresponds to a shingle, this should be a 2-column matrix giving the levels of the shingle. (of the form that would be produced by <code>printing.levels(shingle)</code> ). Otherwise, it should be <code>NULL</code>
<code>strip.names</code>	a logical vector of length 2, indicating whether or not the name of the conditioning variable that corresponds to the strip being drawn is to be written on the strip. The two components give the values for factors and shingles respectively. This argument is ignored for a factor when <code>style</code> is not one of 1 and 3.
<code>strip.levels</code>	a logical vector of length 2, indicating whether or not the level of the conditioning variable that corresponds to the strip being drawn is to be written on the strip. The two components give the values for factors and shingles respectively.
<code>sep</code>	character or expression, serving as a separator if the name and level are both to be shown.
<code>style</code>	integer, with values 1, 2, 3, 4 and 5 currently supported, controlling how the current level of a factor is encoded. Ignored for shingles (actually, when <code>shingle.intervals</code> is non-null. <p>The best way to find out what effect the value of <code>style</code> has is to try them out. Here is a short description: for a style value of 1, the strip is colored in the background color with the strip text (as determined by other arguments) centered on it. A value of 3 is the same, except that a part of the strip is colored in the foreground color, indicating the current level of the factor. For styles 2 and 4, the part corresponding to the current level remains colored in the foreground color, however, for style = 2, the remaining part is not colored at all, whereas for 4, it is colored with the background color. For both these, the names of all the levels of the factor are placed on the strip from left to right. Styles 5 and 6 produce the same effect (they are subtly different in S, this implementation corresponds to 5), they are similar to style 1, except that the strip text is not centered, it is instead positioned according to the current level.</p> <p>Note that unlike S-PLUS, the default value of <code>style</code> is 1. <code>strip.names</code> and <code>strip.levels</code> have no effect if <code>style</code> is not 1 or 3.</p>
<code>horizontal</code>	logical, specifying whether the labels etc should be horizontal. <code>horizontal=FALSE</code> is useful for strips on the left of panels using <code>strip.left=TRUE</code>
<code>par.strip.text</code>	list with parameters controlling the text on each strip, with components <code>col</code> , <code>cex</code> , <code>font</code> , etc.

bg	strip background color.
fg	strip foreground color.
...	arguments to be passed on to <code>strip.default</code> , overriding whatever value it would have normally assumed

### Details

default strip function for trellis functions. Useful mostly because of the `style` argument — non-default styles are often more informative, especially when the names of the levels of the factor `x` are small. Traditional use is as `strip = function(...) strip.default(style=2,...)`, though this can be simplified by the use of `strip.custom`.

### Value

`strip.default` is called for its side-effect, which is to draw a strip appropriate for multi-panel Trellis conditioning plots. `strip.custom` returns a function that is similar to `strip.default`, but with different defaults for the arguments specified in the call.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### See Also

[xyplot](#), [Lattice](#)

### Examples

```
## Traditional use
xyplot(Petal.Length ~ Petal.Width | Species, iris,
       strip = function(..., style) strip.default(..., style = 4))

## equivalent call using strip.custom
xyplot(Petal.Length ~ Petal.Width | Species, iris,
       strip = strip.custom(style = 4))

xyplot(Petal.Length ~ Petal.Width | Species, iris,
       strip = FALSE,
       strip.left = strip.custom(style = 4, horizontal = FALSE))
```

---

D\_trellis.object    *A Trellis Plot Object*

---

### Description

This class of objects is returned by high level lattice functions, and is usually plotted by default by its `print` method.

**Details**

A trellis object, as returned by high level lattice functions like `xyplot`, is a list with the "class" attribute set to "trellis". Many of the components of this list are simply the arguments to the high level function that produced the object. Among them are: `as.table`, `layout`, `page`, `panel`, `prepanel`, `main`, `sub`, `par.strip.text`, `strip`, `skip`, `xlab` `ylab`, `par.settings`, `lattice.options` and `plot.args`. Some other typical components are:

`formula` the Trellis formula used in the call  
`index.cond` list with index for each of the conditioning variables  
`perm.cond` permutation of the order of the conditioning variables  
`aspect.fill` logical, whether aspect is "fill"  
`aspect.ratio` numeric, aspect ratio to be used if `aspect.fill` is FALSE  
`call` call that generated the object.  
`condlevels` list with levels of the conditioning variables  
`legend` list describing the legend(s) to be drawn  
`panel.args` a list as long as the number of panels, each element being a list itself, containing the arguments in named form to be passed to the panel function in that panel.  
`panel.args.common` a list containing the arguments common to all the panel functions in name=value form  
`x.scales` list describing x-scale, can consist of several other lists, paralleling `panel.args`, if x-relation is not "same"  
`y.scales` list describing y-scale, similar to `x.scales`  
`x.between` numeric vector of interpanel x-space  
`y.between` numeric vector of interpanel y-space  
`x.limits` numeric vector of length 2 or list, giving x-axis limits  
`y.limits` similar to `x.limits`  
`packet.sizes` array recording the number of observations in each packet

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[Lattice](#), [xyplot](#), [print.trellis](#)

**Description**

The classic Trellis paradigm is to plot the whole object at once, without the possibility of interacting with it afterwards. However, by keeping track of the grid viewports where the panels and strips are drawn, it is possible to go back to them afterwards and enhance them one panel at a time. These functions provide convenient interfaces to help in this. Note that these are still experimental and the exact details may change in future.



**Usage**

```

panel.identify(x, y = NULL,
              subscripts = seq_along(x),
              labels = subscripts,
              n = length(x), offset = 0.5,
              threshold = 18, ## in points, roughly 0.25 inches
              panel.args = trellis.panelArgs(),
              ...)
panel.identify.qqmath(x, distribution, groups, subscripts, labels,
                    panel.args = trellis.panelArgs(),
                    ...)
panel.identify.cloud(x, y, z, subscripts,
                   perspective, distance,
                   xlim, ylim, zlim,
                   screen, R.mat, aspect, scales.3d,
                   ...,
                   panel.3d.identify,
                   n = length(subscripts),
                   offset = 0.5,
                   threshold = 18,
                   labels = subscripts,
                   panel.args = trellis.panelArgs())
panel.link.splom(threshold = 18, verbose = getOption("verbose"), ...)
panel.brush.splom(threshold = 18, verbose = getOption("verbose"), ...)

trellis.vpname(name = c("position", "split", "split.location", "toplevel",
                      "figure", "panel", "strip", "strip.left", "legend",
                      "main", "sub", "xlab", "ylab", "page"),
              column, row,
              side = c("left", "top", "right", "bottom", "inside"),
              clip.off = FALSE, prefix)
trellis.grobname(name, prefix)
trellis.focus(name, column, row, side, clip.off,
             highlight = interactive(), ...,
             guess = TRUE, verbose = getOption("verbose"))
trellis.switchFocus(name, side, clip.off, highlight, ...)
trellis.unfocus()
trellis.panelArgs(x, packet.number)

```

**Arguments**

*x*, *y*, *z*        variables defining the contents of the panel. In the case of `trellis.panelArgs`, a "trellis" object.

*n*                the number of points to identify by default (overridden by a right click)

*subscripts*      an optional vector of integer indices associated with each point. See details below.

*labels*          an optional vector of labels associated with each point. Defaults to `subscripts`

*distribution*, *groups*    typical panel arguments of `panel.qqmath`. These will usually be obtained from `panel.args`

<code>offset</code>	the labels are printed either below, above, to the left or to the right of the identified point, depending on the relative location of the mouse click. The <code>offset</code> specifies (in "char" units) how far from the identified point the labels should be printed.
<code>threshold</code>	threshold in grid's "points" units. Points further than these from the mouse click position are not considered
<code>panel.args</code>	list that contains components names <code>x</code> (and usually <code>y</code> ), to be used if <code>x</code> is missing. Typically, when called after <code>trellis.focus</code> , this would appropriately be the arguments passed to that panel.
<code>perspective, distance, xlim, ylim, zlim, screen, R.mat, aspect, scales.3d</code>	arguments as passed to <code>panel.cloud</code> . These are required to recompute the relevant three-dimensional projections in <code>panel.identify.cloud</code> .
<code>panel.3d.identify</code>	the function that is responsible for the actual interaction once the data rescaling and rotation computations have been done. By default, an internal function similar to <code>panel.identify</code> is used.
<code>name</code>	<p>character string indicating which viewport or grob we are looking for. Although these do not necessarily provide access to all viewports and grobs created by a lattice plot, they cover most that users might find interesting.</p> <p><code>trellis.vpname</code> and <code>trellis.focus</code> deal with viewport names only, and only accept the values explicitly listed above. <code>trellis.grobname</code> is meant to create names for grobs, and can currently accept any value.</p> <p>If <code>name</code>, as well as <code>column</code> and <code>row</code> is missing in a call to <code>trellis.focus</code>, the user can click inside a panel (or an associated strip) to focus on that panel. Note however that this assumes equal width and height for each panel, and may not work when this is not true.</p> <p>When <code>name</code> is "panel", "strip", or "strip.left", <code>column</code> and <code>row</code> must also be specified. When <code>name</code> is "legend", <code>side</code> must also be specified.</p>
<code>column, row</code>	integers, indicating position of the panel or strip that should be assigned focus in the Trellis layout. Rows are usually calculated from the bottom up, unless the plot was created with <code>as.table=TRUE</code>
<code>guess</code>	logical. If <code>TRUE</code> , and the display has only one panel, that panel will be automatically selected by a call to <code>trellis.focus</code> .
<code>side</code>	character string, relevant only for legends (i.e., when <code>name="legend"</code> ), indicating their position. Partial specification is allowed, as long as it is unambiguous.
<code>clip.off</code>	logical, whether clipping should be off, relevant when <code>name</code> is "panel" or "strip". This is necessary if axes are to be drawn outside the panel or strip. Note that setting <code>clip.off=FALSE</code> does not necessarily mean that clipping is on; that is determined by conditions in effect during printing.
<code>prefix</code>	character string acting as a prefix, meant to distinguish otherwise equivalent viewports in different plots. This only becomes relevant when a particular page is occupied by more than one plot. Defaults to the value appropriate for the last "trellis" object printed, as determined by the <code>prefix</code> argument in <code>print.trellis</code> . Users should not usually need to supply a value for this argument (see note below), however, if supplied explicitly, this has to be a valid R symbol name (briefly, it must start with a letter or a period followed by a letter) and must not contain the grid path separator (currently " : ")

<code>highlight</code>	logical, whether the viewport being assigned focus should be highlighted. For <code>trellis.focus</code> , the default is <code>TRUE</code> in interactive mode, and <code>trellis.switchFocus</code> by default preserves the setting currently active.
<code>packet.number</code>	integer, which panel to get data from. See <code>packet.number</code> for details on how this is calculated
<code>verbose</code>	whether details will be printed
<code>...</code>	For <code>panel.identify.qqmath</code> , extra parameters are passed on to <code>panel.identify</code> . For <code>panel.identify</code> , extra arguments are treated as graphical parameters and are used for labelling. For <code>trellis.focus</code> and <code>trellis.switchFocus</code> , these are used (in combination with <code>lattice.options</code> ) for highlighting the chosen viewport if so requested. Graphical parameters can be supplied for <code>panel.link.splom</code> .

## Details

`panel.identify` is similar to `identify`. When called, it waits for the user to identify points (in the panel being drawn) via mouse clicks. Clicks other than left-clicks terminate the procedure. Although it is possible to call it as part of the panel function, it is more typical to use it to identify points after plotting the whole object, in which case a call to `trellis.focus` first is necessary.

`panel.link.splom` is meant for use with `spлом`, and requires a panel to be chosen using `trellis.focus` before it is called. Clicking on a point causes that and the corresponding projections in other pairwise scatter plots to be highlighted. `panel.brush.splom` is a (misnamed) alias for `panel.link.splom`, retained for back-compatibility.

`panel.identify.qqmath` is a specialized wrapper meant for use with the display produced by `qqmath`. `panel.identify.cloud` is a specialized wrapper meant for use with the display produced by `cloud`. It would be unusual to call them except in a context where default panel function arguments are available through `trellis.panelArgs` (see below).

One way in which `panel.identify` etc. are different from `identify` is in how it uses the `subscripts` argument. In general, when one identifies points in a panel, one wants to identify the origin in the data frame used to produce the plot, and not within that particular panel. This information is available to the panel function, but only in certain situations. One way to ensure that `subscripts` is available is to specify `subscripts = TRUE` in the high level call such as `xyplot`. If `subscripts` is not explicitly specified in the call to `panel.identify`, but is available in `panel.args`, then those values will be used. Otherwise, they default to `seq_along(x)`. In either case, the final return value will be the `subscripts` that were marked.

The process of printing (plotting) a Trellis object builds up a grid layout with named viewports which can then be accessed to modify the plot further. While full flexibility can only be obtained by using grid functions directly, a few lattice functions are available for the more common tasks.

`trellis.focus` can be used to move to a particular panel or strip, identified by its position in the array of panels. It can also be used to focus on the viewport corresponding to one of the labels or a legend, though such usage would be less useful. The exact viewport is determined by the name along with the other arguments, not all of which are relevant for all names. Note that when more than one object is plotted on a page, `trellis.focus` will always go to the plot that was created last. For more flexibility, use grid functions directly (see note below).

After a successful call to `trellis.focus`, the desired viewport (typically panel or strip area) will be made the 'current' viewport (plotting area), which can then be enhanced by calls to standard lattice panel functions as well as grid functions.

It is quite common to have the layout of panels chosen when a "trellis" object is drawn, and not before then. Information on the layout (specifically, how many rows and columns, and which

packet belongs in which position in this layout) is retained for the last "trellis" object plotted, and is available through `trellis.currentLayout`.

`trellis.unfocus` unsets the focus, and makes the top level viewport the current viewport.

`trellis.switchFocus` is a convenience function to switch from one viewport to another, while preserving the current `row` and `column`. Although the rows and columns only make sense for panels and strips, they would be preserved even when the user switches to some other viewport (where row/column is irrelevant) and then switches back.

Once a panel or strip is in focus, `trellis.panelArgs` can be used to retrieve the arguments that were available to the panel function at that position. In this case, it can be called without arguments as

```
trellis.panelArgs()
```

This usage is also allowed when a "trellis" object is being printed, e.g. inside the panel functions or the axis function (but not inside the prepanel function). `trellis.panelArgs` can also retrieve the panel arguments from any "trellis" object. Note that for this usage, one needs to specify the `packet.number` (as described under the `panel` entry in [xyplot](#)) and not the position in the layout, because a layout determines the panel only **after** the object has been printed.

It is usually not necessary to call `trellis.vpname` and `trellis.grobname` directly. However, they can be useful in generating appropriate names in a portable way when using grid functions to interact with the plots directly, as described in the note below.

## Value

`panel.identify` returns an integer vector containing the subscripts of the identified points (see details above). The equivalent of `identify` with `pos=TRUE` is not yet implemented, but can be considered for addition if requested.

`trellis.panelArgs` returns a named list of arguments that were available to the panel function for the chosen panel.

`trellis.vpname` and `trellis.grobname` return character strings.

`trellis.focus` has a meaningful return value only if it has been used to focus on a panel interactively, in which case the return value is a list with components `col` and `row` giving the column and row positions respectively of the chosen panel, unless the choice was cancelled (by a right click), in which case the return value is `NULL`. If click was outside a panel, both `col` and `row` are set to 0.

## Note

The viewports created by `lattice` is accessible to the user only up to a certain extent, as described above. In particular, `trellis.focus` can only be used to manipulate the last plot drawn. For full flexibility, use appropriate functions from the `grid` package directly. For example, `current.vpTree` can be used to inspect the current viewport tree and `seekViewport` or `downViewport` can be used to navigate to these viewports. For such usage, `trellis.vpname` and `trellis.grobname` (with a non-default `prefix` argument) provides a portable way to access the appropriate viewports and grobs by name.

## Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>. Felix Andrews provided initial implementations of `panel.identify.qqmath` and support for focusing on panels interactively.

**See Also**

[identify](#), [Lattice](#), [print.trellis](#), [trellis.currentLayout](#),  
[current.vpTree](#), [viewports](#)

**Examples**

```
## Not run:
xyplot(1:10 ~ 1:10)
trellis.focus("panel", 1, 1)
panel.identify()

## End(Not run)

xyplot(Petal.Length ~ Sepal.Length | Species, iris, layout = c(2, 2))
Sys.sleep(1)

trellis.focus("panel", 1, 1)
do.call("panel.lmline", trellis.panelArgs())
Sys.sleep(0.5)
trellis.unfocus()

trellis.focus("panel", 2, 1)
do.call("panel.lmline", trellis.panelArgs())
Sys.sleep(0.5)
trellis.unfocus()

trellis.focus("panel", 1, 2)
do.call("panel.lmline", trellis.panelArgs())
Sys.sleep(0.5)
trellis.unfocus()

## choosing loess smoothing parameter

p <- xyplot(dist ~ speed, cars)

panel.loessresid <-
  function(x = panel.args$x,
          y = panel.args$y,
          span,
          panel.args = trellis.panelArgs())
  {
    fm <- loess(y ~ x, span = span)
    xgrid <- do.breaks(current.panel.limits()$xlim, 50)
    ygrid <- predict(fm, newdata = data.frame(x = xgrid))
    panel.lines(xgrid, ygrid)
    pred <- predict(fm)
    ## center residuals so that they fall inside panel
    resid <- y - pred + mean(y)
    fm.resid <- loess.smooth(x, resid, span = span)
    ##panel.points(x, resid, col = 1, pch = 4)
    panel.lines(fm.resid, col = 1)
  }

spans <- c(0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8)
```

```

update(p, index.cond = list(rep(1, length(spans))))
panel.locs <- trellis.currentLayout()

i <- 1

for (row in 1:nrow(panel.locs))
  for (column in 1:ncol(panel.locs))
    if (panel.locs[row, column] > 0)
    {
      trellis.focus("panel", row = row, column = column,
                    highlight = FALSE)
      panel.loessresid(span = spans[i])
      grid::grid.text(paste("span = ", spans[i]),
                      x = 0.25,
                      y = 0.75,
                      default.units = "npc")
      trellis.unfocus()
      i <- i + 1
    }

```

---

F\_1\_panel.barchart *Default Panel Function for barchart*

---

## Description

Default panel function for barchart.

## Usage

```

panel.barchart(x, y, box.ratio = 1, box.width,
               horizontal = TRUE,
               origin = NULL, reference = TRUE,
               stack = FALSE,
               groups = NULL,
               col = if (is.null(groups)) plot.polygon$col
                       else superpose.polygon$col,
               border = if (is.null(groups)) plot.polygon$border
                         else superpose.polygon$border,
               lty = if (is.null(groups)) plot.polygon$lty
                      else superpose.polygon$lty,
               lwd = if (is.null(groups)) plot.polygon$lwd
                       else superpose.polygon$lwd,
               ...)

```

## Arguments

x	Extent of Bars. By default, bars start at left of panel, unless origin is specified, in which case they start there
y	Horizontal location of bars, possibly factor
box.ratio	ratio of bar width to inter-bar space

<code>box.width</code>	thickness of bars in absolute units; overrides <code>box.ratio</code> . Useful for specifying thickness when the categorical variable is not a factor, as use of <code>box.ratio</code> alone cannot achieve a thickness greater than 1.
<code>horizontal</code>	logical. If <code>FALSE</code> , the plot is ‘transposed’ in the sense that the behaviours of <code>x</code> and <code>y</code> are switched. <code>x</code> is now the ‘factor’. Interpretation of other arguments change accordingly. See documentation of <code>bwplot</code> for a fuller explanation.
<code>origin</code>	the origin for the bars. For grouped displays with <code>stack = TRUE</code> , this argument is ignored and the origin set to 0. Otherwise, defaults to <code>NULL</code> , in which case bars start at the left (or bottom) end of a panel. This choice is somewhat unfortunate, as it can be misleading, but is the default for historical reasons. For tabular (or similar) data, <code>origin = 0</code> is usually more appropriate; if not, one should reconsider the use of a bar chart in the first place (dot plots are often a good alternative).
<code>reference</code>	logical, whether a reference line is to be drawn at the origin
<code>stack</code>	logical, relevant when <code>groups</code> is non-null. If <code>FALSE</code> (the default), bars for different values of the grouping variable are drawn side by side, otherwise they are stacked.
<code>groups</code>	optional grouping variable
<code>col, border, lty, lwd</code>	Graphical parameters for the bars. By default, the trellis parameter <code>plot.polygon</code> is used if there is no grouping variable, otherwise <code>superpose.polygon</code> is used. <code>col</code> gives the fill color, <code>border</code> the border color, and <code>lty</code> and <code>lwd</code> the line type and width of the borders.
<code>...</code>	extra arguments will be accepted but ignored

### Details

A barchart is drawn in the panel. Note that most arguments controlling the display can be supplied to the high-level `barchart` call directly.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### See Also

[barchart](#)

---

F\_1\_panel.bwplot     *Default Panel Function for bwplot*

---

### Description

This is the default panel function for `bwplot`.

**Usage**

```
panel.bwplot(x, y, box.ratio = 1,
             box.width = box.ratio / (1 + box.ratio),
             horizontal = TRUE,
             pch, col, alpha, cex,
             font, fontfamily, fontface,
             fill, varwidth = FALSE,
             notch = FALSE, notch.frac = 0.5,
             ...,
             levels.fos,
             stats = boxplot.stats,
             coef = 1.5,
             do.out = TRUE)
```

**Arguments**

<code>x, y</code>	numeric vector or factor. Boxplots drawn for each unique value of <code>y</code> ( <code>x</code> ) if <code>horizontal</code> is <code>TRUE</code> ( <code>FALSE</code> )
<code>box.ratio</code>	ratio of box thickness to inter box space
<code>box.width</code>	thickness of box in absolute units; overrides <code>box.ratio</code> . Useful for specifying thickness when the categorical variable is not a factor, as use of <code>box.ratio</code> alone cannot achieve a thickness greater than 1.
<code>horizontal</code>	logical. If <code>FALSE</code> , the plot is ‘transposed’ in the sense that the behaviours of <code>x</code> and <code>y</code> are switched. <code>x</code> is now the ‘factor’. Interpretation of other arguments change accordingly. See documentation of <a href="#">bwplot</a> for a fuller explanation.
<code>pch, col, alpha, cex, font, fontfamily, fontface</code>	graphical parameters controlling the dot. <code>pch=" "</code> is treated specially, by replacing the dot with a line (similar to <a href="#">boxplot</a> )
<code>fill</code>	color to fill the boxplot
<code>varwidth</code>	logical. If <code>TRUE</code> , widths of boxplots are proportional to the number of points used in creating it.
<code>notch</code>	if <code>notch</code> is <code>TRUE</code> , a notch is drawn in each side of the boxes. If the notches of two plots do not overlap this is ‘strong evidence’ that the two medians differ (Chambers et al., 1983, p. 62). See <a href="#">boxplot.stats</a> for the calculations used.
<code>notch.frac</code>	numeric in (0,1). When <code>notch=TRUE</code> , the fraction of the box width that the notches should use.
<code>stats</code>	a function, defaulting to <a href="#">boxplot.stats</a> , that accepts a numeric vector and returns a list similar to the return value of <a href="#">boxplot.stats</a> . The function must accept arguments <code>coef</code> and <code>do.out</code> even if they do not use them (a <code>...</code> argument is good enough). This function is used to determine the box and whisker plot.
<code>coef, do.out</code>	passed to <code>stats</code>
<code>levels.fos</code>	numeric values corresponding to positions of the factor or shingle variable. For internal use.
<code>...</code>	further arguments, ignored.



**Details**

Creates Box and Whisker plot of  $x$  for every level of  $y$  (or the other way round if `horizontal=FALSE`). By default, the actual boxplot statistics are calculated using `boxplot.stats`. Note that most arguments controlling the display can be supplied to the high-level `bwplot` call directly.

Although the graphical parameters for the dot representing the median can be controlled by optional arguments, many others can not. These parameters are obtained from the relevant settings parameters ("`box.rectangle`" for the box, "`box.umbrella`" for the whiskers and "`plot.symbol`" for the outliers).

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[bwplot](#), [boxplot.stats](#)

**Examples**

```
bwplot(voice.part ~ height, data = singer,
       xlab = "Height (inches)",
       panel = function(...) {
         panel.grid(v = -1, h = 0)
         panel.bwplot(...)
       },
       par.settings = list(plot.symbol = list(pch = 4)))

bwplot(voice.part ~ height, data = singer,
       xlab = "Height (inches)",
       notch = TRUE, pch = "|")
```

---

F\_1\_panel.cloud

*Default Panel Function for cloud*

---

**Description**

These are default panel functions controlling `cloud` and `wireframe` displays.

**Usage**

```
panel.cloud(x, y, subscripts, z,
            groups = NULL,
            perspective = TRUE,
            distance = if (perspective) 0.2 else 0,
            xlim, ylim, zlim,
            panel.3d.cloud = "panel.3dscatter",
            panel.3d.wireframe = "panel.3dwire",
            screen = list(z = 40, x = -60),
            R.mat = diag(4), aspect = c(1, 1),
```

```

par.box = NULL,
xlab, ylab, zlab,
xlab.default, ylab.default, zlab.default,
scales.3d,
proportion = 0.6,
wireframe = FALSE,
scpos,
...,
at)
panel.wireframe(...)
panel.3dscatter(x, y, z, rot.mat, distance,
               groups, type = "p",
               xlim.scaled, ylim.scaled, zlim.scaled,
               zero.scaled,
               col, col.point, col.line,
               lty, lwd, cex, pch,
               cross, ..., subscripts)
panel.3dwire(x, y, z, rot.mat = diag(4), distance,
             shade = FALSE,
             shade.colors.palette = trellis.par.get("shade.colors")$palette,
             light.source = c(0, 0, 1000),
             xlim.scaled,
             ylim.scaled,
             zlim.scaled,
             col = if (shade) "transparent" else "black",
             lty = 1, lwd = 1,
             alpha,
             col.groups = superpose.polygon$col,
             polynum = 100,
             ...,
             drape = FALSE,
             at,
             col.regions = regions$col,
             alpha.regions = regions$alpha)

```

### Arguments

`x`, `y`, `z` numeric (or possibly factors) vectors representing the data to be displayed. The interpretation depends on the context. For `panel.cloud` these are essentially the same as the data passed to the high level plot (except if `formula` was a matrix, the appropriate `x` and `y` vectors are generated). By the time they are passed to `panel.3dscatter` and `panel.3dwire`, they have been appropriately subsetted (using `subscripts`) and scaled (to lie inside a bounding box, usually the [-0.5, 0.5] cube).  
Further, for `panel.3dwire`, `x` and `y` are shorter than `z` and represent the sorted locations defining a rectangular grid. Also in this case, `z` may be a matrix if the display is grouped, with each column representing one surface.  
In `panel.cloud` (called from `wireframe`) and `panel.3dwire`, `x`, `y` and `z` could also be matrices (of the same dimension) when they represent a 3-D surface parametrized on a 2-D grid.

`subscripts` index specifying which points to draw. The same `x`, `y` and `z` values (representing the whole data) are passed to `panel.cloud` for each panel. `subscripts`

	specifies the subset of rows to be used for the particular panel.
groups	specification of a grouping variable, passed down from the high level functions.
perspective	logical, whether to plot a perspective view. Setting this to FALSE is equivalent to setting distance to 0
distance	numeric, between 0 and 1, controls amount of perspective. The distance of the viewing point from the origin (in the transformed coordinate system) is $1 / \text{distance}$ . This is described in a little more detail in the documentation for <code>cloud</code>
screen	A list determining the sequence of rotations to be applied to the data before being plotted. The initial position starts with the viewing point along the positive z-axis, and the x and y axes in the usual position. Each component of the list should be named one of "x", "y" or "z" (repetitions are allowed), with their values indicating the amount of rotation about that axis in degrees.
R.mat	initial rotation matrix in homogeneous coordinates, to be applied to the data before <code>screen</code> rotates the view further.
par.box	graphical parameters for box, namely, col, lty and lwd. By default obtained from the parameter <code>box.3d</code>
xlim, ylim, zlim	limits for the respective axes. As with other lattice functions, these could each be a numeric 2-vector or a character vector indicating levels of a factor.
panel.3d.cloud, panel.3d.wireframe	functions that draw the data-driven part of the plot (as opposed to the bounding box and scales) in <code>cloud</code> and <code>wireframe</code> . This function is called after the 'back' of the bounding box is drawn, but before the 'front' is drawn. Any user-defined custom display would probably want to change these functions. The intention is to pass as much information to this function as might be useful (not all of which are used by the defaults). In particular, these functions can expect arguments called <code>xlim</code> , <code>ylim</code> , <code>zlim</code> which give the bounding box ranges in the original data scale and <code>xlim.scaled</code> , <code>ylim.scaled</code> , <code>zlim.scaled</code> which give the bounding box ranges in the transformed scale. More arguments can be considered on request.
aspect	aspect as in <code>cloud</code>
xlab, ylab, zlab	Labels, have to be lists. Typically the user will not manipulate these, but instead control this via arguments to <code>cloud</code> directly.
xlab.default	for internal use
ylab.default	for internal use
zlab.default	for internal use
scales.3d	list defining the scales
proportion	numeric scalar, gives the length of arrows as a proportion of the sides
scpos	A list with three components x, y and z (each a scalar integer), describing which of the 12 sides of the cube the scales should be drawn. The defaults should be OK. Valid values are x: 1, 3, 9, 11; y: 8, 5, 7, 6 and z: 4, 2, 10, 12. (See comments in the source code of <code>panel.cloud</code> to see the details of this enumeration.)
wireframe	logical, indicating whether this is a wireframe plot
drape	logical, whether the facets will be colored by height, in a manner similar to <code>levelplot</code> . This is ignored if <code>shade=TRUE</code> .

`at`, `col.regions`, `alpha.regions`  
 deals with specification of colors when `drape = TRUE` in `wireframe`.  
`at` can be a numeric vector, `col.regions` a vector of colors, and  
`alpha.regions` a numeric scalar controlling transparency. The resulting be-  
 haviour is similar to `levelplot`, `at` giving the breakpoints along the z-axis  
 where colors change, and the other two determining the colors of the facets that  
 fall in between.

`rot.mat` 4x4 transformation matrix in homogeneous coordinates. This gives the rotation  
 matrix combining the `screen` and `R.mat` arguments to `panel.cloud`

`type` character vector, specifying type of cloud plot. Can include one or more of  
 "p", "l", "h" or "b". "p" and "l" mean 'points' and 'lines' respectively,  
 and "b" means 'both'. "h" stands for 'histogram', and causes a line to be  
 drawn from each point to the X-Y plane (i.e., the plane representing  $z = 0$ ), or  
 the lower (or upper) bounding box face, whichever is closer.

`xlim.scaled`, `ylim.scaled`, `zlim.scaled`  
 axis limits (after being scaled to the bounding box)

`zero.scaled` z-axis location (after being scaled to the bounding box) of the X-Y plane in the  
 original data scale, to which lines will be dropped (if within range) from each  
 point when `type = "h"`

`cross` logical, defaults to `TRUE` if `pch = "+"`. `panel.3dscatter` can represent  
 each point by a 3d 'cross' of sorts (it's much easier to understand looking at an  
 example than from a description). This is different from the usual `pch` argu-  
 ment, and reflects the depth of the points and the orientation of the axes. This  
 argument indicates whether this feature will be used.  
 This is useful for two reasons. It can be set to `FALSE` to use "+" as the plotting  
 character in the regular sense. It can also be used to force this feature in grouped  
 displays.

`shade` logical, indicating whether the surface is to be colored using an illumination  
 model with a single light source

`shade.colors.palette`  
 a function (or the name of one) that is supposed to calculate the color of a facet  
 when shading is being used. Three pieces of information are available to the  
 function: first, the cosine of the angle between the incident light ray and the  
 normal to the surface (representing foreshortening); second, the cosine of half  
 the angle between the reflected ray and the viewing direction (useful for non-  
 Lambertian surfaces); and third, the scaled (average) height of that particular  
 facet with respect to the total plot z-axis limits.  
 All three numbers should be between 0 and 1. The  
`shade.colors.palette` function should return a valid color. The  
 default function is obtained from the trellis settings.

`light.source` a 3-vector representing (in cartesian coordinates) the light source. This is rel-  
 ative to the viewing point being (0, 0, 1/distance) (along the positive z-axis),  
 keeping in mind that all observations are bounded within the [-0.5, 0.5] cube

`polynum` quadrilateral faces are drawn in batches of `polynum` at a time. Drawing too few  
 at a time increases the total number of calls to the underlying `grid.polygon`  
 function, which affects speed. Trying to draw too many at once may be unne-  
 cessarily memory intensive. This argument controls the trade-off.

`col.groups` colors for different groups  
`col`, `col.point`, `col.line`, `lty`, `lwd`, `cex`, `pch`, `alpha`  
 graphical parameters  
`...` other parameters, passed down when appropriate

## Details

These functions together are responsible for the content drawn inside each panel in `cloud` and `wireframe`. `panel.wireframe` is a wrapper to `panel.cloud`, which does the actual work.

`panel.cloud` is responsible for drawing the content that does not depend on the data, namely, the bounding box, the arrows/scales, etc. At some point, depending on whether `wireframe` is `TRUE`, it calls either `panel.3d.wireframe` or `panel.3d.cloud`, which draws the data-driven part of the plot.

The arguments accepted by these two functions are different, since they have essentially different purposes. For `cloud`, the data is unstructured, and `x`, `y` and `z` are all passed to the `panel.3d.cloud` function. For `wireframe`, on the other hand, `x` and `y` are increasing vectors with unique values, defining a rectangular grid. `z` must be a matrix with `length(x) * length(y)` rows, and as many columns as the number of groups.

`panel.3dscatter` is the default `panel.3d.cloud` function. It has a `type` argument similar to `panel.xyplot`, and supports grouped displays. It tries to honour depth ordering, i.e., points and lines closer to the camera are drawn later, overplotting more distant ones. (Of course there is no absolute ordering for line segments, so an ad hoc ordering is used. There is no hidden point removal.)

`panel.3dwire` is the default `panel.3d.wireframe` function. It calculates polygons corresponding to the facets one by one, but waits till it has collected information about `plymum` facets, and draws them all at once. This avoids the overhead of drawing `grid.polygon` repeatedly, speeding up the rendering considerably. If `shade = TRUE`, these attempt to color the surface as being illuminated from a light source at `light.source`. `palette.shade` is a simple function that provides the default shading colors

Multiple surfaces are drawn if `groups` is non-null in the call to `wireframe`, however, the algorithm is not sophisticated enough to render intersecting surfaces correctly.

## Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

## See Also

[cloud](#), [utilities.3d](#)

---

F\_1\_panel.densityplot

*Default Panel Function for densityplot*

---

## Description

This is the default panel function for `densityplot`.

## Usage

```
panel.densityplot(x, darg, plot.points = "jitter", ref = FALSE,
                 groups = NULL, weights = NULL,
                 jitter.amount, type, ...)
```

**Arguments**

<code>x</code>	data points for which density is to be estimated
<code>darg</code>	list of arguments to be passed to the <code>density</code> function. Typically, this should be a list with zero or more of the following components : <code>bw</code> , <code>adjust</code> , <code>kernel</code> , <code>window</code> , <code>width</code> , <code>give.Rkern</code> , <code>n</code> , <code>from</code> , <code>to</code> , <code>cut</code> , <code>na.rm</code> (see <a href="#">density</a> for details)
<code>plot.points</code>	logical specifying whether or not the data points should be plotted along with the estimated density. Alternatively, a character string specifying how the points should be plotted. Meaningful values are <code>"rug"</code> , in which case <a href="#">panel.rug</a> is used to plot a 'rug', and <code>"jitter"</code> , in which case the points are jittered vertically to better distinguish overlapping points.
<code>ref</code>	logical, whether to draw x-axis
<code>groups</code>	an optional grouping variable. If present, <a href="#">panel.superpose</a> will be used instead to display each subgroup
<code>weights</code>	numeric vector of weights for the density calculations. If this is specified, the <code>...</code> part must also include a <code>subscripts</code> argument that matches the weights to <code>x</code> .
<code>jitter.amount</code>	when <code>plot.points="jitter"</code> , the value to use as the <code>amount</code> argument to <a href="#">jitter</a> .
<code>type</code>	<code>type</code> argument used to plot points, if requested. This is not expected to be useful, it is available mostly to protect a <code>type</code> argument, if specified, from affecting the density curve.
<code>...</code>	extra graphical parameters. Note that additional arguments to <a href="#">panel.rug</a> cannot be passed on through <code>panel.densityplot</code> .

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[densityplot](#), [jitter](#)

---

F\_1\_panel.dotplot *Default Panel Function for dotplot*

---

**Description**

Default panel function for `dotplot`.

**Usage**

```
panel.dotplot(x, y, horizontal = TRUE,
              pch, col, lty, lwd,
              col.line, levels.fos,
              groups = NULL,
              ...)
```

**Arguments**

<code>x, y</code>	variables to be plotted in the panel. Typically <code>y</code> is the ‘factor’
<code>horizontal</code>	logical. If <code>FALSE</code> , the plot is ‘transposed’ in the sense that the behaviours of <code>x</code> and <code>y</code> are switched. <code>x</code> is now the ‘factor’. Interpretation of other arguments change accordingly. See documentation of <code>bwplot</code> for a fuller explanation.
<code>pch, col, lty, lwd, col.line</code>	graphical parameters
<code>levels.fos</code>	locations where reference lines will be drawn
<code>groups</code>	grouping variable (affects graphical parameters)
<code>...</code>	extra parameters, passed to <code>panel.xyplot</code> which is responsible for drawing the foreground points ( <code>panel.dotplot</code> only draws the background reference lines).

**Details**

Creates (possibly grouped) Dotplot of `x` against `y` or vice versa

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[dotplot](#)

---

F\_1\_panel.histogram

*Default Panel Function for histogram*

---

**Description**

This is the default panel function for histogram.

**Usage**

```
panel.histogram(x,  
                breaks,  
                equal.widths = TRUE,  
                type = "density",  
                nint = round(log2(length(x)) + 1),  
                alpha, col, border, lty, lwd,  
                ...)
```

**Arguments**

<code>x</code>	The data points for which the histogram is to be drawn
<code>breaks</code>	The breakpoints for the histogram
<code>equal.widths</code>	logical used when <code>breaks==NULL</code>
<code>type</code>	Type of histogram, possible values being "percent", "density" and "count"
<code>nint</code>	Number of bins for the histogram
<code>alpha, col, border, lty, lwd</code>	graphical parameters for bars; defaults are obtained from the <code>plot.polygon</code> settings.
<code>...</code>	other arguments, passed to <code>hist</code> when deemed appropriate

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[histogram](#)

---

F\_1\_panel.levelplot

*Panel Functions for levelplot and contourplot*

---

**Description**

These are the default panel functions for `levelplot` and `contourplot`. Also documented is an alternative raster-based panel function for use with `levelplot`.

**Usage**

```
panel.levelplot(x, y, z,
               subscripts,
               at = pretty(z),
               shrink,
               labels,
               label.style = c("mixed", "flat", "align"),
               contour = FALSE,
               region = TRUE,
               col = add.line$col,
               lty = add.line$lty,
               lwd = add.line$lwd,
               border = "transparent",
               ...,
               col.regions = regions$col,
               alpha.regions = regions$alpha)
panel.contourplot(...)

panel.levelplot.raster(x, y, z,
```



```

subscripts,
at = pretty(z),
...,
col.regions = regions$col,
alpha.regions = regions$alpha,
interpolate = FALSE)

```

## Arguments

<code>x, y, z</code>	Variables defining the plot.
<code>subscripts</code>	Integer vector indicating what subset of <code>x</code> , <code>y</code> and <code>z</code> to draw.
<code>at</code>	Numeric vector giving breakpoints along the range of <code>z</code> . See <a href="#">levelplot</a> for details.
<code>shrink</code>	Either a numeric vector of length 2 (meant to work as both <code>x</code> and <code>y</code> components), or a list with components <code>x</code> and <code>y</code> which are numeric vectors of length 2. This allows the rectangles to be scaled proportional to the <code>z</code> -value. The specification can be made separately for widths ( <code>x</code> ) and heights ( <code>y</code> ). The elements of the length 2 numeric vector gives the minimum and maximum proportion of shrinkage (corresponding to min and max of <code>z</code> ).
<code>labels</code>	Either a logical scalar indicating whether the labels are to be drawn, or a character or expression vector giving the labels associated with the <code>at</code> values. Alternatively, <code>labels</code> can be a list with the following components: <code>labels</code> : a character or expression vector giving the labels. This can be omitted, in which case the defaults will be used. <code>col, cex, alpha</code> : graphical parameters for label texts <code>fontfamily, fontface, font</code> : font used for the labels
<code>label.style</code>	Controls how label positions and rotation are determined. A value of "flat" causes the label to be positioned where the contour is flattest, and the label is not rotated. A value of "align" causes the label to be drawn as far from the boundaries as possible, and the label is rotated to align with the contour at that point. The default is to mix these approaches, preferring the flattest location unless it is too close to the boundaries.
<code>contour</code>	A logical flag, specifying whether contour lines should be drawn.
<code>region</code>	A logical flag, specifying whether inter-contour regions should be filled with appropriately colored rectangles.
<code>col, lty, lwd</code>	graphical parameters for contour lines
<code>border</code>	border color for rectangles used when <code>region=TRUE</code> .
<code>...</code>	Extra parameters.
<code>col.regions</code>	A vector of colors, or a function to produce a vector of colors, to be used if <code>region=TRUE</code> . Each interval defined by <code>at</code> is assigned a color, so the number of colors actually used is one less than the length of <code>at</code> . See <a href="#">level.colors</a> for details on how the color assignment is done.
<code>alpha.regions</code>	numeric scalar controlling transparency of facets
<code>interpolate</code>	logical, passed to <a href="#">grid.raster</a> .

**Details**

The same panel function is used for both `levelplot` and `contourplot` (which differ only in default values of some arguments). `panel.contourplot` is a simple wrapper to `panel.levelplot`.

When `contour=TRUE`, the `contourLines` function is used to calculate the contour lines.

`panel.levelplot.raster` is an alternative panel function that uses the raster drawing abilities in R 2.11.0 and higher (through `grid.raster`). It has fewer options (e.g., can only render data on an equispaced grid), but can be more efficient.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[levelplot](#), [level.colors](#), [contourLines](#)

**Examples**

```
require(grid)

levelplot(rnorm(10) ~ 1:10 + sort(runif(10)), panel = panel.levelplot)

suppressWarnings(plot(levelplot(rnorm(10) ~ 1:10 + sort(runif(10))),
                           panel = panel.levelplot.raster,
                           interpolate = TRUE))

levelplot(volcano, panel = panel.levelplot.raster)

levelplot(volcano, panel = panel.levelplot.raster,
           col.regions = topo.colors, cuts = 30, interpolate = TRUE)
```

---

F\_1\_panel.pairs      *Default Superpanel Function for splom*

---

**Description**

This is the default superpanel function for `splom`.

**Usage**

```
panel.pairs(z,
            panel = lattice.getOption("panel.splom"),
            lower.panel = panel,
            upper.panel = panel,
            diag.panel = "diag.panel.splom",
            as.matrix = FALSE,
            groups = NULL,
            panel.subscripts,
            subscripts,
```

```

pscales = 5,

prepanel.limits = function(x) if (is.factor(x)) levels(x) else
  extend.limits(range(as.numeric(x), finite = TRUE)),

varname.col, varname.cex, varname.font,
varname.fontfamily, varname.fontface,
axis.text.col, axis.text.cex, axis.text.font,
axis.text.fontfamily, axis.text.fontface,
axis.line.col, axis.line.lty, axis.line.lwd,
axis.line.alpha, axis.line.tck,
...)
diag.panel.splom(x = NULL,
  varname = NULL, limits, at = NULL, lab = NULL,
  draw = TRUE,
  varname.col, varname.cex,
  varname.lineheight, varname.font,
  varname.fontfamily, varname.fontface,
  axis.text.col, axis.text.alpha,
  axis.text.cex, axis.text.font,
  axis.text.fontfamily, axis.text.fontface,
  axis.line.col, axis.line.alpha,
  axis.line.lty, axis.line.lwd,
  axis.line.tck,
  ...)

```

## Arguments

<code>z</code>	The data frame used for the plot.
<code>panel</code> , <code>lower.panel</code> , <code>upper.panel</code>	The panel function used to display each pair of variables. If specified, <code>lower.panel</code> and <code>upper.panel</code> are used for panels below and above the diagonal respectively.
<code>diag.panel</code>	The panel function used for the diagonals. See arguments to <code>diag.panel.splom</code> to know what arguments this function is passed when called.
<code>as.matrix</code>	logical. If TRUE, the layout of the panels will have origin on the top left instead of bottom left (similar to <code>pairs</code> ). This is in essence the same functionality as provided by <code>as.table</code> for the panel layout
<code>groups</code>	Grouping variable, if any
<code>panel.subscripts</code>	logical specifying whether the panel function accepts an argument named <code>subscripts</code> .
<code>subscripts</code>	The indices of the rows of <code>z</code> that are to be displayed in this (super)panel.
<code>pscales</code>	Controls axis labels, passed down from <code>splom</code> . If <code>pscales</code> is a single number, it indicates the approximate number of equally-spaced ticks that should appear on each axis. If <code>pscales</code> is a list, it should have one component for each column in <code>z</code> , each of which itself a list with the following valid components: <code>at</code> : a numeric vector specifying tick locations <code>labels</code> : character vector labels to go with <code>at</code>

`limits`: numeric 2-vector specifying axis limits (should be made more flexible at some point to handle factors)

These are specifications on a per-variable basis, and used on all four sides in the diagonal cells used for labelling. Factor variables are labelled with the factor names. Use `pscales=0` to suppress the axes entirely.

`prepanel.limits`

The 'regular' high level lattice plots such as `xyplot` use the `prepanel` function for deciding on axis limits from data. This function serves a similar function, and works on a per-variable basis, by calculating the limits, which can be overridden by the corresponding `limits` component in the `pscales` list.

`x` data vector corresponding to that row / column (which will be the same for diagonal 'panels').

`varname` (scalar) character string or expression that is to be written centred within the panel

`limits` numeric of length 2, or, vector of characters, specifying the scale for that panel (used to calculate tick locations when missing)

`at` locations of tick marks

`lab` optional labels for tick marks

`draw` logical, specifying whether to draw the tick marks and labels. If FALSE, only variable names are written

`varname.col`, `varname.cex`, `varname.lineheight`, `varname.font`, `varname.fontfamily`, graphical parameters for the variable name in each diagonal panel

`axis.text.col`, `axis.text.cex`, `axis.text.font`, `axis.text.fontfamily`, `axis.text.f` graphical parameters for axis tick marks and labels

`axis.line.tck`

length of tick marks in diagonal panels

... extra arguments passed on to `panel`, `lower.panel`, `upper.panel` and `diag.panel` from `panel.pairs`. Currently ignored by `diag.panel.splom`.

## Details

`panel.pairs` is the function that is actually passed in as the `panel` function in a trellis object produced by `splom` (taking the `panel` function as its argument).

Note that the axis labeling does not support date-time classes at present.

## Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

## See Also

[splom](#)

---

F\_1\_panel.parallel *Default Panel Function for parallel*

---

### Description

This is the default panel function for `parallel`.

### Usage

```
panel.parallel(x, y, z, subscripts,
              groups = NULL,
              col, lwd, lty, alpha,
              common.scale = FALSE,
              lower,
              upper,
              ...,
              horizontal.axis = TRUE)
```

### Arguments

<code>x, y</code>	dummy variables, ignored.
<code>z</code>	The data frame used for the plot. Each column will be coerced to numeric before being plotted, and an error will be issued if this fails.
<code>subscripts</code>	The indices of the rows of <code>z</code> that are to be displayed in this panel.
<code>groups</code>	An optional grouping variable. If specified, different groups are distinguished by use of different graphical parameters (i.e., rows of <code>z</code> in the same group share parameters).
<code>col, lwd, lty, alpha</code>	graphical parameters (defaults to the settings for <code>superpose.line</code> ). If <code>groups</code> is non-null, these parameters used one for each group. Otherwise, they are recycled and used to distinguish between rows of the data frame <code>z</code> .
<code>common.scale</code>	logical, whether a common scale should be used columns of <code>z</code> . Defaults to <code>FALSE</code> , in which case the horizontal range for each column is different (as determined by <code>lower</code> and <code>upper</code> ).
<code>lower, upper</code>	numeric vectors replicated to be as long as the number of columns in <code>z</code> . Determines the lower and upper bounds to be used for scaling the corresponding columns of <code>z</code> after coercing them to numeric. Defaults to the minimum and maximum of each column. Alternatively, these could be functions (to be applied on each column) that return a scalar.
<code>...</code>	other arguments (ignored)
<code>horizontal.axis</code>	logical indicating whether the parallel axes should be laid out horizontally ( <code>TRUE</code> ) or vertically ( <code>FALSE</code> ).

### Details

Produces parallel coordinate plots, which are easier to understand from an example than through a verbal description. See example for [parallel](#)

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**References**

Inselberg, Alfred (2009) “Parallel Coordinates: Visual Multidimensional Geometry and Its Applications”, Springer. ISBN: 978-0-387-21507-5.

Inselberg, A. (1985) “The Plane with Parallel Coordinates”, *The Visual Computer*.

**See Also**

[parallel](#)

---

F\_1\_panel.qqmath    *Default Panel and Prepanel Function for qqmath*

---

**Description**

This is the default panel function for qqmath.

**Usage**

```
panel.qqmath(x, f.value = NULL,
             distribution = qnorm,
             qtype = 7,
             groups = NULL, ...,
             tails.n = 0)
```

**Arguments**

x	vector (typically numeric, coerced if not) of data values to be used in the panel.
f.value, distribution	Defines how quantiles are calculated. See <a href="#">qqmath</a> for details.
qtype	The type argument to be used in <a href="#">quantile</a>
groups	An optional grouping variable. Within each panel, one Q-Q plot is produced for every level of this grouping variable, differentiated by different graphical parameters.
...	further arguments, often graphical parameters.
tails.n	number of data points to represent exactly on each tail of the distribution. This reproduces the effect of f.value = NULL for the extreme data values, while approximating the remaining data. It has no effect if f.value = NULL. If tails.n is given, qtype is forced to be 1.

**Details**

Creates a Q-Q plot of the data and the theoretical distribution given by distribution. Note that most of the arguments controlling the display can be supplied directly to the high-level qqmath call.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[qqmath](#)

**Examples**

```
set.seed(0)
xx <- rt(10000, df = 10)
qqmath(~ xx, type = c("b", "g"), pch = "+", distribution = qnorm,
  main = c("raw", "ppoints(100)", "tails.n = 50"),
  panel = function(..., f.value) {
    switch(panel.number(),
      panel.qqmath(..., f.value = NULL),
      panel.qqmath(..., f.value = ppoints(100)),
      panel.qqmath(..., f.value = ppoints(100), tails.n = 50)
    ), layout = c(3, 1))[c(1,1,1)]
```

---

F\_1\_panel.stripplot

*Default Panel Function for stripplot*

---

**Description**

This is the default panel function for `stripplot`. Also see `panel.superpose`

**Usage**

```
panel.stripplot(x, y, jitter.data = FALSE,
  factor = 0.5, amount = NULL,
  horizontal = TRUE, groups = NULL,
  ...)
```

**Arguments**

<code>x, y</code>	coordinates of points to be plotted
<code>jitter.data</code>	whether points should be jittered to avoid overplotting. The actual jittering is performed inside <a href="#">panel.xyplot</a> , using its <code>jitter.x</code> or <code>jitter.y</code> argument (depending on the value of <code>horizontal</code> ).
<code>factor, amount</code>	amount of jittering, see <a href="#">jitter</a>
<code>horizontal</code>	logical. If <code>FALSE</code> , the plot is ‘transposed’ in the sense that the behaviours of <code>x</code> and <code>y</code> are switched. <code>x</code> is now the ‘factor’. Interpretation of other arguments change accordingly. See documentation of <a href="#">bwplot</a> for a fuller explanation.
<code>groups</code>	optional grouping variable
<code>...</code>	additional arguments, passed on to <a href="#">panel.xyplot</a>

**Details**

Creates stripplot (one dimensional scatterplot) of  $x$  for each level of  $y$  (or vice versa, depending on the value of `horizontal`)

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[stripplot](#), [jitter](#)

---

F\_1\_panel.xyplot     *Default Panel Function for xyplot*

---

**Description**

This is the default panel function for `xyplot`. Also see `panel.superpose`. The default panel functions for `splom` and `qq` are essentially the same function.

**Usage**

```
panel.xyplot(x, y, type = "p",
             groups = NULL,
             pch, col, col.line, col.symbol,
             font, fontfamily, fontface,
             lty, cex, fill, lwd,
             horizontal = FALSE, ...,
             jitter.x = FALSE, jitter.y = FALSE,
             factor = 0.5, amount = NULL)
panel.splom(...)
panel.qq(...)
```

**Arguments**

<code>x, y</code>	variables to be plotted in the scatterplot
<code>type</code>	character vector consisting of one or more of the following: "p", "l", "h", "b", "o", "s", "S", "r", "a", "g", "smooth". If <code>type</code> has more than one element, an attempt is made to combine the effect of each of the components. The behaviour if any of the first six are included in <code>type</code> is similar to the effect of <code>type</code> in <code>plot</code> (type "b" is actually the same as "o"). "r" adds a regression line (same as <code>panel.lmline</code> , except for default graphical parameters), and "smooth" adds a lowess fit (same as <code>panel.loess</code> ). "g" adds a reference grid using <code>panel.grid</code> in the background. "a" has the effect of calling <code>panel.linejoin</code> , which can be useful for creating interaction plots. The effect of several of these specifications depend on the value of <code>horizontal</code> . Type "s" (and "S") sorts the values along one of the axes (depending on <code>horizontal</code> ); this is unlike the behavior in <code>plot</code> . For the latter behavior, use <code>type = "s"</code> with <code>panel = panel.points</code> . See <code>example(xyplot)</code> and <code>demo(lattice)</code> for examples.



groups an optional grouping variable. If present, `panel.superpose` will be used instead to display each subgroup

col, col.line, col.symbol default colours are obtained from `plot.symbol` and `plot.line` using `trellis.par.get`.

font, fontface, fontfamily font used when pch is a character

pch, lty, cex, lwd, fill other graphical parameters. `fill` serves the purpose of `bg` in `points` for certain values of pch

... extra arguments, if any, for `panel.xyplot`. In most cases `panel.xyplot` ignores these. For types "r" and "smooth", these are passed on to `panel.lmline` and `panel.loess` respectively.

horizontal logical. Controls orientation for certain type's, e.g. one of "h", "s" or "S".

jitter.x, jitter.y logical, whether the data should be jittered before being plotted.

factor, amount controls amount of jittering.

### Details

Creates scatterplot of  $x$  and  $y$ , with various modifications possible via the `type` argument. `panel.qq` draws a 45 degree line before calling `panel.xyplot`.

Note that most of the arguments controlling the display can be supplied directly to the high-level (e.g. `xyplot`) call.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### See Also

`panel.superpose`, `xyplot`, `splom`

### Examples

```
types.plain <- c("p", "l", "o", "r", "g", "s", "S", "h", "a", "smooth")
types.horiz <- c("s", "S", "h", "a", "smooth")
horiz <- rep(c(FALSE, TRUE), c(length(types.plain), length(types.horiz)))

types <- c(types.plain, types.horiz)

x <- sample(seq(-10, 10, length.out = 15), 30, TRUE)
y <- x + 0.25 * (x + 1)^2 + rnorm(length(x), sd = 5)

xyplot(y ~ x | gl(1, length(types)),
       xlab = "type",
       ylab = list(c("horizontal=TRUE", "horizontal=FALSE"), y = c(1/6, 4/6)),
       as.table = TRUE, layout = c(5, 3),
       between = list(y = c(0, 1)),
       strip = function(...) {
         panel.fill(trellis.par.get("strip.background")$col[1])
       })
```

```

    type <- types[panel.number()]
    grid::grid.text(label = sprintf("%s", type),
                   x = 0.5, y = 0.5)
    grid::grid.rect()
  },
  scales = list(alternating = c(0, 2), tck = c(0, 0.7), draw = FALSE),
  par.settings =
  list(layout.widths = list(strip.left = c(1, 0, 0, 0, 0))),
  panel = function(...) {
    type <- types[panel.number()]
    horizontal <- horiz[panel.number()]
    panel.xyplot(...,
                 type = type,
                 horizontal = horizontal)
  })[rep(1, length(types))]

```

---

F\_2\_llines

*Replacements of traditional graphics functions*


---

### Description

These functions are intended to replace common low level traditional graphics functions, primarily for use in panel functions. The originals can not be used (at least not easily) because lattice panel functions need to use grid graphics. Low level drawing functions in grid can be used directly as well, and is often more flexible. These functions are provided for convenience and portability.

### Usage

```

lplot.xy(xy, type, pch, lty, col, cex, lwd,
         font, fontfamily, fontface,
         col.line, col.symbol, alpha, fill,
         origin = 0, ...)

llines(x, ...)
lpoints(x, ...)
ltext(x, ...)

## Default S3 method:
llines(x, y = NULL, type = "l",
       col, alpha, lty, lwd, ...)
## Default S3 method:
lpoints(x, y = NULL, type = "p", col, pch, alpha, fill,
        font, fontfamily, fontface, cex, ...)
## Default S3 method:
ltext(x, y = NULL, labels = seq_along(x),
      col, alpha, cex, srt = 0,
      lineheight, font, fontfamily, fontface,
      adj = c(0.5, 0.5), pos = NULL, offset = 0.5, ...)

lsegments(x0, y0, x1, y1, x2, y2,
          col, alpha, lty, lwd, ...)

```

```

lrect(xleft, ybottom, xright, ytop,
      x = (xleft + xright) / 2,
      y = (ybottom + ytop) / 2,
      width = xright - xleft,
      height = ytop - ybottom,
      col = "transparent",
      border = "black",
      lty = 1, lwd = 1, alpha = 1,
      just = "center",
      hjust = NULL, vjust = NULL,
      ...)
larrow(x0 = NULL, y0 = NULL, x1, y1, x2 = NULL, y2 = NULL,
      angle = 30, code = 2, length = 0.25, unit = "inches",
      ends = switch(code, "first", "last", "both"),
      type = "open",
      col = add.line$col,
      alpha = add.line$alpha,
      lty = add.line$lty,
      lwd = add.line$lwd,
      fill = NULL, ...)
lpolygon(x, y = NULL,
        border = "black", col = "transparent", fill = NULL,
        font, fontface, ...)

panel.lines(...)
panel.points(...)
panel.segments(...)
panel.text(...)
panel.rect(...)
panel.arrows(...)
panel.polygon(...)

```

### Arguments

`x`, `y`, `x0`, `y0`, `x1`, `y1`, `x2`, `y2`, `xy`  
 locations. `x2` and `y2` are available for for S compatibility.

`length`, `unit` determines extent of arrow head. `length` specifies the length in terms of `unit`, which can be any valid grid unit as long as it doesn't need a data argument. `unit` defaults to `inches`, which is the only option in the base version of the function, `arrows`.

`angle`, `code`, `type`, `labels`, `srt`, `adj`, `pos`, `offset`  
 arguments controlling behaviour. See respective base functions for details. For `larrow`s and `panel.larrow`s, `type` is either `"open"` or `"closed"`, indicating the type of arrowhead.

`ends` serves the same function as `code`, using descriptive names rather than integer codes. If specified, this overrides `code`

`col`, `alpha`, `lty`, `lwd`, `fill`, `pch`, `cex`, `lineheight`, `font`, `fontfamily`, `fontface`, `co`  
 graphical parameters. `fill` applies to points when `pch` is in 21:25 and specifies the fill color, similar to the `bg` argument in the base graphics function `points`. For devices that support alpha-transparency, a numeric argument `alpha` between 0 and 1 can controls transparency. Be careful with this, since for devices that do not support alpha-transparency, nothing will be drawn at all

if this is set to anything other than 0. `fill`, `font` and `fontface` are included in `lpolygon` only to ensure that they are not passed down (as `gpar` doesn't like them).

`origin` for `type="h"` or `type="H"`, the value to which lines drop down.  
`xleft`, `ybottom`, `xright`, `ytopy`  
 see [rect](#)  
`width`, `height`, `just`, `hjust`, `vjust`  
 finer control over rectangles, see [grid.rect](#)  
`...` extra arguments, passed on to lower level functions as appropriate.

### Details

These functions are meant to be grid replacements of the corresponding base R graphics functions, to allow existing Trellis code to be used with minimal modification. The functions `panel.*` are essentially identical to the `l*` versions, are recommended for use in new code (as opposed to ported code) as they have more readable names.

See the documentation of the base functions for usage. Not all arguments are always supported. All these correspond to the default methods only.

### Note

There is a new `type="H"` option wherever appropriate, which is similar to `type="h"`, but with horizontal lines.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### See Also

[points](#), [lines](#), [rect](#), [text](#), [segments](#), [arrows](#), [Lattice](#)

---

F\_2\_panel.functions

*Useful Panel Functions*

---

### Description

These are predefined panel functions available in lattice for use in constructing new panel functions (usually on-the-fly).

### Usage

```
panel.abline(a = NULL, b = 0,
             h = NULL, v = NULL,
             reg = NULL, coef = NULL,
             col, col.line, lty, lwd, alpha, type,
             ...,
             reference = FALSE)
panel.refline(...)
```

```

panel.curve(expr, from, to, n = 101,
            curve.type = "l",
            col, lty, lwd, type,
            ...)
panel.rug(x = NULL, y = NULL,
         regular = TRUE,
         start = if (regular) 0 else 0.97,
         end = if (regular) 0.03 else 1,
         x.units = rep("npc", 2),
         y.units = rep("npc", 2),
         col, lty, lwd, alpha,
         ...)
panel.average(x, y, fun = mean, horizontal = TRUE,
             lwd, lty, col, col.line, type,
             ...)
panel.linejoin(x, y, fun = mean, horizontal = TRUE,
              lwd, lty, col, col.line, type,
              ...)

panel.fill(col, border, ...)
panel.grid(h=3, v=3, col, col.line, lty, lwd, ...)
panel.lmline(x, y, ...)
panel.loess(x, y, span = 2/3, degree = 1,
           family = c("symmetric", "gaussian"),
           evaluation = 50,
           lwd, lty, col, col.line, type,
           horizontal = FALSE,
           ...)
panel.mathdensity(dmath = dnorm, args = list(mean=0, sd=1),
                 n = 50, col, col.line, lwd, lty, type,
                 ...)

```

### Arguments

<code>x, y</code>	variables defining the contents of the panel
<code>a, b</code>	Coefficients of the line to be added by <code>panel.abline</code> . <code>a</code> can be a vector of length 2, representing the coefficients of the line to be added, in which case <code>b</code> should be missing. <code>a</code> can also be an appropriate 'regression' object, i.e., an object which has a <code>coef</code> method that returns a length 2 numeric vector. The corresponding line will be plotted. The <code>reg</code> argument will override <code>a</code> if specified.
<code>coef</code>	Coefficients of the line to be added as a length 2 vector
<code>reg</code>	A regression object. The corresponding fitted line will be drawn
<code>h, v</code>	For <code>panel.abline</code> , these are numeric vectors giving locations respectively of horizontal and vertical lines to be added to the plot, in native coordinates. For <code>panel.grid</code> , these usually specify the number of horizontal and vertical reference lines to be added to the plot. Alternatively, they can be negative numbers. <code>h=-1</code> and <code>v=-1</code> are intended to make the grids aligned with the axis

labels. This doesn't always work; all that actually happens is that the locations are chosen using `pretty`, which is also how the label positions are chosen in the most common cases (but not for factor or date-time variables, for instance). `h` and `v` can be negative numbers other than `-1`, in which case `-h` and `-v` (as appropriate) is supplied as the `n` argument to `pretty`.

<code>reference</code>	logical indicating whether the default graphical parameters for <code>panel.abline</code> should be taken from the "reference.line" parameter settings. The default is to take them from the "add.line" settings. The <code>panel.refline</code> function is a wrapper around <code>panel.abline</code> that calls it with <code>reference=TRUE</code> .
<code>expr</code>	expression as a function of <code>x</code> or a function to plot as a curve
<code>n</code>	the number of points to use for drawing the curve
<code>regular</code>	logical indicating whether the 'rug' is to be drawn on the regular side (left / bottom) or not (right / top)
<code>start, end</code>	endpoints of rug segments, in normalized parent coordinates (between 0 and 1). Defaults depend on value of <code>regular</code> , and cover 3% of the panel width and height
<code>x.units, y.units</code>	character vector, replicated to be of length two. Specifies the (grid) units associated with <code>start</code> and <code>end</code> above. <code>x.units</code> and <code>y.units</code> are for the rug on the x-axis and y-axis respectively (and thus are associated with <code>start</code> and <code>end</code> values on the y and x scales respectively).
<code>from, to</code>	optional lower and upper x-limits of curve. If missing, limits of current panel are used
<code>curve.type</code>	type of curve ("p" for points, etc), passed to <code>llines</code>
<code>col, col.line, lty, lwd, alpha, border</code>	graphical parameters
<code>type</code>	Usually ignored by the panel functions documented here; the argument is present only to make sure an explicitly specified <code>type</code> argument (perhaps meant for another function) doesn't affect the display.
<code>span, degree, family, evaluation</code>	arguments to <code>loess.smooth</code> , for which <code>panel.loess</code> is essentially a wrapper.
<code>fun</code>	the function that will be applied to the subset of <code>x(y)</code> determined by the unique values of <code>y(x)</code>
<code>horizontal</code>	logical. If <code>FALSE</code> , the plot is 'transposed' in the sense that the behaviours of <code>x</code> and <code>y</code> are switched. <code>x</code> is now the 'factor'. Interpretation of other arguments change accordingly. See documentation of <code>bwplot</code> for a fuller explanation.
<code>dmath</code>	A vectorized function that produces density values given a numeric vector named <code>x</code> , e.g., <code>dnorm</code>
<code>args</code>	list giving additional arguments to be passed to <code>dmath</code>
<code>...</code>	graphical parameters can be supplied. see function definition for details. Color can usually be specified by <code>col</code> , <code>col.line</code> and <code>col.symbol</code> , the last two overriding the first for lines and points respectively.

## Details

`panel.abline` adds a line of the form  $y=a+bx$  or vertical and/or horizontal lines. Graphical parameters are obtained from the "add.line" settings by default. `panel.refline` is similar, but uses the "reference.line" settings for the defaults.

`panel.grid` draws a reference grid.

`panel.curve` adds a curve, similar to what `curve` does with `add = TRUE`. Graphical parameters for the line are obtained from the `add.line` setting.

`panel.average` treats one of `x` and `y` as a factor (according to the value of `horizontal`), calculates `fun` applied to the subsets of the other variable determined by each unique value of the factor, and joins them by a line. Can be used in conjunction with `panel.xyplot` and more commonly with `panel.superpose` to produce interaction plots. See [xyplot](#) documentation for an example. `panel.linejoin` is an alias for `panel.average` retained for back-compatibility and may go away in future.

`panel.mathdensity` plots a (usually theoretical) probability density function. This can be useful in conjunction with `histogram` and `densityplot` to visually estimate goodness of fit (note, however, that `qqmath` is more suitable for this).

`panel.rug` adds a *rug* representation of the (marginal) data to the panel, much like [rug](#).

`panel.lmline(x, y)` is equivalent to `panel.abline(lm(y~x))`.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### See Also

[loess.smooth](#), [panel.axis](#), [panel.identify](#) [identify](#), [trellis.par.set](#)

---

F\_2\_panel.qqmathline

*Useful panel function with qqmath*

---

### Description

Useful panel function with `qqmath`. Draws a line passing through the points (usually) determined by the .25 and .75 quantiles of the sample and the theoretical distribution.

### Usage

```
panel.qqmathline(x, y = x,
                 distribution = qnorm,
                 probs = c(0.25, 0.75),
                 qtype = 7,
                 groups = NULL,
                 ...)
```

### Arguments

<code>x</code>	The original sample, possibly reduced to a fewer number of quantiles, as determined by the <code>f.value</code> argument to <code>qqmath</code>
<code>y</code>	an alias for <code>x</code> for backwards compatibility
<code>distribution</code>	quantile function for reference theoretical distribution.
<code>probs</code>	numeric vector of length two, representing probabilities. Corresponding quantile pairs define the line drawn.

qtype	the type of quantile computation used in <a href="#">quantile</a>
groups	optional grouping variable. If non-null, a line will be drawn for each group.
...	other arguments.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[prepanel.qqmathline](#), [qqmath](#), [quantile](#)

---

F\_2\_panel.smoothScatter

*Lattice panel function analogous to smoothScatter*

---

**Description**

This function allows the user to place `smoothScatter` plots in lattice graphics.

**Usage**

```
panel.smoothScatter(x, y = NULL,
                    nbin = 64, cuts = 255,
                    bandwidth,
                    colramp,
                    nrpoints = 100,
                    transformation = function(x) x^0.25,
                    pch = ".",
                    cex = 1, col="black",
                    range.x,
                    ...,
                    raster = FALSE,
                    subscripts)
```

**Arguments**

x	Numeric vector containing x-values or n by 2 matrix containing x and y values.
y	Numeric vector containing y-values (optional). The length of x must be the same as that of y.
nbin	Numeric vector of length 1 (for both directions) or 2 (for x and y separately) containing the number of equally spaced grid points for the density estimation.
cuts	number of cuts defining the color gradient
bandwidth	Numeric vector: the smoothing bandwidth. If missing, these functions come up with a more or less useful guess. This parameter then gets passed on to the function <a href="#">bkde2D</a> .
colramp	Function accepting an integer n as an argument and returning n colors.



<code>nrpoints</code>	Numeric vector of length 1 giving number of points to be superimposed on the density image. The first <code>nrpoints</code> points from those areas of lowest regional densities will be plotted. Adding points to the plot allows for the identification of outliers. If all points are to be plotted, choose <code>nrpoints = Inf</code> .
<code>transformation</code>	Function that maps the density scale to the color scale.
<code>pch, cex</code>	graphical parameters for the <code>nrpoints</code> “outlying” points shown in the display
<code>range.x</code>	see <a href="#">bkde2D</a> for details.
<code>col</code>	<a href="#">points</a> color parameter
<code>...</code>	Further arguments that are passed on to <a href="#">panel.levelplot</a> .
<code>raster</code>	logical; if TRUE, <a href="#">panel.levelplot.raster</a> is used, making potentially smaller output files.
<code>subscripts</code>	ignored, but necessary for handling of <code>...</code> in certain situations. Likely to be removed in future.

### Details

This replicates the display part of the `smoothScatter` function by replacing standard graphics calls by grid-compatible ones.

### Value

The function is called for its side effects, namely the production of the appropriate plots on a graphics device.

### Author(s)

Deepayan Sarkar <[deepayan.sarkar@r-project.org](mailto:deepayan.sarkar@r-project.org)>

### Examples

```
ddf <- as.data.frame(matrix(rnorm(40000), ncol = 4) + 3 * rnorm(10000))
ddf[, c(2,4)] <- (-ddf[, c(2,4)])
xyplot(V1 ~ V2 + V3, ddf, outer = TRUE,
       panel = panel.smoothScatter, aspect = "iso")
splom(ddf, panel = panel.smoothScatter, nbin = 64, raster = TRUE)
```

---

F\_2\_panel.superpose

*Panel Function for Display Marked by groups*

---

### Description

These are panel functions for Trellis displays useful when a grouping variable is specified for use within panels. The `x` (and `y` where appropriate) variables are plotted with different graphical parameters for each distinct value of the grouping variable.

**Usage**

```

panel.superpose(x, y = NULL, subscripts, groups,
               panel.groups = "panel.xyplot",
               ...,
               col, col.line, col.symbol,
               pch, cex, fill, font,
               fontface, fontfamily,
               lty, lwd, alpha,
               type = "p",
               distribute.type = FALSE)
panel.superpose.2(..., distribute.type = TRUE)

panel.superpose.plain(...,
                     col, col.line, col.symbol,
                     pch, cex, fill, font,
                     fontface, fontfamily,
                     lty, lwd, alpha)

```

**Arguments**

<code>x, y</code>	coordinates of the points to be displayed
<code>panel.groups</code>	the panel function to be used for each group of points. Defaults to <code>panel.xyplot</code> (behaviour in S). To be able to distinguish between different levels of the originating group inside <code>panel.groups</code> , it will be supplied two special arguments called <code>group.number</code> and <code>group.value</code> which will hold the numeric code and factor level corresponding to the current level of <code>groups</code> . No special care needs to be taken when writing a <code>panel.groups</code> function if this feature is not used.
<code>subscripts</code>	subscripts giving indices in original data frame
<code>groups</code>	a grouping variable. Different graphical parameters will be used to plot the subsets of observations given by each distinct value of <code>groups</code> . The default graphical parameters are obtained from <code>superpose.symbol</code> and <code>superpose.line</code> using <code>trellis.par.get</code> wherever appropriate
<code>type</code>	usually a character vector specifying what should be drawn for each group, passed on to the <code>panel.groups</code> function, which must know what to do with it. By default, this is <code>panel.xyplot</code> , whose help page describes the admissible values. The functions <code>panel.superpose</code> and <code>panel.superpose.2</code> differ only in the default value of <code>distribute.type</code> , which controls the way the <code>type</code> argument is interpreted. If <code>distribute.type = FALSE</code> , then the interpretation is the same as for <code>panel.xyplot</code> for each of the unique groups. In other words, if <code>type</code> is a vector, all the individual components are honoured concurrently. If <code>distribute.type = TRUE</code> , <code>type</code> is replicated to be as long as the number of unique values in <code>groups</code> , and one component used for the points corresponding to the each different group. Even in this case, it is possible to request multiple types per group, specifying <code>type</code> as a list, each component being the desired <code>type</code> vector for the corresponding group. If <code>distribute.type = FALSE</code> , any occurrence of "g" in <code>type</code> causes a grid to be drawn, and all such occurrences are removed before <code>type</code> is passed on to <code>panel.groups</code> .

`col`, `col.line`, `col.symbol`, `pch`, `cex`, `fill`, `font`, `fontface`, `fontfamily`, `lty`, `lwd`, graphical parameters, replicated to be as long as the number of groups. These are eventually passed down to `panel.groups`, but as scalars rather than vectors. When `panel.groups` is called for the *i*-th level of groups, the corresponding element of each graphical parameter is passed to it.

... Extra arguments. Passed down to `panel.superpose` from `panel.superpose.2`, and to `panel.groups` from `panel.superpose`.

`distribute.type`  
logical controlling interpretation of the `type` argument.

### Details

`panel.superpose` and `panel.superpose.2` differ essentially in how `type` is interpreted by default. The default behaviour in `panel.superpose` is the opposite of that in S, which is the same as that of `panel.superpose.2`.

`panel.superpose.plain` is the same as `panel.superpose`, except that the default settings for the style arguments are the same for all groups and are taken from the default plot style. It is used in [xyplot.ts](#).

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org> (`panel.superpose.2` originally contributed by Neil Klepeis)

### See Also

Different functions when used as `panel.groups` gives different types of plots, for example [panel.xyplot](#), [panel.dotplot](#) and [panel.linejoin](#) (This can be used to produce interaction plots).

See [Lattice](#) for an overview of the package.

---

F\_2\_panel.violin    *Panel Function to create Violin Plots*

---

### Description

This is a panel function that can create a violin plot. It is typically used in a high-level call to `bwplot`.

### Usage

```
panel.violin(x, y, box.ratio = 1, box.width,
             horizontal = TRUE,
             alpha, border, lty, lwd, col,
             varwidth = FALSE,
             bw, adjust, kernel, window,
             width, n = 50, from, to, cut,
             na.rm, ...)
```

**Arguments**

<code>x, y</code>	numeric vector or factor. Violin plots are drawn for each unique value of <code>y</code> ( <code>x</code> ) if <code>horizontal</code> is <code>TRUE</code> ( <code>FALSE</code> )
<code>box.ratio</code>	ratio of the thickness of each violin and inter violin space
<code>box.width</code>	thickness of the violins in absolute units; overrides <code>box.ratio</code> . Useful for specifying thickness when the categorical variable is not a factor, as use of <code>box.ratio</code> alone cannot achieve a thickness greater than 1.
<code>horizontal</code>	logical. If <code>FALSE</code> , the plot is ‘transposed’ in the sense that the behaviours of <code>x</code> and <code>y</code> are switched. <code>x</code> is now the ‘factor’. See documentation of <code>bwplot</code> for a fuller explanation.
<code>alpha, border, lty, lwd, col</code>	graphical parameters controlling the violin. Defaults are taken from the "plot.polygon" settings.
<code>varwidth</code>	logical. If <code>FALSE</code> , the densities are scaled separately for each group, so that the maximum value of the density reaches the limit of the allocated space for each violin (as determined by <code>box.ratio</code> ). If <code>TRUE</code> , densities across violins will have comparable scale.
<code>bw, adjust, kernel, window, width, n, from, to, cut, na.rm</code>	arguments to <code>density</code> , passed on as appropriate
<code>...</code>	arguments passed on to <code>density</code> .

**Details**

Creates Violin plot of `x` for every level of `y`. Note that most arguments controlling the display can be supplied to the high-level (typically `bwplot`) call directly.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[bwplot](#), [density](#)

**Examples**

```
bwplot(voice.part ~ height, singer,
       panel = function(..., box.ratio) {
         panel.violin(..., col = "transparent",
                     varwidth = FALSE, box.ratio = box.ratio)
         panel.bwplot(..., fill = NULL, box.ratio = .1)
       } )
```

---

F\_3\_prepanel.default

*Default Prepanel Functions*


---

**Description**

These prepanel functions are used as fallback defaults in various high level plot functions in Lattice. These are rarely useful to normal users but may be helpful in developing new displays.

**Usage**

```
prepanel.default.bwplot(x, y, horizontal, nlevels, origin, stack, ...)
prepanel.default.histogram(x, breaks, equal.widths, type, nint, ...)
prepanel.default.qq(x, y, ...)
prepanel.default.xyplot(x, y, type, subscripts, groups, ...)
prepanel.default.cloud(perspective, distance,
                        xlim, ylim, zlim,
                        screen = list(z = 40, x = -60),
                        R.mat = diag(4),
                        aspect = c(1, 1), panel.aspect = 1,
                        ..., zoom = 0.8)
prepanel.default.levelplot(x, y, subscripts, ...)
prepanel.default.qqmath(x, f.value, distribution, qtype,
                        groups, subscripts, ..., tails.n = 0)
prepanel.default.densityplot(x, darg, groups, weights, subscripts, ...)
prepanel.default.parallel(x, y, z, ..., horizontal.axis)
prepanel.default.splom(z, ...)
```

**Arguments**

<code>x, y</code>	x and y values, numeric or factor
<code>horizontal</code>	logical, applicable when one of the variables is to be treated as categorical (factor or shingle).
<code>horizontal.axis</code>	logical indicating whether the parallel axes should be laid out horizontally (TRUE) or vertically (FALSE).
<code>nlevels</code>	number of levels of such a categorical variable.
<code>origin, stack</code>	for barcharts or the <code>type="h"</code> plot type
<code>breaks, equal.widths, type, nint</code>	details of histogram calculations. <code>type</code> has a different meaning in <code>prepanel.default.xyplot</code> (see <a href="#">panel.xyplot</a> )
<code>groups, subscripts</code>	See <a href="#">xyplot</a> . Whenever appropriate, calculations are done separately for each group and then combined.
<code>weights</code>	numeric vector of weights for the density calculations. If this is specified, it is subsetted by <code>subscripts</code> to match it to <code>x</code> .

perspective, distance, xlim, ylim, zlim, screen, R.mat, aspect, panel.aspect, zoom  
 see [panel.cloud](#)  
 f.value, distribution, tails.n  
 see [panel.qqmath](#)  
 darg list of arguments passed to [density](#)  
 z see [panel.parallel](#) and [panel.pairs](#)  
 qtype type of [quantile](#)  
 ... other arguments, usually ignored

**Value**

A list with components `xlim`, `ylim`, `dx` and `dy`, and possibly `xat` and `yat`, the first two being used to calculate panel axes limits, the last two for banking computations. The form of these components are described in the help page for [xyplot](#).

**Author(s)**

Deepayan Sarkar <[Deepayan.Sarkar@R-project.org](mailto:Deepayan.Sarkar@R-project.org)>

**See Also**

[xyplot](#), [banking](#), [Lattice](#). See documentation of corresponding panel functions for more details about the arguments.

---

F\_3\_prepanel.functions

*Useful Prepanel Function for Lattice*

---

**Description**

These are predefined prepanel functions available in Lattice.

**Usage**

```
prepanel.lmline(x, y, ...)
prepanel.loess(x, y, span, degree, family, evaluation, ...)
prepanel.qqmathline(x, y = x, distribution = qnorm,
                    probs = c(0.25, 0.75), qtype = 7,
                    groups, subscripts,
                    ...)
```

**Arguments**

`x`, `y` x and y values, numeric or factor  
`distribution` quantile function for theoretical distribution. This is automatically passed in when this is used as a prepanel function in `qqmath`.  
`qtype` type of [quantile](#)  
`probs` numeric vector of length two, representing probabilities. If used with `aspect="xy"`, the aspect ratio will be chosen to make the line passing through the corresponding quantile pairs as close to 45 degrees as possible.

```
span, degree, family, evaluation
      arguments controlling the underlying loess smooth
groups, subscripts
      See xyplot. Whenever appropriate, calculations are done separately for each
      group and then combined.
...
      other arguments
```

### Value

usually a list with components `xlim`, `ylim`, `dx` and `dy`, the first two being used to calculate panel axes limits, the last two for banking computations. The form of these components are described under `xyplot`. There are also several prepanel functions that serve as the default for high level functions, see `prepanel.default.xyplot`

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### See Also

`trellis.par.get`, `xyplot`, `banking`, `Lattice`. See `loess.smooth` for further options to `prepanel.loess`

---

G\_axis.default

*Default axis annotation utilities*

---

### Description

Lattice functions provide control over how the plot axes are annotated through a common interface. There are two levels of control. The `xscale.components` and `yscale.components` arguments can be functions that determine tick mark locations and labels given a packet. For more direct control, the `axis` argument can be a function that actually draws the axes. The functions documented here are the defaults for these arguments. They can additionally be used as components of user written replacements.

### Usage

```
xscale.components.default(lim,
                          packet.number = 0,
                          packet.list = NULL,
                          top = TRUE,
                          ...)
yscale.components.default(lim,
                          packet.number = 0,
                          packet.list = NULL,
                          right = TRUE,
                          ...)
axis.default(side = c("top", "bottom", "left", "right"),
            scales, components, as.table,
            labels = c("default", "yes", "no"),
            ticks = c("default", "yes", "no"),
            ...)
```

**Arguments**

<code>lim</code>	the range of the data in that packet (data subset corresponding to a combination of levels of the conditioning variable). The range is not necessarily numeric; e.g. for factors, they could be character vectors representing levels, and for the various date-time representations, they could be vectors of length 2 with the corresponding class.
<code>packet.number</code>	which packet (counted according to the packet order, described in <code>print.trellis</code> ) is being processed. In cases where all panels have the same limits, this function is called only once (rather than once for each packet), in which case this argument will have the value 0.
<code>packet.list</code>	list, as long as the number of packets, giving all the actual packets. Specifically, each component is the list of arguments given to the panel function when and if that packet is drawn in a panel. (This has not yet been implemented.)
<code>top, right</code>	the value of the <code>top</code> and <code>right</code> components of the result, as appropriate. See below for interpretation.
<code>side</code>	on which side the axis is to be drawn. The usual partial matching rules apply.
<code>scales</code>	the appropriate component of the <code>scales</code> argument supplied to the high level function, suitably standardized.
<code>components</code>	list, similar to those produced by <code>xscale.components.default</code> and <code>yscale.components.default</code> .
<code>as.table</code>	the <code>as.table</code> argument in the high level function.
<code>labels</code>	whether labels are to be drawn. By default, the rules determined by <code>scales</code> are used.
<code>ticks</code>	whether labels are to be drawn. By default, the rules determined by <code>scales</code> are used.
<code>...</code>	many other arguments may be supplied, and are passed on to other internal functions.

**Details**

These functions are part of a new API introduced in `lattice 0.14` to provide the user more control over how axis annotation is done. While the API has been designed in anticipation of use that was previously unsupported, the implementation has initially focused on reproducing existing capabilities, rather than test new features. At the time of writing, several features are unimplemented. If you require them, please contact the maintainer.

**Value**

`xscale.components.default` and `yscale.components.default` return a list of the form suitable as the `components` argument of `axis.default`. Valid components in the return value of `xscale.components.default` are:

<code>num.limit</code>	A numeric limit for the box.
<code>bottom</code>	A list with two elements, <code>ticks</code> and <code>labels</code> . <code>ticks</code> must be a list with components <code>at</code> and <code>tick</code> which give the location and lengths of tick marks. <code>tick</code> can be a vector, and will be recycled to be as long as <code>at</code> . <code>labels</code> must be a list with components <code>at</code> , <code>labels</code> , and <code>check.overlap</code> . <code>at</code> and <code>labels</code> give the location and labels of the tick labels; this is usually the same as the location



of the ticks, but is not required to be so. `check.overlap` is a logical flag indicating whether overlapping of labels should be avoided by omitting some of the labels while rendering.

`top` This can be a logical flag; if `TRUE`, `top` is treated as being the same as `bottom`; if `FALSE`, axis annotation for the top axis is omitted. Alternatively, `top` can be a list like `bottom`.

Valid components in the return value of `yscale.components.default` are `left` and `right`. Their interpretations are analogous to (respectively) the `bottom` and `top` components described above.

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### See Also

[Lattice](#), [xyplot](#), [print.trellis](#)

### Examples

```
str(xscale.components.default(c(0, 1)))

set.seed(36872)
rln <- rlnorm(100)

densityplot(rln,
  scales = list(x = list(log = 2), alternating = 3),
  xlab = "Simulated lognormal variates",
  xscale.components = function(...) {
    ans <- xscale.components.default(...)
    ans$top <- ans$bottom
    ans$bottom$labels$labels <- parse(text = ans$bottom$labels$labels)
    ans$top$labels$labels <-
      if (require(MASS))
        fractions(2^(ans$top$labels$at))
      else
        2^(ans$top$labels$at)
    ans
  })

## Direct use of axis to show two temperature scales (Celcius and
## Fahrenheit). This does not work for multi-row plots, and doesn't
## do automatic allocation of space

F2C <- function(f) 5 * (f - 32) / 9
C2F <- function(c) 32 + 9 * c / 5

axis.CF <-
  function(side, ...)
  {
    ylim <- current.panel.limits()$ylim
    switch(side,
      left = {
```

```

        prettyF <- pretty(ylim)
        labF <- parse(text = sprintf("%s ~ degree * F", prettyF))
        panel.axis(side = side, outside = TRUE,
                  at = prettyF, labels = labF)
    },
    right = {
        prettyC <- pretty(F2C(ylim))
        labC <- parse(text = sprintf("%s ~ degree * C", prettyC))
        panel.axis(side = side, outside = TRUE,
                  at = C2F(prettyC), labels = labC)
    },
    axis.default(side = side, ...))
}

xyplot(nhtemp ~ time(nhtemp), aspect = "xy", type = "o",
       scales = list(y = list(alternating = 3)),
       axis = axis.CF, xlab = "Year", ylab = "Temperature",
       main = "Yearly temperature in New Haven, CT")

## version using yscale.components

yscale.components.CF <-
  function(...)
  {
    ans <- yscale.components.default(...)
    ans$right <- ans$left
    ans$left$labels$labels <-
      parse(text = sprintf("%s ~ degree * F", ans$left$labels$at))
    prettyC <- pretty(F2C(ans$num.limit))
    ans$right$ticks$at <- C2F(prettyC)
    ans$right$labels$at <- C2F(prettyC)
    ans$right$labels$labels <-
      parse(text = sprintf("%s ~ degree * C", prettyC))
    ans
  }

xyplot(nhtemp ~ time(nhtemp), aspect = "xy", type = "o",
       scales = list(y = list(alternating = 3)),
       yscale.components = yscale.components.CF,
       xlab = "Year", ylab = "Temperature",
       main = "Yearly temperature in New Haven, CT")

```

---

G\_banking

*Banking*


---

### Description

Calculates banking slope

### Usage

```
banking(dx, dy)
```



**Arguments**

model	the model/formula to be parsed. This can be in either of two possible forms, one for 2d and one for 3d formulas, determined by the <code>dimension</code> argument. The 2d formulas are of the form $y \sim x \mid g_1 * \dots * g_n$ , and the 3d formulas are of the form $z \sim x * y \mid g_1 * \dots * g_n$ . In the first form, $y$ may be omitted. The conditioning variables $g_1, \dots, g_n$ can be omitted in either case.
data	the environment/dataset where the variables in the formula are evaluated.
dimension	dimension of the model, see above
subset	index for choosing a subset of the data frame
groups	the grouping variable, if present
multiple, outer	logicals, determining how a '+' in the y and x components of the formula are processed. See <a href="#">xyplot</a> for details
subscripts	logical, whether subscripts are to be calculated
drop	logical or list, similar to the <code>drop.unused.levels</code> argument in <a href="#">xyplot</a> , indicating whether unused levels of conditioning factors and data variables that are factors are to be dropped.

**Value**

returns a list with several components, including `left`, `right`, `left.name`, `right.name`, `condition` for 2-D, and `left`, `right.x`, `right.y`, `left.name`, `right.x.name`, `right.y.name`, `condition` for 3-D. Other possible components are `groups`, `subscr`

**Author(s)**

Saikat DebRoy, Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[xyplot](#), [Lattice](#)

---

G\_packet.panel.default

*Associating Packets with Panels*

---

**Description**

When a "trellis" object is plotted, panels are always drawn in an order such that columns vary the fastest, then rows and then pages. An optional function can be specified that determines, given the column, row and page and other relevant information, the packet (if any) which should be used in that panel. The function documented here implements the default behaviour, which is to match panel order with packet order, determined by varying the first conditioning variable the fastest, then the second, and so on. This matching is performed after any reordering and/or permutation of the conditioning variables.

**Usage**

```
packet.panel.default(layout, condlevels, page, row, column,
                    skip, all.pages.skip = TRUE)
```

**Arguments**

`layout`            the `layout` argument in high level functions, suitably standardized.

`condlevels`       a list of levels of conditioning variables, after relevant permutations and/or re-ordering of levels

`page, row, column`       the location of the panel in the coordinate system of pages, rows and columns.

`skip`             the `skip` argument in high level functions

`all.pages.skip`       whether `skip` should be replicated over all pages. If `FALSE`, `skip` will be replicated to be only as long as the number of positions on a page, and that template will be used for all pages.

**Value**

A suitable combination of levels of the conditioning variables in the form of a numeric vector as long as the number of conditioning variables, with each element an integer indexing the levels of the corresponding variable. Specifically, if the return value is `p`, then the `i`-th conditioning variable will have level `condlevels[[i]][p[i]]`.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[Lattice](#), [xyplot](#)

**Examples**

```
packet.panel.page <- function(n)
{
  ## returns a function that when used as the 'packet.panel'
  ## argument in print.trellis plots page number 'n' only
  function(layout, page, ...) {
    stopifnot(layout[3] == 1)
    packet.panel.default(layout = layout, page = n, ...)
  }
}

data(mtcars)
HP <- equal.count(mtcars$hp, 6)
p <-
  xyplot(mpg ~ disp | HP * factor(cyl),
         mtcars, layout = c(0, 6, 1))

print(p, packet.panel = packet.panel.page(1))
print(p, packet.panel = packet.panel.page(2))
```

G\_panel.axis

*Panel Function for Drawing Axis Ticks and Labels***Description**

panel.axis is the function used by lattice to draw axes. It is typically not used by users, except those wishing to create advanced annotation. Keep in mind issues of clipping when trying to use it as part of the panel function. current.panel.limits can be used to retrieve a panel's x and y limits.

**Usage**

```
panel.axis(side = c("bottom", "left", "top", "right"),
           at,
           labels = TRUE,
           draw.labels = TRUE,
           check.overlap = FALSE,
           outside = FALSE,
           ticks = TRUE,
           half = !outside,
           which.half,
           tck = as.numeric(ticks),
           rot = if (is.logical(labels)) 0 else c(90, 0),
           text.col, text.alpha, text.cex, text.font,
           text.fontfamily, text.fontface,
           line.col, line.lty, line.lwd, line.alpha)

current.panel.limits(unit = "native")
```

**Arguments**

side	character string indicating which side axes are to be drawn on. Partial specification is allowed.
at	location of labels
labels	the labels to go along with at. The labels can be a character vector or a vector of expressions. Alternatively, this can be a logical. If TRUE, the labels are derived from at, otherwise, labels are empty.
draw.labels	logical indicating whether labels are to be drawn
check.overlap	logical, whether to check for overlapping of labels. This also has the effect of removing at values that are 'too close' to the limits.
outside	logical, whether to the labels draw outside the panel or inside. Note that outside=TRUE will only have a visible effect if clipping is disabled for the viewport (panel).
ticks	logical, whether to draw the tickmarks
half	logical, whether only half of scales will be drawn for each side
which.half	character string, one of "lower" and "upper". Indicates which half is to be used for tick locations if half=TRUE. Defaults to whatever is suitable for <a href="#">splom</a>

`tck`                numeric scalar, multiplier for tick length. Can be negative.  
`rot`                rotation angles for labels in degrees. Can be a vector of length 2 for x- and y-axes respectively  
`text.col`, `text.alpha`, `text.cex`, `text.font`, `text.fontfamily`, `text.fontface`, `line.`  
                      graphical parameters  
`unit`                which grid `unit` the values should be in

### Details

`panel.axis` can draw axis tick marks inside or outside a panel (more precisely, a grid viewport). It honours the (native) axis scales. Used in `panel.pairs` for `splom`, as well as for all the usual axis drawing by the print method for "trellis" objects. It can also be used to enhance plots 'after the fact' by adding axes.

### Value

`current.panel.limits` returns a list with components `xlim` and `ylim`, which are both numeric vectors of length 2, giving the scales of the current panel (viewport). The values correspond to the unit system specified by `unit`, by default "native".

### Author(s)

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

### See Also

`Lattice`, `xyplot`, `trellis.focus`, `unit`

---

`G_panel.number`

*Accessing Auxiliary Information During Plotting*

---

### Description

Control over lattice plots are provided through a collection of user specifiable functions that perform various tasks during the plotting. Not all information is available to all functions. The functions documented here attempt to provide a consistent interface to access relevant information from within these user specified functions, namely those specified as the `panel`, `strip` and `axis` functions.

### Usage

```

current.row()
current.column()
panel.number()
packet.number()
which.packet()

trellis.currentLayout(which = c("packet", "panel"))
  
```

**Arguments**

`which` whether return value (a matrix) should contain panel numbers or packet numbers, which are usually, but not necessarily, the same (see below for details).

**Value**

`trellis.currentLayout` returns a matrix with as many rows and columns as in the layout of panels in the current plot. Entries in the matrix are integer indices indicating which packet (or panel; see below) occupies that position, with 0 indicating the absence of a panel. `current.row` and `current.column` return integer indices specifying which row and column in the layout are currently active. `panel.number` returns an integer counting which panel is being drawn (starting from 1 for the first panel, a.k.a. the panel order). `packet.number` gives the packet number according to the packet order, which is determined by varying the first conditioning variable the fastest, then the second, and so on. `which.packet` returns the combination of levels of the conditioning variables in the form of a numeric vector as long as the number of conditioning variables, with each element an integer indexing the levels of the corresponding variable.

**Note**

The availability of these functions make redundant some features available in earlier versions of lattice, namely optional arguments called `panel.number` and `packet.number` that were made available to `panel` and `strip`. If you have written such functions, it should be enough to replace instances of `panel.number` and `packet.number` by the corresponding function calls. You should also remove `panel.number` and `packet.number` from the argument list of your function to avoid a warning.

If these accessor functions are not enough for your needs, feel free to contact the maintainer and ask for more.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[Lattice](#), [xyplot](#)

---

G\_Rows

*Extract rows from a list*

---

**Description**

Convenience function to extract subset of a list. Usually used in creating keys.

**Usage**

```
Rows(x, which)
```

**Arguments**

`x` list with each member a vector of the same length  
`which` index for members of `x`



**Value**

A list similar to `x`, with each `x[[i]]` replaced by `x[[i]][which]`

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[xyplot](#), [Lattice](#)

---

G\_utilities.3d      *Utility functions for 3-D plots*

---

**Description**

These are (related to) the default panel functions for `cloud` and `wireframe`.

**Usage**

```
ltransform3dMatrix(screen, R.mat)
ltransform3dto3d(x, R.mat, dist)
```

**Arguments**

<code>x</code>	<code>x</code> can be a numeric matrix with 3 rows for <code>ltransform3dto3d</code>
<code>screen</code>	list, as described in <a href="#">panel.cloud</a>
<code>R.mat</code>	4x4 transformation matrix in homogeneous coordinates
<code>dist</code>	controls transformation to account for perspective viewing

**Details**

`ltransform3dMatrix` and `ltransform3dto3d` are utility functions to help in computation of projections. These functions are used inside the panel functions for `cloud` and `wireframe`. They may be useful in user-defined panel functions as well.

The first function takes a list of the form of the `screen` argument in `cloud` and `wireframe` and a `R.mat`, a 4x4 transformation matrix in homogeneous coordinates, to return a new 4x4 transformation matrix that is the result of applying `R.mat` followed by the rotations in `screen`. The second function applies a 4x4 transformation matrix in homogeneous coordinates to a 3xn matrix representing points in 3-D space, and optionally does some perspective computations. (There has been no testing with non-trivial transformation matrices, and my knowledge of the homogeneous coordinate system is very limited, so there may be bugs here.)

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>

**See Also**

[cloud](#), [panel.cloud](#)

H\_barley

*Yield data from a Minnesota barley trial***Description**

Total yield in bushels per acre for 10 varieties at 6 sites in each of two years.

**Usage**

```
barley
```

**Format**

A data frame with 120 observations on the following 4 variables.

**yield** Yield (averaged across three blocks) in bushels/acre.

**variety** Factor with levels "Svansota", "No. 462", "Manchuria", "No. 475", "Velvet", "Peatland", "Glabron", "No. 457", "Wisconsin No. 38", "Trobi".

**year** Factor with levels 1932, 1931

**site** Factor with 6 levels: "Grand Rapids", "Duluth", "University Farm", "Morris", "Crookston", "Waseca"

**Details**

These data are yields in bushels per acre, of 10 varieties of barley grown in 1/40 acre plots at University Farm, St. Paul, and at the five branch experiment stations located at Waseca, Morris, Crookston, Grand Rapids, and Duluth (all in Minnesota). The varieties were grown in three randomized blocks at each of the six stations during 1931 and 1932, different land being used each year of the test.

Immer et al. (1934) present the data for each Year\*Site\*Variety\*Block. The data here is the average yield across the three blocks.

Immer et al. (1934) refer (once) to the experiment as being conducted in 1930 and 1931, then later refer to it (repeatedly) as being conducted in 1931 and 1932. Later authors have continued the confusion.

Cleveland (1993) suggests that the data for the Morris site may have had the years switched.

**Author(s)**

Documentation contributed by Kevin Wright.

**Source**

Immer, R. F., H. K. Hayes, and LeRoy Powers. (1934). Statistical Determination of Barley Varietal Adaptation. *Journal of the American Society of Agronomy*, **26**, 403–419.

**References**

Cleveland, William S. (1993). *Visualizing Data*. Hobart Press, Summit, New Jersey.

Fisher, R. A. (1971). *The Design of Experiments*. Hafner, New York, 9th edition.

**See Also**

`immer` in the MASS package for data from the same experiment (expressed as total yield for 3 blocks) for a subset of varieties.

**Examples**

```
# Graphic suggesting the Morris data switched the years 1931 and 1932
# Figure 1.1 from Cleveland
dotplot(variety ~ yield | site, data = barley, groups = year,
        key = simpleKey(levels(barley$year), space = "right"),
        xlab = "Barley Yield (bushels/acre) ",
        aspect=0.5, layout = c(1,6), ylab=NULL)
```

---

H\_environmental      *Atmospheric environmental conditions in New York City*

---

**Description**

Daily measurements of ozone concentration, wind speed, temperature and solar radiation in New York City from May to September of 1973.

**Usage**

```
environmental
```

**Format**

A data frame with 111 observations on the following 4 variables.

**ozone** Average ozone concentration (of hourly measurements) of in parts per billion.

**radiation** Solar radiation (from 08:00 to 12:00) in langleys.

**temperature** Maximum daily emperature in degrees Fahrenheit.

**wind** Average wind speed (at 07:00 and 10:00) in miles per hour.

**Author(s)**

Documentation contributed by Kevin Wright.

**Source**

Bruntz, S. M., W. S. Cleveland, B. Kleiner, and J. L. Warner. (1974). The Dependence of Ambient Ozone on Solar Radiation, Wind, Temperature, and Mixing Height. In *Symposium on Atmospheric Diffusion and Air Pollution*, pages 125–128. American Meterological Society, Boston.

**References**

Cleveland, William S. (1993). *Visualizing Data*. Hobart Press, Summit, New Jersey.

**Examples**

```

# Scatter plot matrix with loess lines
splom(~environmental,
      panel=function(x,y){
        panel.xyplot(x,y)
        panel.loess(x,y)
      }
)

# Conditioned plot similar to figure 5.3 from Cleveland
attach(environmental)
Temperature <- equal.count(temperature, 4, 1/2)
Wind <- equal.count(wind, 4, 1/2)
xyplot((ozone^(1/3)) ~ radiation | Temperature * Wind,
       aspect=1,
       prepanel = function(x, y)
         prepanel.loess(x, y, span = 1),
       panel = function(x, y){
         panel.grid(h = 2, v = 2)
         panel.xyplot(x, y, cex = .5)
         panel.loess(x, y, span = 1)
       },
       xlab = "Solar radiation (langleys)",
       ylab = "Ozone (cube root ppb)")
detach()

# Similar display using the coplot function
with(environmental,{
  coplot((ozone^.33) ~ radiation | temperature * wind,
        number=c(4,4),
        panel = function(x, y, ...) panel.smooth(x, y, span = .8, ...),
        xlab="Solar radiation (langleys)",
        ylab="Ozone (cube root ppb)")
})

```

---

H\_ethanol

*Engine exhaust fumes from burning ethanol*


---

**Description**

Ethanol fuel was burned in a single-cylinder engine. For various settings of the engine compression and equivalence ratio, the emissions of nitrogen oxides were recorded.

**Usage**

```
ethanol
```

**Format**

A data frame with 88 observations on the following 3 variables.

**NOx** Concentration of nitrogen oxides (NO and NO<sub>2</sub>) in micrograms/J.

**C** Compression ratio of the engine.

**E** Equivalence ratio—a measure of the richness of the air and ethanol fuel mixture.

**Author(s)**

Documentation contributed by Kevin Wright.

**Source**

Brinkman, N.D. (1981) Ethanol Fuel—A Single-Cylinder Engine Study of Efficiency and Exhaust Emissions. *SAE transactions*, **90**, 1410–1424.

**References**

Cleveland, William S. (1993). *Visualizing Data*. Hobart Press, Summit, New Jersey.

**Examples**

```
## Constructing panel functions on the fly
EE <- equal.count(ethanol$E, number=9, overlap=1/4)
xyplot(NOx ~ C | EE, data = ethanol,
       prepanel = function(x, y) prepanel.loess(x, y, span = 1),
       xlab = "Compression ratio", ylab = "NOx (micrograms/J)",
       panel = function(x, y) {
         panel.grid(h=-1, v= 2)
         panel.xyplot(x, y)
         panel.loess(x,y, span=1)
       },
       aspect = "xy")

# Wireframe loess surface fit. See Figure 4.61 from Cleveland.
require(stats)
with(ethanol, {
  eth.lo <- loess(NOx ~ C * E, span = 1/3, parametric = "C",
                 drop.square = "C", family="symmetric")
  eth.marginal <- list(C = seq(min(C), max(C), length.out = 25),
                     E = seq(min(E), max(E), length.out = 25))
  eth.grid <- expand.grid(eth.marginal)
  eth.fit <- predict(eth.lo, eth.grid)
  wireframe(eth.fit ~ eth.grid$C * eth.grid$E,
            shade=TRUE,
            screen = list(z = 40, x = -60, y=0),
            distance = .1,
            xlab = "C", ylab = "E", zlab = "NOx")
})
```

---

H\_melanoma

*Melanoma skin cancer incidence*

---

**Description**

These data from the Connecticut Tumor Registry present age-adjusted numbers of melanoma skin-cancer incidences per 100,000 people in Connecticut for the years from 1936 to 1972.

**Usage**

melanoma

**Format**

A data frame with 37 observations on the following 2 variables.

**year** Years 1936 to 1972.

**incidence** Rate of melanoma cancer per 100,000 population.

**Note**

This dataset is not related to the `melanoma` dataset in the `boot` package with the same name.

The S-PLUS 6.2 help for the melanoma data says that the incidence rate is per *million*, but this is not consistent with data found at the National Cancer Institute (<http://www.nci.nih.gov>).

**Author(s)**

Documentation contributed by Kevin Wright.

**Source**

Houghton, A., E. W. Munster, and M. V. Viola. (1978). Increased Incidence of Malignant Melanoma After Peaks of Sunspot Activity. *The Lancet*, **8**, 759–760.

**References**

Cleveland, William S. (1993). *Visualizing Data*. Hobart Press, Summit, New Jersey.

**Examples**

```
# Time-series plot. Figure 3.64 from Cleveland.
xyplot(incidence ~ year,
       data = melanoma,
       aspect = "xy",
       panel = function(x, y)
         panel.xyplot(x, y, type="o", pch = 16),
       ylim = c(0, 6),
       xlab = "Year",
       ylab = "Incidence")
```

---

H\_singer

*Heights of New York Choral Society singers*

---

**Description**

Heights in inches of the singers in the New York Choral Society in 1979. The data are grouped according to voice part. The vocal range for each voice part increases in pitch according to the following order: Bass 2, Bass 1, Tenor 2, Tenor 1, Alto 2, Alto 1, Soprano 2, Soprano 1.

**Usage**

`singer`

**Format**

A data frame with 235 observations on the following 2 variables.

**height** Height in inches of the singers.

**voice.part** (Unordered) factor with levels "Bass 2", "Bass 1", "Tenor 2", "Tenor 1", "Alto 2", "Alto 1", "Soprano 2", "Soprano 1".

**Author(s)**

Documentation contributed by Kevin Wright.

**Source**

Chambers, J.M., W. S. Cleveland, B. Kleiner, and P. A. Tukey. (1983). *Graphical Methods for Data Analysis*. Chapman and Hall, New York.

**References**

Cleveland, William S. (1993). *Visualizing Data*. Hobart Press, Summit, New Jersey.

**Examples**

```
# Separate histogram for each voice part (Figure 1.2 from Cleveland)
histogram(~ height | voice.part,
          data = singer,
          aspect=1,
          layout = c(2, 4),
          nint=15,
          xlab = "Height (inches)")

# Quantile-Quantile plot (Figure 2.11 from Cleveland)
qqmath(~ height | voice.part,
       data=singer,
       aspect=1,
       layout=c(2,4),
       prepanel = prepanel.qqmathline,
       panel = function(x, ...) {
         panel.grid()
         panel.qqmathline(x, ...)
         panel.qqmath(x, ...)
       },
       xlab = "Unit Normal Quantile",
       ylab="Height (inches)")
```

---

I\_lset

---

*Interface to modify Trellis Settings - Deprecated*


---

**Description**

A (hopefully) simpler alternative to `trellis.par.get/set`. This is deprecated, and the same functionality is now available with `trellis.par.set`

**Usage**

```
lset(theme = col.whitebg())
```

**Arguments**

`theme` a list describing how to change the settings of the current active device. Valid components are those in the list returned by `trellis.par.get()`. Each component must itself be a list, with one or more of the appropriate components (need not have all components). Changes are made to the settings for the currently active device only.

**Author(s)**

Deepayan Sarkar <Deepayan.Sarkar@R-project.org>





## Chapter 18

# The mgcv package

---

mgcv-package

*GAMs with GCV/AIC/REML smoothness estimation and GAMMs by REML/PQL*

---

### Description

mgcv provides functions for generalized additive modelling ([gam](#) and [bam](#)) and generalized additive mixed modelling ([gamm](#), and [random.effects](#)). The term GAM is taken to include any GLM estimated by quadratically penalized (possibly quasi-) likelihood maximization.

Particular features of the package are facilities for automatic smoothness selection, and the provision of a variety of smooths of more than one variable. User defined smooths can be added. A Bayesian approach to confidence/credible interval calculation is provided. Linear functionals of smooths, penalization of parametric model terms and linkage of smoothing parameters are all supported. Lower level routines for generalized ridge regression and penalized linearly constrained least squares are also available.

### Details

mgcv provides generalized additive modelling functions [gam](#), [predict.gam](#) and [plot.gam](#), which are very similar in use to the S functions of the same name designed by Trevor Hastie (with some extensions). However the underlying representation and estimation of the models is based on a penalized regression spline approach, with automatic smoothness selection. A number of other functions such as [summary.gam](#) and [anova.gam](#) are also provided, for extracting information from a fitted [gamObject](#).

Use of [gam](#) is much like use of [glm](#), except that within a [gam](#) model formula, isotropic smooths of any number of predictors can be specified using [s](#) terms, while scale invariant smooths of any number of predictors can be specified using [te](#) terms. [smooth.terms](#) provides an overview of the built in smooth classes, and [random.effects](#) should be referred to for an overview of random effects terms. Estimation is by penalized likelihood or quasi-likelihood maximization, with smoothness selection by GCV, GACV, gAIC/UBRE or (RE)ML. See [gam](#), [gam.models](#), [linear.functional.terms](#) and [gam.selection](#) for some discussion of model specification and selection. For detailed control of fitting see [gam.convergence](#), [gam](#) arguments [method](#) and [optimizer](#) and [gam.control](#). For checking and visualization see [gam.check](#), [choose.k](#), [vis.gam](#) and [plot.gam](#). While a number of types of smoother are built into the package, it is also extendable with user defined smooths, see [smooth.construct](#), for example.

A Bayesian approach to smooth modelling is used to derive standard errors on predictions, and hence credible intervals. The Bayesian covariance matrix for the model coefficients is returned in `Vp` of the `gamObject`. See `predict.gam` for examples of how this can be used to obtain credible regions for any quantity derived from the fitted model, either directly, or by direct simulation from the posterior distribution of the model coefficients. Approximate p-values can also be obtained for testing individual smooth terms for equality to the zero function, using similar ideas. Frequentist approximations can be used for hypothesis testing based model comparison. See `anova.gam` and `summary.gam` for more on hypothesis testing.

For large datasets (that is large `n`) see `bam` which is a version of `gam` with a much reduced memory footprint.

The package also provides a generalized additive mixed modelling function, `gamm`, based on a PQL approach and `lme` from the `nlme` library (for an `lme4` based version, see package `gamm4`). `gamm` is particularly useful for modelling correlated data (i.e. where a simple independence model for the residual variation is inappropriate). In addition, low level routine `magic` can fit models to data with a known correlation structure.

Some underlying GAM fitting methods are available as low level fitting functions: see `magic` and `mgcv`. But there is little functionality that can not be more conveniently accessed via `gam`. Penalized weighted least squares with linear equality and inequality constraints is provided by `pcls`.

For a complete list of functions type `library(help=mgcv)`.

### Author(s)

Simon Wood <simon.wood@r-project.org>

with contributions and/or help from Kurt Hornik, Mike Lonergan, Henric Nilsson and Brian Ripley.

Maintainer: Simon Wood <simon.wood@r-project.org>

### References

Wood, S.N. (2004) Stable and efficient multiple smoothing parameter estimation for generalized additive models. *J. Amer. Statist. Ass.* 99:673-686.

Wood, S.N. (2006) *Generalized Additive Models: an introduction with R*, CRC

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. *J.R.Statist.Soc.B* 70(3):495-518

### Examples

```
## see examples for gam and gamm
```

---

anova.gam

*Approximate hypothesis tests related to GAM fits*

---

### Description

Performs hypothesis tests relating to one or more fitted `gam` objects. For a single fitted `gam` object, Wald tests of the significance of each parametric and smooth term are performed. Otherwise the fitted models are compared using an analysis of deviance table. The tests are usually approximate, unless the models are un-penalized. Simulation evidence suggests that best p-value performance results from using ML estimated smoothing parameters.

**Usage**

```
## S3 method for class 'gam':
anova(object, ..., dispersion = NULL, test = NULL,
       alpha = 0, freq = FALSE)
## S3 method for class 'anova.gam':
print(x, digits = max(3, getOption("digits") - 3), ...)
```

**Arguments**

<code>object, ...</code>	fitted model objects of class <code>gam</code> as produced by <code>gam()</code> .
<code>x</code>	an <code>anova.gam</code> object produced by a single model call to <code>anova.gam()</code> .
<code>dispersion</code>	a value for the dispersion parameter: not normally used.
<code>test</code>	what sort of test to perform for a multi-model call. One of "Chisq", "F" or "Cp".
<code>alpha</code>	adjustment to degrees of freedom per estimated smoothing parameter for a term when called with a single model object. See <a href="#">summary.gam</a> for details.
<code>freq</code>	whether to use frequentist or Bayesian approximations for single smooth term p-values. See <a href="#">summary.gam</a> for details.
<code>digits</code>	number of digits to use when printing output.

**Details**

If more than one fitted model is provided than `anova.glm` is used. If only one model is provided then the significance of each model term is assessed using Wald tests: see [summary.gam](#) for details of the actual computations. In the latter case `print.anova.gam` is used as the printing method. Note that the p-values for smooth terms are approximate only: simulation evidence suggests that they work best with REML or ML smoothness selection.

**Value**

In the multi-model case `anova.gam` produces output identical to [anova.glm](#), which it in fact uses.

In the single model case an object of class `anova.gam` is produced, which is in fact an object returned from [summary.gam](#).

`print.anova.gam` simply produces tabulated output.

**WARNING**

P-values for smooth terms are only approximate.

**Author(s)**

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)> with substantial improvements by Henric Nilsson.

**See Also**

[gam](#), [predict.gam](#), [gam.check](#), [summary.gam](#)

**Examples**

```
library(mgcv)
set.seed(0)
dat <- gamSim(5, n=200, scale=2)

b<-gam(y ~ x0 + s(x1) + s(x2) + s(x3), data=dat)
anova(b)
b1<-gam(y ~ x0 + s(x1) + s(x2), data=dat)
anova(b, b1, test="F")
```

bam

*Generalized additive models for very large datasets***Description**

Fits a generalized additive model (GAM) to a very large data set, the term ‘GAM’ being taken to include any quadratically penalized GLM. The degree of smoothness of model terms is estimated as part of fitting. In use the function is much like `gam`, except that the numerical methods are designed for datasets containing upwards of several tens of thousands of data. The advantage of `bam` is much lower memory footprint than `gam`, but it can also be much faster, for large datasets.

**Usage**

```
bam(formula, family=gaussian(), data=list(), weights=NULL, subset=NULL,
    na.action=na.omit, offset=NULL, method="REML", control=gam.control(),
    scale=0, gamma=1, knots=NULL, sp=NULL, min.sp=NULL, paraPen=NULL,
    chunk.size=10000, ...)
```

**Arguments**

<code>formula</code>	A GAM formula (see <code>formula.gam</code> and also <code>gam.models</code> ). This is exactly like the formula for a GLM except that smooth terms, <code>s</code> and <code>te</code> can be added to the right hand side to specify that the linear predictor depends on smooth functions of predictors (or linear functionals of these).
<code>family</code>	This is a family object specifying the distribution and link to use in fitting etc. See <code>glm</code> and <code>family</code> for more details. A negative binomial family is provided: see <code>negbin</code> , but only the known theta case is supported by <code>bam</code> .
<code>data</code>	A data frame or list containing the model response variable and covariates required by the formula. By default the variables are taken from <code>environment(formula)</code> : typically the environment from which <code>gam</code> is called.
<code>weights</code>	prior weights on the data.
<code>subset</code>	an optional vector specifying a subset of observations to be used in the fitting process.
<code>na.action</code>	a function which indicates what should happen when the data contain ‘NA’s. The default is set by the ‘na.action’ setting of ‘options’, and is ‘na.fail’ if that is unset. The “factory-fresh” default is ‘na.omit’.
<code>offset</code>	Can be used to supply a model offset for use in fitting. Note that this offset will always be completely ignored when predicting, unlike an offset included in <code>formula</code> : this conforms to the behaviour of <code>lm</code> and <code>glm</code> .

method	The smoothing parameter estimation method. "GCV.Cp" to use GCV for unknown scale parameter and Mallows' Cp/UBRE/AIC for known scale. "GACV.Cp" is equivalent, but using GACV in place of GCV. "REML" for REML estimation, including of unknown scale, "P-REML" for REML estimation, but using a Pearson estimate of the scale. "ML" and "P-ML" are similar, but using maximum likelihood in place of REML.
control	A list of fit control parameters returned by <code>gam.control</code> .
scale	If this is positive then it is taken as the known scale parameter. Negative signals that the scale parameter is unknown. 0 signals that the scale parameter is 1 for Poisson and binomial and unknown otherwise. Note that (RE)ML methods can only work with scale parameter 1 for the Poisson and binomial cases.
gamma	It is sometimes useful to inflate the model degrees of freedom in the GCV or UBRE/AIC score by a constant multiplier. This allows such a multiplier to be supplied.
knots	this is an optional list containing user specified knot values to be used for basis construction. For most bases the user simply supplies the knots to be used, which must match up with the <code>k</code> value supplied (note that the number of knots is not always just <code>k</code> ). See <code>tprs</code> for what happens in the " <code>t<sub>p</sub></code> " / " <code>t<sub>s</sub></code> " case. Different terms can use different numbers of knots, unless they share a covariate.
sp	A vector of smoothing parameters can be provided here. Smoothing parameters must be supplied in the order that the smooth terms appear in the model formula. Negative elements indicate that the parameter should be estimated, and hence a mixture of fixed and estimated parameters is possible. If smooths share smoothing parameters then <code>length(sp)</code> must correspond to the number of underlying smoothing parameters.
min.sp	Lower bounds can be supplied for the smoothing parameters. Note that if this option is used then the smoothing parameters <code>full.sp</code> , in the returned object, will need to be added to what is supplied here to get the smoothing parameters actually multiplying the penalties. <code>length(min.sp)</code> should always be the same as the total number of penalties (so it may be longer than <code>sp</code> , if smooths share smoothing parameters).
paraPen	optional list specifying any penalties to be applied to parametric model terms. <code>gam.models</code> explains more.
chunk.size	The model matrix is created in chunks of this size, rather than ever being formed whole.
...	further arguments for passing on e.g. to <code>gam.fit</code> (such as <code>mustart</code> ).

## Details

`bam` operates by first setting up the basis characteristics for the smooths, using a representative subsample of the data. Then the model matrix is constructed in blocks using `predict.gam`. For each block the factor `R`, from the QR decomposition of the whole model matrix is updated, along with `Q'y` and the sum of squares of `y`. At the end of block processing, fitting takes place, without the need to ever form the whole model matrix.

In the generalized case, the same trick is used with the weighted model matrix and weighted pseudodata, at each step of the PIRLS. Smoothness selection is performed on the working model at each stage (performance oriented iteration), to maintain the small memory footprint. This is easy to justify in the case of GCV or Cp/UBRE/AIC based model selection, and also for REML/ML with known scale parameter. It is slightly less well justified in the REML/ML unknown scale parameter case, but it seems unlikely that this case actually behaves any less well.

Note that POI is not as stable as the default nested iteration used with `gam`, but that for very large, information rich, datasets, this is unlikely to matter much.

Note that it is possible to spend most of the computational time on basis evaluation, if an expensive basis is used. In practice this means that the default "tp" basis should be avoided: almost any other basis (e.g. "cr" or "ps") can be used in the 1D case, and tensor product smooths (te) are typically much less costly in the multi-dimensional case.

### Value

An object of class "gam" as described in `gamObject`.

### WARNINGS

The routine will be slow if the default "tp" basis is used.

You must have more unique combinations of covariates than the model has total parameters. (Total parameters is sum of basis dimensions plus sum of non-spline terms less the number of spline terms).

This routine is less stable than 'gam' for a the same dataset.

The negbin family is only supported for the \*known theta\* case.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>

### References

<http://www.maths.bath.ac.uk/~sw283/>

### See Also

`mgcv-package`, `gamObject`, `gam.models`, `smooth.terms`,  
`linear.functional.terms`, `s`, `te` `predict.gam`, `plot.gam`,  
`summary.gam`, `gam.side`, `gam.selection`, `mgcv`, `gam.control` `gam.check`,  
`linear.functional.terms` `negbin`, `magic`, `vis.gam`

### Examples

```
library(mgcv)
## following is not *very* large, for obvious reasons...

dat <- gamSim(1, n=15000, dist="normal", scale=20)
bs <- "ps"; k <- 20
b<-bam(y ~ s(x0, bs=bs, k=k) + s(x1, bs=bs, k=k) + s(x2, bs=bs, k=k) +
        s(x3, bs=bs, k=k), data=dat, method="REML")
summary(b)
plot(b, pages=1, rug=FALSE) ## plot smooths, but not rug
plot(b, pages=1, rug=FALSE, seWithMean=TRUE) ## `with intercept' CIs

ba<-bam(y ~ s(x0, bs=bs, k=k) + s(x1, bs=bs, k=k) + s(x2, bs=bs, k=k) +
        s(x3, bs=bs, k=k), data=dat, method="GCV.Cp") ## use GCV
summary(ba)

## A Poisson example...
```

```
dat <- gamSim(1, n=15000, dist="poisson", scale=.1)
b1<-bam(y ~ s(x0, bs=bs, k=k) + s(x1, bs=bs, k=k) + s(x2, bs=bs, k=k) +
        s(x3, bs=bs, k=k), data=dat, method="ML", family=poisson())
b1
```

bam.update

*Update a strictly additive bam model for new data.***Description**

Strictly additive models fitted by `bam` can be efficiently updated as new data becomes available, by simply updating the QR decomposition on which estimation is based, and re-optimizing the smoothing parameters, starting from the previous estimates. This routine implements this.

**Usage**

```
bam.update(b, data, chunk.size=10000)
```

**Arguments**

<code>b</code>	A gam object fitted by <code>bam</code> and representing a strictly additive model (i.e. gaussian errors, identity link).
<code>data</code>	Extra data to augment the original data used to obtain <code>b</code> . Must include a column of weights if the original fit was weighted.
<code>chunk.size</code>	size of subsets of data to process in one go when getting fitted values.

**Details**

`bam.update` updates the QR decomposition of the (weighted) model matrix of the GAM represented by `b` to take account of the new data. The orthogonal factor multiplied by the response vector is also updated. Given these updates the model and smoothing parameters can be re-estimated, as if the whole dataset (original and the new data) had been fitted in one go.

Note that there may be small numerical differences in fit between fitting the data all at once, and fitting in stages by updating, if the smoothing bases used have any of their details set with reference to the data (e.g. default knot locations).

**Value**

An object of class "gam" as described in `gamObject`.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

<http://www.maths.bath.ac.uk/~sw283/>



**See Also**

[mgcv-package](#), [bam](#)

**Examples**

```
library(mgcv)
## following is not *very* large, for obvious reasons...
set.seed(8)

dat <- gamSim(1, n=5000, dist="normal", scale=5)
dat[c(50, 13, 3000, 3005, 3100), ] <- NA
dat1 <- dat[4001:5000, ]
dat0 <- dat[1:4000, ]
bs <- "ps"; k <- 20
method <- "GCV.Cp"
b <- bam(y ~ s(x0, bs=bs, k=k) + s(x1, bs=bs, k=k) + s(x2, bs=bs, k=k) +
         s(x3, bs=bs, k=k), data=dat0, method=method)

b1 <- bam.update(b, dat1)

b2 <- bam.update(bam.update(b, dat1[1:500, ]), dat1[501:1000, ])

b3 <- bam(y ~ s(x0, bs=bs, k=k) + s(x1, bs=bs, k=k) + s(x2, bs=bs, k=k) +
         s(x3, bs=bs, k=k), data=dat, method=method)
b1; b2; b3

summary(b1); summary(b2); summary(b3)
```

---

choose.k

*Basis dimension choice for smooths*

---

**Description**

Choosing the basis dimension, and checking the choice, when using penalized regression smoothers.

Penalized regression smoothers gain computational efficiency by virtue of being defined using a basis of relatively modest size,  $k$ . When setting up models in the `mgcv` package, using `s` or `te` terms in a model formula,  $k$  must be chosen: the defaults are essentially arbitrary.

In practice  $k-1$  (or  $k$ ) sets the upper limit on the degrees of freedom associated with an `s` smooth (1 degree of freedom is usually lost to the identifiability constraint on the smooth). For `te` smooths the upper limit of the degrees of freedom is given by the product of the  $k$  values provided for each marginal smooth less one, for the constraint. However the actual effective degrees of freedom are controlled by the degree of penalization selected during fitting, by GCV, AIC, REML or whatever is specified. The exception to this is if a smooth is specified using the `fx=TRUE` option, in which case it is unpenalized.

So, exact choice of  $k$  is not generally critical: it should be chosen to be large enough that you are reasonably sure of having enough degrees of freedom to represent the underlying ‘truth’ reasonably well, but small enough to maintain reasonable computational efficiency. Clearly ‘large’ and ‘small’ are dependent on the particular problem being addressed.

As with all model assumptions, it is useful to be able to check the choice of  $k$  informally. If the effective degrees of freedom for a model term are estimated to be much less than  $k-1$  then this is unlikely to be very worthwhile, but as the EDF approach  $k-1$ , checking can be important. A useful general purpose approach goes as follows: (i) fit your model and extract the deviance residuals; (ii) for each smooth term in your model, fit an equivalent, single, smooth to the residuals, using a substantially increased  $k$  to see if there is pattern in the residuals that could potentially be explained by increasing  $k$ . Examples are provided below.

The obvious, but more costly, alternative is simply to increase the suspect  $k$  and refit the original model. If there are no statistically important changes as a result of doing this, then  $k$  was large enough. (Change in the smoothness selection criterion, and/or the effective degrees of freedom, when  $k$  is increased, provide the obvious numerical measures for whether the fit has changed substantially.)

One scenario that can cause confusion is this: a model is fitted with  $k=10$  for a smooth term, and the EDF for the term is estimated as 7.6, some way below the maximum of 9. The model is then refitted with  $k=20$  and the EDF increases to 8.7 - what is happening - how come the EDF was not 8.7 the first time around? The explanation is that the function space with  $k=20$  contains a larger subspace of functions with EDF 8.7 than did the function space with  $k=10$ : one of the functions in this larger subspace fits the data a little better than did any function in the smaller subspace. These subtleties seldom have much impact on the statistical conclusions to be drawn from a model fit, however.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>

### References

Wood, S.N. (2006) Generalized Additive Models: An Introduction with R. CRC.  
<http://www.maths.bath.ac.uk/~sw283/>

### Examples

```
## Simulate some data ....
library(mgcv)
set.seed(0)
dat <- gamSim(1,n=400,scale=2)

## fit a GAM with quite low `k`
b<-gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=6)+s(x3,k=6),data=dat)
plot(b,pages=1)

## Economical tactic (see below for more obvious approach)....
## check for residual pattern, removeable by increasing `k`
## typically `k`, below, should be substantially larger than
## the original, `k` but certainly less than n/2.
## Note use of cheap "cs" shrinkage smoothers, and gamma=1.4
## to reduce chance of overfitting...
rsd <- residuals(b)
gam(rsd~s(x0,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x1,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x2,k=40,bs="cs"),gamma=1.4,data=dat) ## `k` too low
gam(rsd~s(x3,k=40,bs="cs"),gamma=1.4,data=dat) ## fine

## similar example with multi-dimensional smooth
```

```

b1 <- gam(y~s(x0)+s(x1,x2,k=15)+s(x3),data=dat)
rsd <- residuals(b1)
gam(rsd~s(x0,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x1,x2,k=100,bs="ts"),gamma=1.4,data=dat) ## `k' too low
gam(rsd~s(x3,k=40,bs="cs"),gamma=1.4,data=dat) ## fine

## and a `te' example
b2 <- gam(y~s(x0)+te(x1,x2,k=4)+s(x3),data=dat)
rsd <- residuals(b2)
gam(rsd~s(x0,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~te(x1,x2,k=10,bs="cs"),gamma=1.4,data=dat) ## `k' too low
gam(rsd~s(x3,k=40,bs="cs"),gamma=1.4,data=dat) ## fine

## same approach works with other families in the original model
dat <- gamSim(1,n=400,scale=.25,dist="poisson")
bp<-gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=6)+s(x3,k=6),
        family=poisson,data=dat)
rsd <- residuals(bp)
gam(rsd~s(x0,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x1,k=40,bs="cs"),gamma=1.4,data=dat) ## fine
gam(rsd~s(x2,k=40,bs="cs"),gamma=1.4,data=dat) ## `k' too low
gam(rsd~s(x3,k=40,bs="cs"),gamma=1.4,data=dat) ## fine

rm(dat)

## More obvious, but more expensive tactic... Just increase
## suspicious k until fit is stable.

set.seed(0)
dat <- gamSim(1,n=400,scale=2)
## fit a GAM with quite low `k'
b <- gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=6)+s(x3,k=6),
        data=dat,method="REML")
b
## edf for 3rd smooth is highest as proportion of k -- increase k
b <- gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=12)+s(x3,k=6),
        data=dat,method="REML")
b
## edf substantially up, -ve REML substantially down
b <- gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=24)+s(x3,k=6),
        data=dat,method="REML")
b
## slight edf increase and -ve REML change
b <- gam(y~s(x0,k=6)+s(x1,k=6)+s(x2,k=40)+s(x3,k=6),
        data=dat,method="REML")
b
## definitely stabilized (but really k around 20 would have been fine)

```

---

cSplineDes

*Evaluate cyclic B spline basis*


---

### Description

Uses `splineDesign` to set up the model matrix for a cyclic B-spline basis.

**Usage**

```
cSplineDes(x, knots, ord = 4)
```

**Arguments**

x	covariate values for smooth.
knots	The knot locations: the range of these must include all the data.
ord	order of the basis. 4 is a cubic spline basis. Must be >1.

**Details**

The routine is a wrapper that sets up a B-spline basis, where the basis functions wrap at the first and last knot locations.

**Value**

A matrix with `length(x)` rows and `length(knots)-1` columns.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**See Also**

[cyclic.p.spline](#)

**Examples**

```
## create some x's and knots...
n <- 200
x <- 0:(n-1)/(n-1);k<- 0:5/5
X <- cSplineDes(x,k) ## cyclic spline design matrix
## plot evaluated basis functions...
plot(x,X[,1],type="l"); for (i in 2:5) lines(x,X[,i],col=i)
## check that the ends match up....
ee <- X[1,]-X[n,];ee
tol <- .Machine$double.eps^.75
if (all.equal(ee,ee*0,tol=tol)!=TRUE)
  stop("cyclic spline ends don't match!")

## similar with uneven data spacing...
x <- sort(runif(n)) + 1 ## sorting just makes end checking easy
k <- seq(min(x),max(x),length=8) ## create knots
X <- cSplineDes(x,k) ## get cyclic spline model matrix
plot(x,X[,1],type="l"); for (i in 2:ncol(X)) lines(x,X[,i],col=i)
ee <- X[1,]-X[n,];ee ## do ends match??
tol <- .Machine$double.eps^.75
if (all.equal(ee,ee*0,tol=tol)!=TRUE)
  stop("cyclic spline ends don't match!")
```

---

`exclude.too.far`      *Exclude prediction grid points too far from data*

---

### Description

Takes two arrays defining the nodes of a grid over a 2D covariate space and two arrays defining the location of data in that space, and returns a logical vector with elements `TRUE` if the corresponding node is too far from data and `FALSE` otherwise. Basically a service routine for `vis.gam` and `plot.gam`.

### Usage

```
exclude.too.far(g1, g2, d1, d2, dist)
```

### Arguments

<code>g1</code>	co-ordinates of grid relative to first axis.
<code>g2</code>	co-ordinates of grid relative to second axis.
<code>d1</code>	co-ordinates of data relative to first axis.
<code>d2</code>	co-ordinates of data relative to second axis.
<code>dist</code>	how far away counts as too far. Grid and data are first scaled so that the grid lies exactly in the unit square, and <code>dist</code> is a distance within this unit square.

### Details

Linear scalings of the axes are first determined so that the grid defined by the nodes in `g1` and `g2` lies exactly in the unit square (i.e. on  $[0,1]$  by  $[0,1]$ ). These scalings are applied to `g1`, `g2`, `d1` and `d2`. The minimum Euclidean distance from each node to a datum is then determined and if it is greater than `dist` the corresponding entry in the returned array is set to `TRUE` (otherwise to `FALSE`). The distance calculations are performed in compiled code for speed without storage overheads.

### Value

A logical array with `TRUE` indicating a node in the grid defined by `g1`, `g2` that is ‘too far’ from any datum.

### Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

### References

<http://www.maths.bath.ac.uk/~sw283/>

### See Also

[vis.gam](#)

**Examples**

```
library(mgcv)
x<-rnorm(100);y<-rnorm(100) # some "data"
n<-40 # generate a grid...
mx<-seq(min(x),max(x),length=n)
my<-seq(min(y),max(y),length=n)
gx<-rep(mx,n);gy<-rep(my,rep(n,n))
tf<-exclude.too.far(gx,gy,x,y,0.1)
plot(gx[!tf],gy[!tf],pch=".");points(x,y,col=2)
```

---

extract.lme.cov	<i>Extract the data covariance matrix from an lme object</i>
-----------------	--

---

**Description**

This is a service routine for [gamm](#). Extracts the estimated covariance matrix of the data from an `lme` object, allowing the user control about which levels of random effects to include in this calculation. `extract.lme.cov` forms the full matrix explicitly: `extract.lme.cov2` tries to be more economical than this.

**Usage**

```
extract.lme.cov(b, data, start.level=1)
extract.lme.cov2(b, data, start.level=1)
```

**Arguments**

<code>b</code>	A fitted model object returned by a call to <a href="#">lme</a> .
<code>data</code>	The data frame/ model frame that was supplied to <a href="#">lme</a> .
<code>start.level</code>	The level of nesting at which to start including random effects in the calculation. This is used to allow smooth terms to be estimated as random effects, but treated like fixed effects for variance calculations.

**Details**

The random effects, correlation structure and variance structure used for a linear mixed model combine to imply a covariance matrix for the response data being modelled. These routines extract that covariance matrix. The process is slightly complicated, because different components of the fitted model object are stored in different orders (see function code for details!).

The `extract.lme.cov` calculation is not optimally efficient, since it forms the full matrix, which may in fact be sparse. `extract.lme.cov2` is more efficient. If the covariance matrix is diagonal, then only the leading diagonal is returned; if it can be written as a block diagonal matrix (under some permutation of the original data) then a list of matrices defining the non-zero blocks is returned along with an index indicating which row of the original data each row/column of the block diagonal matrix relates to. The block sizes are defined by the coarsest level of grouping in the random effect structure.

[gamm](#) uses `extract.lme.cov2`.

`extract.lme.cov` does not currently deal with the situation in which the grouping factors for a correlation structure are finer than those for the random effects. `extract.lme.cov2` does deal with this situation.

**Value**

For `extract.lme.cov` an estimated covariance matrix.

For `extract.lme.cov2` a list containing the estimated covariance matrix and an indexing array. The covariance matrix is stored as the elements on the leading diagonal, a list of the matrices defining a block diagonal matrix, or a full matrix if the previous two options are not possible.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

For `lme` see:

Pinheiro J.C. and Bates, D.M. (2000) Mixed effects Models in S and S-PLUS. Springer

For details of how GAMMs are set up here for estimation using `lme` see:

Wood, S.N. (2006) Low rank scale invariant tensor product smooths for Generalized Additive Mixed Models. *Biometrics* 62(4):1025-1036

or

Wood S.N. (2006) Generalized Additive Models: An Introduction with R. Chapman and Hall/CRC Press.

<http://www.maths.bath.ac.uk/~sw283/>

**See Also**

[gamm](#), [formXtViX](#)

**Examples**

```
library(nlme)
data(Rail)
b <- lme(travel~1,Rail,~1|Rail)
extract.lme.cov(b,Rail)
```

---

fix.family.link      *Modify families for use in GAM fitting*

---

**Description**

Generalized Additive Model fitting by ‘outer’ iteration, requires extra derivatives of the variance and link functions to be added to family objects. The functions add what is needed.

**Usage**

```
fix.family.link(fam)
fix.family.var(fam)
fix.family.ls(fam)
```

**Arguments**

fam                      A family.

## Details

Outer iteration GAM estimation requires derivatives of the GCV, UBRE/gAIC, GACV, REML or ML score, which are obtained by finding the derivatives of the model coefficients w.r.t. the log smoothing parameters, using the implicit function theorem. The expressions for the derivatives require the second and third derivatives of the link w.r.t. the mean (and the 4th derivatives if Fisher scoring is not used). Also required are the first and second derivatives of the variance function w.r.t. the mean (plus the third derivative if Fisher scoring is not used). Finally REML or ML estimation of smoothing parameters requires the log saturated likelihood and its first two derivatives w.r.t. the scale parameter. These functions add functions evaluating these quantities to a family.

If the family already has functions `dvar`, `d2var`, `d3var`, `d2link`, `d3link`, `d4link` and for RE/ML `ls`, then these functions simply return the family unmodified: this allows non-standard links to be used with `gam` when using outer iteration (performance iteration operates with unmodified families). Note that if you only need Fisher scoring then `d4link` and `d3var` can be dummy, as they are ignored. Similarly `ls` is only needed for RE/ML.

The `dvar` function is a function of a mean vector, `mu`, and returns a vector of corresponding first derivatives of the family variance function. The `d2link` function is also a function of a vector of mean values, `mu`: it returns a vector of second derivatives of the link, evaluated at `mu`. Higher derivatives are defined similarly.

If modifying your own family, note that you can often get away with supplying only a `dvar` and `d2var`, function if your family only requires links that occur in one of the standard families.

## Value

A family object with extra component functions `dvar`, `d2var`, `d2link`, `d3link`, `d4link` and `ls`.

## Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

## See Also

[gam.fit3](#)

---

fixDependence

*Detect linear dependencies of one matrix on another*

---

## Description

Identifies columns of a matrix `X2` which are linearly dependent on columns of a matrix `X1`. Primarily of use in setting up identifiability constraints for nested GAMs.

## Usage

```
fixDependence(X1, X2, tol=.Machine$double.eps^.5)
```



**Arguments**

X1	A matrix.
X2	A matrix, the columns of which may be partially linearly dependent on the columns of X1.
tol	The tolerance to use when assessing linear dependence.

**Details**

The algorithm uses a simple approach based on QR decomposition: see Wood (2006, section 4.10.2) for details.

**Value**

An array of the columns of X2 which are linearly dependent on columns of X1. NULL if the two matrices are independent.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

Wood S.N. (2006) Generalized Additive Models: An Introduction with R. Chapman and Hall/CRC Press.

**Examples**

```
n<-20;c1<-4;c2<-7
X1<-matrix(runif(n*c1),n,c1)
X2<-matrix(runif(n*c2),n,c2)
X2[,3]<-X1[,2]+X2[,4]*.1
X2[,5]<-X1[,1]*.2+X1[,2]*.04
fixDependence(X1,X2)
```

---

formula.gam

*GAM formula*

---

**Description**

Description of [gam](#) formula (see Details), and how to extract it from a fitted gam object.

**Usage**

```
## S3 method for class 'gam':
formula(x, ...)
```

**Arguments**

x	fitted model objects of class gam (see <a href="#">gamObject</a> ) as produced by gam().
...	un-used in this case

## Details

The formula supplied to `gam` is exactly like that supplied to `glm` except that smooth terms, `s` and `te` can be added to the right hand side (and `.` is not supported in `gam` formulae).

Smooth terms are specified by expressions of the form:

```
s(x1, x2, . . . , k=12, fx=FALSE, bs="tp", by=z, id=1)
```

where `x1`, `x2`, etc. are the covariates which the smooth is a function of, and `k` is the dimension of the basis used to represent the smooth term. If `k` is not specified then basis specific defaults are used. `fx` is used to indicate whether or not this term should be unpenalized, and therefore have a fixed number of degrees of freedom set by `k` (almost always `k-1`). `bs` indicates the basis to use for the smooth: the built in options are described in `smooth.terms`, and user defined smooths can be added (see `user.defined.smooth`). If `bs` is not supplied then the default "tp" (`tprs`) basis is used. `by` can be used to specify a variable by which the smooth should be multiplied. For example `gam(y~s(x, by=z))` would specify a model  $E(y) = f(x)z$  where  $f(\cdot)$  is a smooth function. The `by` option is particularly useful for models in which different functions of the same variable are required for each level of a factor and for ‘varying coefficient models’: see `gam.models`. `id` is used to give smooths identities: smooths with the same identity have the same basis, penalty and smoothing parameter (but different coefficients, so they are different functions).

An alternative for specifying smooths of more than one covariate is e.g.:

```
te(x, z, bs=c("tp", "tp"), m=c(2, 3), k=c(5, 10))
```

which would specify a tensor product smooth of the two covariates `x` and `z` constructed from marginal t.p.r.s. bases of dimension 5 and 10 with marginal penalties of order 2 and 3. Any combination of basis types is possible, as is any number of covariates. `te` provides further information.

Both `s` and `te` terms accept an `sp` argument of supplied smoothing parameters: positive values are taken as fixed values to be used, negative to indicate that the parameter should be estimated. If `sp` is supplied then it over-rides whatever is in the `sp` argument to `gam`, if it is not supplied then it defaults to all negative, but does not over-ride the `sp` argument to `gam`.

Formulae can involve nested or “overlapping” terms such as

```
y~s(x) + s(z) + s(x, z) or y~s(x, z) + s(z, v):
```

see `gam.side` for further details and examples.

Smooth terms in a `gam` formula will accept matrix arguments as covariates (and corresponding `by` variable), in which case a ‘summation convention’ is invoked. Consider the example of `s(X, Z, by=L)` where `X`, `Z` and `L` are `n` by `m` matrices. Let `F` be the `n` by `m` matrix that results from evaluating the smooth at the values in `X` and `Z`. Then the contribution to the linear predictor from the term will be `rowSums(F*L)` (note the element-wise multiplication). This convention allows the linear predictor of the GAM to depend on (a discrete approximation to) any linear functional of a smooth: see `linear.functional.terms` for more information and examples (including functional linear models/signal regression).

Note that `gam` allows any term in the model formula to be penalized (possibly by multiple penalties), via the `paraPen` argument. See `gam.models` for details and example code.

## Value

Returns the model formula, `x$formula`. Provided so that `anova` methods print an appropriate description of the model.

## Author(s)

Simon N. Wood <simon.wood@r-project.org>

**See Also**[gam](#)

---

`formXtViX`*Form component of GAMM covariance matrix*

---

**Description**

This is a service routine for [gamm](#). Given,  $V$ , an estimated covariance matrix obtained using [extract.lme.cov2](#) this routine forms  $X^T V^{-1} X$  as efficiently as possible, given the structure of  $V$  (usually sparse).

**Usage**`formXtViX(V, X)`**Arguments**

<code>V</code>	A data covariance matrix list returned from <a href="#">extract.lme.cov2</a>
<code>X</code>	A model matrix.

**Details**

The covariance matrix returned by [extract.lme.cov2](#) may be in a packed and re-ordered format, since it is usually sparse. Hence a special service routine is required to form the required products involving this matrix.

**Value**

A matrix.

**Author(s)**

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

**References**

For `lme` see:

Pinheiro J.C. and Bates, D.M. (2000) Mixed effects Models in S and S-PLUS. Springer

For details of how GAMMs are set up for estimation using `lme` see:

Wood, S.N. (2006) Low rank scale invariant tensor product smooths for Generalized Additive Mixed Models. *Biometrics* 62(4):1025-1036

<http://www.maths.bath.ac.uk/~sw283/>

**See Also**

[gamm](#), [extract.lme.cov2](#)

---

full.score	<i>GCV/UBRE score for use within nlm</i>
------------	--

---

### Description

Evaluates GCV/UBRE score for a GAM, given smoothing parameters. The routine calls `gam.fit` to fit the model, and is usually called by `nlm` to optimize the smoothing parameters.

This is basically a service routine for `gam`, and is not usually called directly by users. It is only used in this context for GAMs fitted by outer iteration (see `gam.outer`) when the the outer method is "nlm.fd" (see `gam` argument `optimizer`).

### Usage

```
full.score(sp, G, family, control, gamma, ...)
```

### Arguments

<code>sp</code>	The logs of the smoothing parameters
<code>G</code>	a list returned by <code>mgcv::gam.setup</code>
<code>family</code>	The family object for the GAM.
<code>control</code>	a list returned by <code>gam.control</code>
<code>gamma</code>	the degrees of freedom inflation factor (usually 1).
<code>...</code>	other arguments, typically for passing on to <code>gam.fit</code> .

### Value

The value of the GCV/UBRE score, with attribute "full.gam.object" which is the full object returned by `gam.fit`.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>

---

gam	<i>Generalized additive models with integrated smoothness estimation</i>
-----	--

---

### Description

Fits a generalized additive model (GAM) to data, the term 'GAM' being taken to include any quadratically penalized GLM. The degree of smoothness of model terms is estimated as part of fitting. `gam` can also fit any GLM subject to multiple quadratic penalties (including estimation of degree of penalization). Isotropic or scale invariant smooths of any number of variables are available as model terms, as are linear functionals of such smooths; confidence/credible intervals are readily available for any quantity predicted using a fitted model; `gam` is extendable: users can add smooths.

Smooth terms are represented using penalized regression splines (or similar smoothers) with smoothing parameters selected by GCV/UBRE/AIC/REML or by regression splines with fixed degrees of freedom (mixtures of the two are permitted). Multi-dimensional smooths are

available using penalized thin plate regression splines (isotropic) or tensor product splines (when an isotropic smooth is inappropriate). For an overview of the smooths available see [smooth.terms](#). For more on specifying models see [gam.models](#), [random.effects](#) and [linear.functional.terms](#). For more on model selection see [gam.selection](#).

`gam()` is not a clone of what S-PLUS provides: the major differences are (i) that by default estimation of the degree of smoothness of model terms is part of model fitting, (ii) a Bayesian approach to variance estimation is employed that makes for easier confidence interval calculation (with good coverage probabilities), (iii) that the model can depend on any (bounded) linear functional of smooth terms, and, (iv) the parametric part of the model can be penalized, (v) simple random effects can be incorporated, and (vi) the facilities for incorporating smooths of more than one variable are different: specifically there are no `lo` smooths, but instead (a) `s` terms can have more than one argument, implying an isotropic smooth and (b) `te` smooths are provided as an effective means for modelling smooth interactions of any number of variables via scale invariant tensor product smooths. If you want a clone of what S-PLUS provides use [gam](#) from package `gam`.

For very large datasets see [bam](#), for mixed GAM see [gamm](#) and [random.effects](#).

## Usage

```
gam(formula, family=gaussian(), data=list(), weights=NULL, subset=NULL,
    na.action, offset=NULL, method="GCV.Cp",
    optimizer=c("outer", "newton"), control=gam.control(), scale=0,
    select=FALSE, knots=NULL, sp=NULL, min.sp=NULL, H=NULL, gamma=1,
    fit=TRUE, paraPen=NULL, G=NULL, in.out, ...)
```

## Arguments

<code>formula</code>	A GAM formula (see <a href="#">formula.gam</a> and also <a href="#">gam.models</a> ). This is exactly like the formula for a GLM except that smooth terms, <code>s</code> and <code>te</code> can be added to the right hand side to specify that the linear predictor depends on smooth functions of predictors (or linear functionals of these).
<code>family</code>	This is a family object specifying the distribution and link to use in fitting etc. See <a href="#">glm</a> and <a href="#">family</a> for more details. A negative binomial family is provided: see <a href="#">negbin</a> .
<code>data</code>	A data frame or list containing the model response variable and covariates required by the formula. By default the variables are taken from <code>environment(formula)</code> : typically the environment from which <code>gam</code> is called.
<code>weights</code>	prior weights on the data.
<code>subset</code>	an optional vector specifying a subset of observations to be used in the fitting process.
<code>na.action</code>	a function which indicates what should happen when the data contain 'NA's. The default is set by the 'na.action' setting of 'options', and is 'na.fail' if that is unset. The "factory-fresh" default is 'na.omit'.
<code>offset</code>	Can be used to supply a model offset for use in fitting. Note that this offset will always be completely ignored when predicting, unlike an offset included in <code>formula</code> : this conforms to the behaviour of <code>lm</code> and <code>glm</code> .
<code>control</code>	A list of fit control parameters returned by <a href="#">gam.control</a> .
<code>method</code>	The smoothing parameter estimation method. "GCV.Cp" to use GCV for unknown scale parameter and Mallows' Cp/UBRE/AIC for known scale. "GACV.Cp" is equivalent, but using GACV in place of GCV. "REML" for

	REML estimation, including of unknown scale, "P-REML" for REML estimation, but using a Pearson estimate of the scale. "ML" and "P-ML" are similar, but using maximum likelihood in place of REML.
optimizer	An array specifying the numerical optimization method to use to optimize the smoothing parameter estimation criterion (given by method). "perf" for performance iteration. "outer" for the more stable direct approach. "outer" can use several alternative optimizers, specified in the second element of optimizer: "newton" (default), "bfgs", "optim", "nlm" and "nlm.fd" (the latter is based entirely on finite differenced derivatives and is very slow).
scale	If this is positive then it is taken as the known scale parameter. Negative signals that the scale parameter is unknown. 0 signals that the scale parameter is 1 for Poisson and binomial and unknown otherwise. Note that (RE)ML methods can only work with scale parameter 1 for the Poisson and binomial cases.
select	If this is TRUE then gam can add an extra penalty to each term so that it can be penalized to zero. This means that the smoothing parameter estimation that is part of fitting can completely remove terms from the model. If the corresponding smoothing parameter is estimated as zero then the extra penalty has no effect.
knots	this is an optional list containing user specified knot values to be used for basis construction. For most bases the user simply supplies the knots to be used, which must match up with the k value supplied (note that the number of knots is not always just k). See <code>tprs</code> for what happens in the "tp"/"ts" case. Different terms can use different numbers of knots, unless they share a covariate.
sp	A vector of smoothing parameters can be provided here. Smoothing parameters must be supplied in the order that the smooth terms appear in the model formula. Negative elements indicate that the parameter should be estimated, and hence a mixture of fixed and estimated parameters is possible. If smooths share smoothing parameters then <code>length(sp)</code> must correspond to the number of underlying smoothing parameters.
min.sp	Lower bounds can be supplied for the smoothing parameters. Note that if this option is used then the smoothing parameters <code>full.sp</code> , in the returned object, will need to be added to what is supplied here to get the smoothing parameters actually multiplying the penalties. <code>length(min.sp)</code> should always be the same as the total number of penalties (so it may be longer than <code>sp</code> , if smooths share smoothing parameters).
H	A user supplied fixed quadratic penalty on the parameters of the GAM can be supplied, with this as its coefficient matrix. A common use of this term is to add a ridge penalty to the parameters of the GAM in circumstances in which the model is close to un-identifiable on the scale of the linear predictor, but perfectly well defined on the response scale.
gamma	It is sometimes useful to inflate the model degrees of freedom in the GCV or UBRE/AIC score by a constant multiplier. This allows such a multiplier to be supplied.
fit	If this argument is TRUE then gam sets up the model and fits it, but if it is FALSE then the model is set up and an object G containing what would be required to fit is returned. See argument G.
paraPen	optional list specifying any penalties to be applied to parametric model terms. <a href="#">gam.models</a> explains more.

G	Usually NULL, but may contain the object returned by a previous call to <code>gam</code> with <code>fit=FALSE</code> , in which case all other arguments are ignored except for <code>gamma</code> , <code>in.out</code> , <code>scale</code> , <code>control</code> , <code>method</code> optimizer and <code>fit</code> .
<code>in.out</code>	optional list for initializing outer iteration. If supplied then this must contain two elements: <code>sp</code> should be an array of initialization values for all smoothing parameters (there must be a value for all smoothing parameters, whether fixed or to be estimated, but those for fixed s.p.s are not used); <code>scale</code> is the typical scale of the GCV/UBRE function, for passing to the outer optimizer.
...	further arguments for passing on e.g. to <code>gam.fit</code> (such as <code>mustart</code> ).

## Details

A generalized additive model (GAM) is a generalized linear model (GLM) in which the linear predictor is given by a user specified sum of smooth functions of the covariates plus a conventional parametric component of the linear predictor. A simple example is:

$$\log(E(y_i)) = f_1(x_{1i}) + f_2(x_{2i})$$

where the (independent) response variables  $y_i \sim \text{Poi}$ , and  $f_1$  and  $f_2$  are smooth functions of covariates  $x_1$  and  $x_2$ . The log is an example of a link function.

If absolutely any smooth functions were allowed in model fitting then maximum likelihood estimation of such models would invariably result in complex overfitting estimates of  $f_1$  and  $f_2$ . For this reason the models are usually fit by penalized likelihood maximization, in which the model (negative log) likelihood is modified by the addition of a penalty for each smooth function, penalizing its ‘wiggleness’. To control the tradeoff between penalizing wiggleness and penalizing badness of fit each penalty is multiplied by an associated smoothing parameter: how to estimate these parameters, and how to practically represent the smooth functions are the main statistical questions introduced by moving from GLMs to GAMs.

The `mgcv` implementation of `gam` represents the smooth functions using penalized regression splines, and by default uses basis functions for these splines that are designed to be optimal, given the number basis functions used. The smooth terms can be functions of any number of covariates and the user has some control over how smoothness of the functions is measured.

`gam` in `mgcv` solves the smoothing parameter estimation problem by using the Generalized Cross Validation (GCV) criterion

$$nD/(n - DoF)^2$$

or an Un-Biased Risk Estimator (UBRE) criterion

$$D/n + 2sDoF/n - s$$

where  $D$  is the deviance,  $n$  the number of data,  $s$  the scale parameter and  $DoF$  the effective degrees of freedom of the model. Notice that UBRE is effectively just AIC rescaled, but is only used when  $s$  is known.

Alternatives are GACV, or a Laplace approximation to REML. There is some evidence that the latter may actually be the most effective choice.

Smoothing parameters are chosen to minimize the GCV, UBRE/AIC, GACV or REML scores for the model, and the main computational challenge solved by the `mgcv` package is to do this efficiently and reliably. Various alternative numerical methods are provided which can be set by argument `optimizer`.

Broadly `gam` works by first constructing basis functions and one or more quadratic penalty coefficient matrices for each smooth term in the model formula, obtaining a model matrix for the strictly parametric part of the model formula, and combining these to obtain a complete model

matrix (/design matrix) and a set of penalty matrices for the smooth terms. Some linear identifiability constraints are also obtained at this point. The model is fit using `gam.fit`, a modification of `glm.fit`. The GAM penalized likelihood maximization problem is solved by Penalized Iteratively Reweighted Least Squares (P-IRLS) (see e.g. Wood 2000). Smoothing parameter selection is integrated in one of two ways. (i) ‘Performance iteration’ uses the fact that at each P-IRLS iteration a penalized weighted least squares problem is solved, and the smoothing parameters of that problem can be estimated by GCV or UBRE. Eventually, in most cases, both model parameter estimates and smoothing parameter estimates converge. (ii) Alternatively the P-IRLS scheme is iterated to convergence for each trial set of smoothing parameters, and GCV, UBRE or REML scores are only evaluated on convergence - optimization is then ‘outer’ to the P-IRLS loop: in this case the P-IRLS iteration has to be differentiated, to facilitate optimization, and `gam.fit3` is used in place of `gam.fit`. The default is the second method, outer iteration.

Several alternative basis-penalty types are built in for representing model smooths, but alternatives can easily be added (see `smooth.terms` for an overview and `smooth.construct` for how to add smooth classes). In practice the default basis is usually the best choice, but the choice of the basis dimension ( $k$  in the `s` and `te` terms) is something that should be considered carefully (the exact value is not critical, but it is important not to make it restrictively small, nor very large and computationally costly). The basis should be chosen to be larger than is believed to be necessary to approximate the smooth function concerned. The effective degrees of freedom for the smooth will then be controlled by the smoothing penalty on the term, and (usually) selected automatically (with an upper limit set by  $k-1$  or occasionally  $k$ ). Of course the  $k$  should not be made too large, or computation will be slow (or in extreme cases there will be more coefficients to estimate than there are data).

Note that `gam` assumes a very inclusive definition of what counts as a GAM: basically any penalized GLM can be used: to this end `gam` allows the non smooth model components to be penalized via argument `paraPen` and allows the linear predictor to depend on general linear functionals of smooths, via the summation convention mechanism described in `linear.functional.terms`.

Details of the default underlying fitting methods are given in Wood (2004 and 2008). Some alternative methods are discussed in Wood (2000 and 2006).

### Value

If `fit=FALSE` the function returns a list `G` of items needed to fit a GAM, but doesn’t actually fit it. Otherwise the function returns an object of class "gam" as described in `gamObject`.

### WARNINGS

You must have more unique combinations of covariates than the model has total parameters. (Total parameters is sum of basis dimensions plus sum of non-spline terms less the number of spline terms).

Automatic smoothing parameter selection is not likely to work well when fitting models to very few response data.

For data with many zeroes clustered together in the covariate space it is quite easy to set up GAMs which suffer from identifiability problems, particularly when using Poisson or binomial families. The problem is that with e.g. log or logit links, mean value zero corresponds to an infinite range on the linear predictor scale.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>



Front end design inspired by the S function of the same name based on the work of Hastie and Tibshirani (1990). Underlying methods owe much to the work of Wahba (e.g. 1990) and Gu (e.g. 2002).

## References

Key References on this implementation:

Wood, S.N. (2004) Stable and efficient multiple smoothing parameter estimation for generalized additive models. *J. Amer. Statist. Ass.* 99:673-686. [Default method for additive case (but no longer for generalized)]

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. *J.R.Statist.Soc.B* 70(3):495-518. [Generalized additive model methods]

Wood, S.N. (2003) Thin plate regression splines. *J.R.Statist.Soc.B* 65(1):95-114

Wood, S.N. (2006a) Low rank scale invariant tensor product smooths for generalized additive mixed models. *Biometrics* 62(4):1025-1036

Wood S.N. (2006b) *Generalized Additive Models: An Introduction with R*. Chapman and Hall/CRC Press.

Wood, S.N. (2006c) On confidence intervals for generalized additive models based on penalized regression splines. *Australian and New Zealand Journal of Statistics.* 48(4): 445-464.

Key Reference on GAMs and related models:

Hastie (1993) in Chambers and Hastie (1993) *Statistical Models in S*. Chapman and Hall.

Hastie and Tibshirani (1990) *Generalized Additive Models*. Chapman and Hall.

Wahba (1990) *Spline Models of Observational Data*. SIAM

Wood, S.N. (2000) Modelling and Smoothing Parameter Estimation with Multiple Quadratic Penalties. *J.R.Statist.Soc.B* 62(2):413-428 [The original mgcv paper, but no longer the default methods.]

Background References:

Green and Silverman (1994) *Nonparametric Regression and Generalized Linear Models*. Chapman and Hall.

Gu and Wahba (1991) Minimizing GCV/GML scores with multiple smoothing parameters via the Newton method. *SIAM J. Sci. Statist. Comput.* 12:383-398

Gu (2002) *Smoothing Spline ANOVA Models*, Springer.

O'Sullivan, Yandall and Raynor (1986) Automatic smoothing of regression functions in generalized linear models. *J. Am. Statist.Ass.* 81:96-103

Wood (2001) mgcv:GAMs and Generalized Ridge Regression for R. *R News* 1(2):20-25

Wood and Augustin (2002) GAMs with integrated model selection using penalized regression splines and applications to environmental modelling. *Ecological Modelling* 157:157-177

<http://www.maths.bath.ac.uk/~sw283/>

## See Also

`mgcv-package`, `gamObject`, `gam.models`, `smooth.terms`,  
`linear.functional.terms`, `s`, `te` `predict.gam`, `plot.gam`,  
`summary.gam`, `gam.side`, `gam.selection`, `mgcv`, `gam.control` `gam.check`,  
`linear.functional.terms` `negbin`, `magic`, `vis.gam`

**Examples**

```

library(mgcv)
set.seed(0) ## simulate some data...
dat <- gamSim(1,n=400,dist="normal",scale=2)
b<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat)
summary(b)
plot(b,pages=1,residuals=TRUE) ## show partial residuals
plot(b,pages=1,seWithMean=TRUE) ## `with intercept' CIs

## same fit in two parts .....
G<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),fit=FALSE,data=dat)
b<-gam(G=G)
print(b)

## change the smoothness selection method to REML
b0<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat,method="REML")
plot(b,pages=1)

## ... and do automatic terms selection as well
b1<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat,
        method="REML",select=TRUE)
plot(b1,pages=1)

## set the smoothing parameter for the first term, estimate rest ...
bp<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),sp=c(0.01,-1,-1,-1),data=dat)
plot(bp,pages=1)
## alternatively...
bp <- gam(y~s(x0,sp=.01)+s(x1)+s(x2)+s(x3),data=dat)

# set lower bounds on smoothing parameters ....
bp<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),
        min.sp=c(0.001,0.01,0,10),data=dat)
print(b);print(bp)

# same with REML
bp<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),
        min.sp=c(0.1,0.1,0,10),data=dat,method="REML")
print(b0);print(bp)

## now a GAM with 3df regression spline term & 2 penalized terms

b0<-gam(y~s(x0,k=4,fx=TRUE,bs="tp")+s(x1,k=12)+s(x2,k=15),data=dat)
plot(b0,pages=1)

## now fit a 2-d term to x0,x1
b1<-gam(y~s(x0,x1)+s(x2)+s(x3),data=dat)
par(mfrow=c(2,2))
plot(b1)

par(mfrow=c(1,1))
## now simulate poisson data...
dat <- gamSim(1,n=4000,dist="poisson",scale=.1)

```

```

## use "cr" basis to save time, with 4000 data...
b2<-gam(y~s(x0,bs="cr")+s(x1,bs="cr")+s(x2,bs="cr")+
        s(x3,bs="cr"),family=poisson,data=dat,method="REML")
plot(b2,pages=1)

## drop x3, but initialize sp's from previous fit, to
## save more time...

b2a<-gam(y~s(x0,bs="cr")+s(x1,bs="cr")+s(x2,bs="cr"),
        family=poisson,data=dat,method="REML",
        in.out=list(sp=b2$sp[1:3],scale=1))
par(mfrow=c(2,2))
plot(b2a)

par(mfrow=c(1,1))
## similar example using performance iteration
dat <- gamSim(1,n=400,dist="poisson",scale=.25)

b3<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=poisson,
        data=dat,optimizer="perf")
plot(b3,pages=1)

## repeat using GACV as in Wood 2008...

b4<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=poisson,
        data=dat,method="GACV.Cp",scale=-1)
plot(b4,pages=1)

## repeat using REML as in Wood 2009...

b5<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=poisson,
        data=dat,method="REML")
plot(b5,pages=1)

## a binary example (see later for large dataset version)...

dat <- gamSim(1,n=400,dist="binary",scale=.33)

lr.fit <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=binomial,
             data=dat,method="REML")
## plot model components with truth overlaid in red
op <- par(mfrow=c(2,2))
fn <- c("f0","f1","f2","f3");xn <- c("x0","x1","x2","x3")
for (k in 1:4) {
  plot(lr.fit,residuals=TRUE,select=k)
  ff <- dat[[fn[k]]];xx <- dat[[xn[k]]]
  ind <- sort.int(xx,index.return=TRUE)$ix
  lines(xx[ind],(ff-mean(ff))[ind]*.33,col=2)
}
par(op)
anova(lr.fit)
lr.fit1 <- gam(y~s(x0)+s(x1)+s(x2),family=binomial,
             data=dat,method="REML")
lr.fit2 <- gam(y~s(x1)+s(x2),family=binomial,
             data=dat,method="REML")
AIC(lr.fit,lr.fit1,lr.fit2)

```

```

## A Gamma example, by modify `gamSim' output...

dat <- gamSim(1,n=400,dist="normal",scale=1)
dat$f <- dat$f/4 ## true linear predictor
Ey <- exp(dat$f);scale <- .5 ## mean and GLM scale parameter
## Note that `shape' and `scale' in `rgamma' are almost
## opposite terminology to that used with GLM/GAM...
dat$y <- rgamma(Ey*0,shape=1/scale,scale=Ey*scale)
bg <- gam(y~ s(x0)+ s(x1)+s(x2)+s(x3),family=Gamma(link=log),
          data=dat,method="REML")
plot(bg,pages=1)

## For inverse Gaussian, see ?rig

## now a 2D smoothing example...

eg <- gamSim(2,n=500,scale=.1)
attach(eg)

op <- par(mfrow=c(2,2),mar=c(4,4,1,1))

contour(truth$x,truth$z,truth$f) ## contour truth
b4 <- gam(y~s(x,z),data=data) ## fit model
fit1 <- matrix(predict.gam(b4,pr,se=FALSE),40,40)
contour(truth$x,truth$z,fit1) ## contour fit
persp(truth$x,truth$z,truth$f) ## persp truth
vis.gam(b4) ## persp fit
detach(eg)
par(op)

#####
## largish dataset example with user defined knots
#####

par(mfrow=c(1,1))
eg <- gamSim(2,n=10000,scale=.5)
attach(eg)

ind<-sample(1:10000,1000,replace=FALSE)
b5<-gam(y~s(x,z,k=50),data=data,
        knots=list(x=data$x[ind],z=data$z[ind]))
vis.gam(b5)

## and a pure "knot based" spline of the same data
b6<-gam(y~s(x,z,k=100),data=data,knots=list(x= rep((1:10-0.5)/10,10),
        z=rep((1:10-0.5)/10,rep(10,10))))
vis.gam(b6,color="heat")

## varying the default large dataset behaviour via `xt'
b7 <- gam(y~s(x,z,k=50,xt=list(max.knots=1000,seed=2)),data=data)
vis.gam(b7)
detach(eg)

#####
## Approximate large dataset logistic regression for rare events
## based on subsampling the zeroes, and adding an offset to

```

```

## approximately allow for this.
## Doing the same thing, but upweighting the sampled zeroes
## leads to problems with smoothness selection, and CIs.
#####
n <- 100000 ## simulate n data
dat <- gamSim(1,n=n,dist="binary",scale=.33)
p <- binomial()$linkinv(dat$f-6) ## make 1's rare
dat$y <- rbinom(p,1,p) ## re-simulate rare response

## Now sample all the 1's but only proportion S of the 0's
S <- 0.02 ## sampling fraction of zeroes
dat <- dat[dat$y==1 | runif(n) < S,] ## sampling

## Create offset based on total sampling fraction
dat$s <- rep(log(nrow(dat)/n),nrow(dat))

lr.fit <- gam(y~s(x0,bs="cr")+s(x1,bs="cr")+s(x2,bs="cr")+s(x3,bs="cr")+
  offset(s),family=binomial,data=dat,method="REML")

## plot model components with truth overlaid in red
op <- par(mfrow=c(2,2))
fn <- c("f0","f1","f2","f3");xn <- c("x0","x1","x2","x3")
for (k in 1:4) {
  plot(lr.fit,select=k,scale=0)
  ff <- dat[[fn[k]]];xx <- dat[[xn[k]]]
  ind <- sort.int(xx,index.return=TRUE)$ix
  lines(xx[ind],(ff-mean(ff))[ind]*.33,col=2)
}
par(op)
rm(dat)

```

---

gam.check

*Some diagnostics for a fitted gam model*


---

## Description

Takes a fitted `gam` object produced by `gam()` and produces some diagnostic information about the fitting procedure and results. The default is to produce 4 residual plots, and some information about the convergence of the smoothness selection optimization.

## Usage

```
gam.check(b, ...)
```

## Arguments

`b` a fitted `gam` object as produced by `gam()`.

`...` extra graphics parameters to pass to plotting functions.

## Details

This function plots 4 standard diagnostic plots, and some other convergence diagnostics. Usually the 4 plots are various residual plots. The printed information relates to the optimization used to select smoothing parameters. For the default optimization methods the information is summarized in a readable way, but for other optimization methods, whatever is returned by way of convergence diagnostics is simply printed.

## Author(s)

Simon N. Wood <simon.wood@r-project.org>

## References

Wood S.N. (2006) Generalized Additive Models: An Introduction with R. Chapman and Hall/CRC Press.

<http://www.maths.bath.ac.uk/~sw283/>

## See Also

[choose.k](#), [gam](#), [mgcv](#), [magic](#)

## Examples

```
library(mgcv)
set.seed(0)
dat <- gamSim(1, n=200)
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3), data=dat)
plot(b, pages=1)
gam.check(b)
```

---

gam.control

*Setting GAM fitting defaults*

---

## Description

This is an internal function of package `mgcv` which allows control of the numerical options for fitting a GAM. Typically users will want to modify the defaults if model fitting fails to converge, or if the warnings are generated which suggest a loss of numerical stability during fitting. To change the default choice of fitting method, see `gam` arguments `method` and `optimizer`.

## Usage

```
gam.control(irls.reg=0.0, epsilon = 1e-06, maxit = 100,
            mgcv.tol=1e-7, mgcv.half=15, trace = FALSE,
            rank.tol=.Machine$double.eps^0.5,
            nlm=list(), optim=list(), newton=list(),
            outerPIsteps=0, idLinksBases=TRUE, scalePenalty=TRUE,
            keepData=FALSE)
```

**Arguments**

<code>irls.reg</code>	For most models this should be 0. The iteratively re-weighted least squares method by which GAMs are fitted can fail to converge in some circumstances. For example, data with many zeroes can cause problems in a model with a log link, because a mean of zero corresponds to an infinite range of linear predictor values. Such convergence problems are caused by a fundamental lack of identifiability, but do not show up as lack of identifiability in the penalized linear model problems that have to be solved at each stage of iteration. In such circumstances it is possible to apply a ridge regression penalty to the model to impose identifiability, and <code>irls.reg</code> is the size of the penalty.
<code>epsilon</code>	This is used for judging conversion of the GLM IRLS loop in <code>gam.fit</code> or <code>gam.fit3</code> .
<code>maxit</code>	Maximum number of IRLS iterations to perform.
<code>mgcv.tol</code>	The convergence tolerance parameter to use in GCV/UBRE optimization.
<code>mgcv.half</code>	If a step of the GCV/UBRE optimization method leads to a worse GCV/UBRE score, then the step length is halved. This is the number of halvings to try before giving up.
<code>trace</code>	Set this to TRUE to turn on diagnostic output.
<code>rank.tol</code>	The tolerance used to estimate the rank of the fitting problem, for methods which deal with rank deficient cases (basically all except those based on <code>mgcv</code> ).
<code>nlm</code>	list of control parameters to pass to <code>nlm</code> if this is used for outer estimation of smoothing parameters (not default). See details.
<code>optim</code>	list of control parameters to pass to <code>optim</code> if this is used for outer estimation of smoothing parameters (not default). See details.
<code>newton</code>	list of control parameters to pass to default Newton optimizer used for outer estimation of log smoothing parameters. See details.
<code>outerPIsteps</code>	The number of performance iteration steps used to initialize outer iteration.
<code>idLinksBases</code>	If smooth terms have their smoothing parameters linked via the <code>id</code> mechanism (see <code>s</code> ), should they also have the same bases. Set this to FALSE only if you are sure you know what you are doing (you should almost surely set <code>scalePenalty</code> to FALSE as well in this case).
<code>scalePenalty</code>	<code>gamm</code> is somewhat sensitive to the absolute scaling of the penalty matrices of a smooth relative to its model matrix. This option rescales the penalty matrices to accomodate this problem. Probably should be set to FALSE if you are linking smoothing parameters but have set <code>idLinkBases</code> to FALSE.
<code>keepData</code>	Should a copy of the original <code>data</code> argument be kept in the <code>gam</code> object? Strict compatibility with class <code>glm</code> would keep it, but it wastes space to do so.

**Details**

Outer iteration using `newton` is controlled by the list `newton` with the following elements: `conv.tol` (default 1e-6) is the relative convergence tolerance; `maxNstep` is the maximum length allowed for an element of the Newton search direction (default 5); `maxSstep` is the maximum length allowed for an element of the steepest descent direction (only used if Newton fails - default 2); `maxHalf` is the maximum number of step halvings to permit before giving up (default 30).

If outer iteration using `nlm` is used for fitting, then the control list `nlm` stores control arguments for calls to routine `nlm`. The list has the following named elements: (i) `ndigit` is the number of significant digits in the GCV/UBRE score - by default this is worked out from `epsilon`; (ii)

`gradtol` is the tolerance used to judge convergence of the gradient of the GCV/UBRE score to zero - by default set to  $10 \times \text{epsilon}$ ; (iii) `stepmax` is the maximum allowable log smoothing parameter step - defaults to 2; (iv) `steptol` is the minimum allowable step length - defaults to  $1e-4$ ; (v) `iterlim` is the maximum number of optimization steps allowed - defaults to 200; (vi) `check.analyticals` indicates whether the built in exact derivative calculations should be checked numerically - defaults to FALSE. Any of these which are not supplied and named in the list are set to their default values.

Outer iteration using `optim` is controlled using list `optim`, which currently has one element: `factr` which takes default value  $1e7$ .

### Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

### References

Wood, S.N. (2004) Stable and efficient multiple smoothing parameter estimation for generalized additive models. *J. Amer. Statist. Ass.* 99:673-686.

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. *J.R.Statist.Soc.B* 70(3):495-518.

<http://www.maths.bath.ac.uk/~sw283/>

### See Also

[gam](#), [gam.fit](#), [glm.control](#)

---

gam.convergence

*GAM convergence and performance issues*

---

### Description

When fitting GAMs there is a tradeoff between speed of fitting and probability of fit convergence. The default fitting options, specified by `gam` arguments `method` and `optimizer`, opt for certainty of convergence over speed of fit. In the Generalized Additive Model case it means using ‘outer’ iteration in preference to ‘performance iteration’: see [gam.outer](#) for details.

It is possible for the default ‘outer’ iteration to fail when finding initial smoothing parameters using a few steps of performance iteration (if you get a convergence failure message from `magic` when outer iterating, then this is what has happened): lower `outerPIsteps` in [gam.control](#) to fix this.

There are three things that you can try to speed up GAM fitting. (i) if you have large numbers of smoothing parameters in the generalized case, then try the `"bfgs"` method option in `gam` argument `optimizer`: this can be faster than the default. (ii) Change the `optimizer` argument to `gam` so that ‘performance iteration’ is used in place of the default outer iteration. Usually performance iteration converges well and it can sometimes be quicker than the default outer iteration. (iii) For large datasets it may be worth changing the smoothing basis to use `bs="cr"` (see [s](#) for details) for 1-d smooths, and to use `te` smooths in place of `s` smooths for smooths of more than one variable. This is because the default thin plate regression spline basis `"tp"` is costly to set up for large datasets (much over 1000 data, say).



If the GAM estimation process fails to converge when using performance iteration, then switch to outer iteration via the `optimizer` argument of `gam`. If it still fails, try increasing the number of IRLS iterations (see `gam.control`) or perhaps experiment with the convergence tolerance.

If you still have problems, it's worth noting that a GAM is just a (penalized) GLM and the IRLS scheme used to estimate GLMs is not guaranteed to converge. Hence non convergence of a GAM may relate to a lack of stability in the basic IRLS scheme. Therefore it is worth trying to establish whether the IRLS iterations are capable of converging. To do this fit the problematic GAM with all smooth terms specified with `fx=TRUE` so that the smoothing parameters are all fixed at zero. If this 'largest' model can converge then, then the maintainer would quite like to know about your problem! If it doesn't converge, then its likely that your model is just too flexible for the IRLS process itself. Having tried increasing `maxit` in `gam.control`, there are several other possibilities for stabilizing the iteration. It is possible to try (i) setting lower bounds on the smoothing parameters using the `min.sp` argument of `gam`: this may or may not change the model being fitted; (ii) reducing the flexibility of the model by reducing the basis dimensions `k` in the specification of `s` and `te` model terms: this obviously changes the model being fitted somewhat; (iii) introduce a small regularization term into the fitting via the `irls.reg` argument of `gam.control`: this option obviously changes the nature of the fit somewhat, since parameter estimates are pulled towards zero by doing this.

Usually, a major contributor to fitting difficulties is that the model is a very poor description of the data.

#### Author(s)

Simon N. Wood <simon.wood@r-project.org>

---

gam.fit

*GAM P-IRLS estimation with GCV/UBRE smoothness estimation*

---

#### Description

This is an internal function of package `mgcv`. It is a modification of the function `glm.fit`, designed to be called from `gam`. The major modification is that rather than solving a weighted least squares problem at each IRLS step, a weighted, penalized least squares problem is solved at each IRLS step with smoothing parameters associated with each penalty chosen by GCV or UBRE, using routine `magic`. For further information on usage see code for `gam`. Some regularization of the IRLS weights is also permitted as a way of addressing identifiability related problems (see `gam.control`). Negative binomial parameter estimation is supported.

The basic idea of estimating smoothing parameters at each step of the P-IRLS is due to Gu (1992), and is termed 'performance iteration' or 'performance oriented iteration'.

#### Usage

```
gam.fit(G, start = NULL, etastart = NULL,
        mustart = NULL, family = gaussian(),
        control = gam.control(), gamma=1,
        fixedSteps=(control$maxit+1), ...)
```

**Arguments**

G	An object of the type returned by <code>gam</code> when <code>fit=FALSE</code> .
start	Initial values for the model coefficients.
etastart	Initial values for the linear predictor.
mustart	Initial values for the expected response.
family	The family object, specifying the distribution and link to use.
control	Control option list as returned by <code>gam.control</code> .
gamma	Parameter which can be increased to up the cost of each effective degree of freedom in the GCV or AIC/UBRE objective.
fixedSteps	How many steps to take: useful when only using this routine to get rough starting values for other methods.
...	Other arguments: ignored.

**Value**

A list of fit information.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

- Gu (1992) Cross-validating non-Gaussian data. *J. Comput. Graph. Statist.* 1:169-179
- Gu and Wahba (1991) Minimizing GCV/GML scores with multiple smoothing parameters via the Newton method. *SIAM J. Sci. Statist. Comput.* 12:383-398
- Wood, S.N. (2000) Modelling and Smoothing Parameter Estimation with Multiple Quadratic Penalties. *J.R.Statist.Soc.B* 62(2):413-428
- Wood, S.N. (2004) Stable and efficient multiple smoothing parameter estimation for generalized additive models. *J. Amer. Statist. Ass.* 99:637-686

**See Also**

[gam.fit3](#), [gam](#), [magic](#)

---

gam.fit3

*P-IRLS GAM estimation with GCV & UBRE/AIC or RE/ML derivative calculation*

---

**Description**

Estimation of GAM smoothing parameters is most stable if optimization of the UBRE/AIC, GCV, GACV, REML or ML score is outer to the penalized iteratively re-weighted least squares scheme used to estimate the model given smoothing parameters.

This routine estimates a GAM (any quadratically penalized GLM) given log smoothing parameters, and evaluates derivatives of the smoothness selection scores of the model with respect to the log smoothing parameters. Calculation of exact derivatives is generally faster than approximating them

by finite differencing, as well as generally improving the reliability of GCV/UBRE/AIC/REML score minimization.

The approach is to run the P-IRLS to convergence, and only then to iterate for first and second derivatives.

Not normally called directly, but rather service routines for `gam`.

### Usage

```
gam.fit3(x, y, sp, Eb, UrS=list(),
        weights = rep(1, nobs), start = NULL, etastart = NULL,
        mustart = NULL, offset = rep(0, nobs), U1 = diag(ncol(x)),
        Mp = -1, family = gaussian(), control = gam.control(),
        intercept = TRUE, deriv=2, gamma=1, scale=1,
        printWarn=TRUE, scoreType="REML", null.coef=rep(0, ncol(x)),
        pearson.extra=0, dev.extra=0, n.true=-1, ...)
```

### Arguments

<code>x</code>	The model matrix for the GAM (or any penalized GLM).
<code>y</code>	The response variable.
<code>sp</code>	The log smoothing parameters.
<code>Eb</code>	A balanced version of the total penalty matrix: used for numerical rank determination.
<code>UrS</code>	List of square root penalties premultiplied by transpose of orthogonal basis for the total penalty.
<code>weights</code>	prior weights for fitting.
<code>start</code>	optional starting parameter guesses.
<code>etastart</code>	optional starting values for the linear predictor.
<code>mustart</code>	optional starting values for the mean.
<code>offset</code>	the model offset
<code>U1</code>	An orthogonal basis for the range space of the penalty — required for ML smoothness estimation only.
<code>Mp</code>	The dimension of the total penalty null space — required for ML smoothness estimation only.
<code>family</code>	the family - actually this routine would never be called with <code>gaussian()</code>
<code>control</code>	control list as returned from <code>glm.control</code>
<code>intercept</code>	does the model have an intercept, TRUE or FALSE
<code>deriv</code>	Should derivatives of the GCV and UBRE/AIC scores be calculated? 0, 1 or 2, indicating the maximum order of differentiation to apply.
<code>gamma</code>	The weight given to each degree of freedom in the GCV and UBRE scores can be varied (usually increased) using this parameter.
<code>scale</code>	The scale parameter - needed for the UBRE/AIC score.
<code>printWarn</code>	Set to FALSE to suppress some warnings. Useful in order to ensure that some warnings are only printed if they apply to the final fitted model, rather than an intermediate used in optimization.
<code>scoreType</code>	specifies smoothing parameter selection criterion to use.

<code>null.coef</code>	coefficients for a model which gives some sort of upper bound on deviance. This allows immediate divergence problems to be controlled.
<code>pearson.extra</code>	Extra component to add to numerator of pearson statistic in P-REML/P-ML smoothness selection criteria.
<code>dev.extra</code>	Extra component to add to deviance for REML/ML type smoothness selection criteria.
<code>n.true</code>	Number of data to assume in smoothness selection criteria. $\leq 0$ indicates that it should be the number of rows of X.
<code>...</code>	Other arguments: ignored.

### Details

This routine is basically `glm.fit` with some modifications to allow (i) for quadratic penalties on the log likelihood; (ii) derivatives of the model coefficients with respect to log smoothing parameters to be obtained by use of the implicit function theorem and (iii) derivatives of the GAM GCV, UBRE/AIC, REML or ML scores to be evaluated at convergence.

In addition the routines apply step halving to any step that increases the penalized deviance substantially.

The most costly parts of the calculations are performed by calls to compiled C code (which in turn calls LAPACK routines) in place of the compiled code that would usually perform least squares estimation on the working model in the IRLS iteration.

Estimation of smoothing parameters by optimizing GCV scores obtained at convergence of the P-IRLS iteration was proposed by O'Sullivan et al. (1986), and is here termed 'outer' iteration.

Note that use of non-standard families with this routine requires modification of the families as described in [fix.family.link](#).

### Author(s)

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The routine has been modified from `glm.fit` in R 2.0.1, written by the R core (see `glm.fit` for further credits).

### References

O'Sullivan, Yandall & Raynor (1986) Automatic smoothing of regression functions in generalized linear models. J. Amer. Statist. Assoc. 81:96-103.

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. J.R.Statist. Soc. B 70(3):495-518

<http://www.maths.bath.ac.uk/~sw283/>

### See Also

[gam.fit](#), [gam](#), [mgcv](#), [magic](#)

## Description

This page is intended to provide some more information on how to specify GAMs. A GAM is a GLM in which the linear predictor depends, in part, on a sum of smooth functions of predictors and (possibly) linear functionals of smooth functions of (possibly dummy) predictors.

Specifically let  $y_i$  denote an independent random variable with mean  $\mu_i$  and an exponential family distribution, or failing that a known mean variance relationship suitable for use of quasi-likelihood methods. Then the the linear predictor of a GAM has a structure something like

$$g(\mu_i) = \mathbf{X}_i\beta + f_1(x_{1i}, x_{2i}) + f_2(x_{3i}) + L_i f_3(x_4) + \dots$$

where  $g$  is a known smooth monotonic ‘link’ function,  $\mathbf{X}_i\beta$  is the parametric part of the linear predictor, the  $x_j$  are predictor variables, the  $f_j$  are smooth functions and  $L_i$  is some linear functional of  $f_3$ . There may of course be multiple linear functional terms, or none.

The key idea here is that the dependence of the response on the predictors can be represented as a parametric sub-model plus the sum of some (functionals of) smooth functions of one or more of the predictor variables. Thus the model is quite flexible relative to strictly parametric linear or generalized linear models, but still has much more structure than the completely general model that says that the response is just some smooth function of all the covariates.

Note one important point. In order for the model to be identifiable the smooth functions usually have to be constrained to have zero mean (usually taken over the set of covariate values). The constraint is needed if the term involving the smooth includes a constant function in its span. `gam` always applies such constraints unless there is a `by` variable present, in which case an assessment is made of whether the constraint is needed or not (see below).

The following sections discuss specifying model structures for `gam`. Specification of the distribution and link function is done using the `family` argument to `gam` and works in the same way as for `glm`. This page therefore concentrates on the model formula for `gam`.

## Models with simple smooth terms

Consider the example model.

$$g(\mu_i) = \beta_0 + \beta_1 x_{1i} + \beta_2 x_{2i} + f_1(x_{3i}) + f_2(x_{4i}, x_{5i})$$

where the response variables  $y_i$  has expectation  $\mu_i$  and  $g$  is a link function.

The `gam` formula for this would be

```
y ~ x1 + x2 + s(x3) + s(x4, x5).
```

This would use the default basis for the smooths (a thin plate regression spline basis for each), with automatic selection of the effective degrees of freedom for both smooths. The dimension of the smoothing basis is given a default value as well (the dimension of the basis sets an upper limit on the maximum possible degrees of freedom for the basis - the limit is typically one less than basis dimension). Full details of how to control smooths are given in `s` and `te`, and further discussion of basis dimension choice can be found in `choose.k`. For the moment suppose that we would like to change the basis of the first smooth to a cubic regression spline basis with a dimension of 20, while fixing the second term at 25 degrees of freedom. The appropriate formula would be:

```
y ~ x1 + x2 + s(x3, bs="cr", k=20) + s(x4, x5, k=26, fx=TRUE).
```

The above assumes that  $x_4$  and  $x_5$  are naturally on similar scales (e.g. they might be co-ordinates), so that isotropic smoothing is appropriate. If this assumption is false then tensor product smoothing might be better (see [te](#)).

$y \sim x_1 + x_2 + s(x_3) + te(x_4, x_5)$

would generate a tensor product smooth of  $x_4$  and  $x_5$ . By default this smooth would have basis dimension 25 and use cubic regression spline marginals. Varying the defaults is easy. For example  $y \sim x_1 + x_2 + s(x_3) + te(x_4, x_5, bs=c("cr", "ps"), k=c(6, 7))$  specifies that the tensor product should use a rank 6 cubic regression spline marginal and a rank 7 P-spline marginal to create a smooth with basis dimension 42.

### Nested terms

Another common modelling task is to decide if a model like:

$$E(y_i) = f(x_i, z_i)$$

is really necessary or whether:

$$E(y_i) = f_1(x_i) + f_2(z_i)$$

would do just as well. One possibility is to examine the results of fitting:

$y \sim s(x) + s(z) + s(x, z)$ .

gam automatically generates side conditions to make this model identifiable. You can also estimate ‘overlapping’ models like:

$y \sim s(x, z) + s(z, v)$ .

Note that optimum interpretability of such models is obtained by ensuring that lower order terms are strictly nested with higher order ones. This is most easily achieved by employing tensor product smooths for multidimensional terms, and ensuring that lower order terms are using the same (marginal) bases as higher order ones. For example:

$y \sim s(x, bs="cr", k=5) + s(z, bs="cr", k=5) + te(x, z)$

would ensure strict nesting of the main effects within the interaction (given the [te](#) default `bs` and `k` arguments), since the main effects employ the same bases used as marginals for the [te](#) term.

### ‘by’ variables

by variables are the means for constructing ‘varying-coefficient models’ (geographic regression models) and for letting smooths ‘interact’ with factors or parametric terms. They are also the key to specifying general linear functionals of smooths.

The `s` and `te` terms used to specify smooths accept an argument `by`, which is a numeric or factor variable of the same dimension as the covariates of the smooth. If a `by` variable is numeric, then its  $i^{th}$  element multiplies the  $i^{th}$  row of the model matrix corresponding to the smooth term concerned. If a `by` variable is a factor then it generates an indicator vector for each level of the factor. The model matrix for the smooth term is then replicated for each factor level, and each copy has its rows multiplied by the corresponding rows of its indicator variable. The smoothness penalties are also duplicated for each factor level. In short a different smooth is generated for each factor level (the `id` argument to `s` and `te` can be used to force all such smooths to have the same smoothing parameter).

As an example, consider the model

$$E(y_i) = \beta_0 + f(x_i)z_i$$

where  $f$  is a smooth function, and  $z_i$  is a numeric variable. The appropriate formula is:

$y \sim s(x, by=z)$

- the `by` argument ensures that the smooth function gets multiplied by covariate  $z$ . Note that when

using factor variables, then the presence of centering constraints usually means that the by variable should be included as a parametric term, as well.

The example code below also illustrates the use of factor by variables.

by variables may be supplied as numeric matrices as part of specifying general linear functional terms.

If a by variable is present and numeric (rather than a factor) then the corresponding smooth is only subjected to an identifiability constraint if (i) the by variable is a constant vector, or, (ii) for a matrix by variable,  $L$ , if  $L \%*\% \text{rep}(1, \text{ncol}(L))$  is constant or (iii) if a user defined smooth constructor supplies an identifiability constraint explicitly.

### Linking smooths with ‘id’

It is sometimes desirable to insist that different smooth terms have the same degree of smoothness. This can be done by using the `id` argument to `s` or `te` terms. Smooths which share an `id` will have the same smoothing parameter. Really this only makes sense if the smooths use the same basis functions, and the default behaviour is to force this to happen: all smooths sharing an `id` have the same basis functions as the first smooth occurring with that `id`. Note that if you want exactly the same function for each smooth, then this is best achieved by making use of the summation convention covered under ‘linear functional terms’.

As an example suppose that  $E(y_i) \equiv \mu_i$  and

$$g(\mu_i) = f_1(x_{1i}) + f_2(x_{2i}, x_{3i}) + f_3(x_{4i})$$

but that  $f_1$  and  $f_3$  should have the same smoothing parameters (and  $x_2$  and  $x_3$  are on different scales). Then the `gam` formula

```
y ~ s(x1, id=1) + te(x_2, x3) + s(x4, id=1)
```

would achieve the desired result. `id` can be numbers or character strings. Giving an `id` to a term with a factor by variable causes the smooths at each level of the factor to have the same smoothing parameter.

Smooth term `ids` are not supported by `gamm`.

### Linear functional terms

General linear functional terms have a long history in the spline literature including in the penalized GLM context (see e.g. Wahba 1990). Such terms encompass varying coefficient models/ geographic regression, functional GLMs (i.e. GLMs with functional predictors), GLASS models, etc, and allow smoothing with respect to aggregated covariate values, for example.

Such terms are implemented in `mgcv` using a simple ‘summation convention’ for smooth terms: If the covariates of a smooth are supplied as matrices, then summation of the evaluated smooth over the columns of the matrices is implied. Each covariate matrix and any by variable matrix must be of the same dimension. Consider, for example the term

```
s(X, Z, by=L)
```

where  $X$ ,  $Z$  and  $L$  are  $n \times p$  matrices. Let  $f$  denote the thin plate regression spline specified. The resulting contribution to the  $i^{\text{th}}$  element of the linear predictor is

$$\sum_{j=1}^p L_{ij} f(X_{ij}, Z_{ij})$$

If no  $L$  is supplied then all its elements are taken as 1. In R code terms, let  $F$  denote the  $n \times p$  matrix obtained by evaluating the smooth at the values in  $X$  and  $Z$ . Then the contribution of the term to the linear predictor is `rowSums(L*F)` (note that it’s element by element multiplication here!).

The summation convention applies to `te` terms as well as `s` terms. More details and examples are provided in [linear.functional.terms](#).

## Random effects

Random effects can be added to gam models using `s(...,bs="re")` terms (see [smooth.construct.re.smooth.spec](#)), or the `paraPen` argument to `gam` covered below. See [gam.vcomp](#), [random.effects](#) and [smooth.construct.re.smooth.spec](#) for further details. An alternative is to use the approach of `gamm`.

## Penalizing the parametric terms

In case the ability to add smooth classes, smooth identities, by variables and the summation convention are still not sufficient to implement exactly the penalized GLM that you require, `gam` also allows you to penalize the parametric terms in the model formula. This is mostly useful in allowing one or more matrix terms to be included in the formula, along with a sequence of quadratic penalty matrices for each.

Suppose that you have set up a model matrix  $\mathbf{X}$ , and want to penalize the corresponding coefficients,  $\beta$  with two penalties  $\beta^T \mathbf{S}_1 \beta$  and  $\beta^T \mathbf{S}_2 \beta$ . Then something like the following would be appropriate: `gam(y ~ X - 1, paraPen=list(X=list(S1, S1)))`

The `paraPen` argument should be a list with elements having names corresponding to the terms being penalized. Each element of `paraPen` is itself a list, with optional elements `L`, `rank` and `sp`: all other elements must be penalty matrices. If present, `rank` is a vector giving the rank of each penalty matrix (if absent this is determined numerically). `L` is a matrix that maps underlying log smoothing parameters to the log smoothing parameters that actually multiply the individual quadratic penalties: taken as the identity if not supplied. `sp` is a vector of (underlying) smoothing parameter values: positive values are taken as fixed, negative to signal that the smoothing parameter should be estimated. Taken as all negative if not supplied.

An obvious application of `paraPen` is to incorporate random effects, and an example of this is provided below. In this case the supplied penalty matrices will be (generalized) inverse covariance matrices for the random effects — i.e. precision matrices. The final estimate of the covariance matrix corresponding to one of these penalties is given by the (generalized) inverse of the penalty matrix multiplied by the estimated scale parameter and divided by the estimated smoothing parameter for the penalty. For example, if you use an identity matrix to penalize some coefficients that are to be viewed as i.i.d. Gaussian random effects, then their estimated variance will be the estimated scale parameter divided by the estimate of the smoothing parameter, for this penalty. See the ‘rail’ example below.

## Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

## References

- Wahba (1990) Spline Models of Observational Data SIAM.  
 Wood S.N. (2006) Generalized Additive Models: An Introduction with R. Chapman and Hall/CRC Press.

## Examples

```
set.seed(10)
## simulate data from y = f(x2)*x1 + error
dat <- gamSim(3,n=400)

b<-gam(y ~ s(x2,by=x1),data=dat)
plot(b,pages=1)
```



```

summary(b)

## Factor `by' variable example (with a spurious covariate x0)
## simulate data...

dat <- gamSim(4)

## fit model...
b <- gam(y ~ fac+s(x2,by=fac)+s(x0),data=dat)
plot(b,pages=1)
summary(b)

## note that the preceding fit is the same as...
b1<-gam(y ~ s(x2,by=as.numeric(fac==1))+s(x2,by=as.numeric(fac==2))+
        s(x2,by=as.numeric(fac==3))+s(x0)-1,data=dat)
## ... the `-1' is because the intercept is confounded with the
## *uncentred* smooths here.
plot(b1,pages=1)
summary(b1)

## repeat forcing all s(x2) terms to have the same smoothing param
## (not a very good idea for these data!)
b2 <- gam(y ~ fac+s(x2,by=fac,id=1)+s(x0),data=dat)
plot(b2,pages=1)
summary(b2)

rm(dat)

## An example of a simple random effects term implemented via
## penalization of the parametric part of the model...

dat <- gamSim(1,n=400,scale=2) ## simulate 4 term additive truth
## Now add some random effects to the simulation. Response is
## grouped into one of 20 groups by `fac' and each groups has a
## random effect added....
fac <- as.factor(sample(1:20,400,replace=TRUE))
dat$X <- model.matrix(~fac-1)
b <- rnorm(20)*.5
dat$y <- dat$y + dat$X%*%b

## now fit appropriate random effect model...
PP <- list(X=list(rank=20,diag(20)))
rm <- gam(y~ X+s(x0)+s(x1)+s(x2)+s(x3),data=dat,paraPen=PP)
plot(rm,pages=1)
## Get estimated random effects standard deviation...
sig.b <- sqrt(rm$sig2/rm$sp[1]);sig.b

## a much simpler approach uses "re" terms...

rm1 <- gam(y ~ s(fac,bs="re")+s(x0)+s(x1)+s(x2)+s(x3),data=dat,method="ML")
gam.vcomp(rm1)

## Simple comparison with lme, using Rail data. See ?random.effects for a simpler method
require(nlme)
b0 <- lme(travel~1,data=Rail,~1|Rail,method="ML")
Z <- model.matrix(~Rail-1,data=Rail,
                 contrasts.arg=list(Rail="contr.treatment"))

```

```

b <- gam(travel~Z,data=Rail,paraPen=list(Z=list(diag(6))),method="ML")

b0
(b$reml.scale/b$sp)^.5 ## `gam' ML estimate of Rail sd
b$reml.scale^.5        ## `gam' ML estimate of residual sd

b0 <- lme(travel~1,data=Rail,~1|Rail,method="REML")
Z <- model.matrix(~Rail-1,data=Rail,
  contrasts.arg=list(Rail="contr.treatment"))
b <- gam(travel~Z,data=Rail,paraPen=list(Z=list(diag(6))),method="REML")

b0
(b$reml.scale/b$sp)^.5 ## `gam' REML estimate of Rail sd
b$reml.scale^.5        ## `gam' REML estimate of residual sd

```

gam.outer

*Minimize GCV or UBRE score of a GAM using 'outer' iteration***Description**

Estimation of GAM smoothing parameters is most stable if optimization of the smoothness selection score (GCV, GACV, UBRE/AIC, REML, ML etc) is outer to the penalized iteratively re-weighted least squares scheme used to estimate the model given smoothing parameters.

This routine optimizes a smoothness selection score in this way. Basically the score is evaluated for each trial set of smoothing parameters by estimating the GAM for those smoothing parameters. The score is minimized w.r.t. the parameters numerically, using `newton` (default), `bfgs`, `optim` or `nlm`. Exact (first and second) derivatives of the score can be used by fitting with `gam.fit3`. This improves efficiency and reliability relative to relying on finite difference derivatives.

Not normally called directly, but rather a service routine for `gam`.

**Usage**

```
gam.outer(lsp, fscale, family, control, method, optimizer,
  criterion, scale, gamma, G, ...)
```

**Arguments**

<code>lsp</code>	The log smoothing parameters.
<code>fscale</code>	Typical scale of the GCV or UBRE/AIC score.
<code>family</code>	the model family.
<code>control</code>	control argument to pass to <code>gam.fit</code> if pure finite differencing is being used.
<code>method</code>	method argument to <code>gam</code> defining the smoothness criterion to use (but depending on whether or not scale known).
<code>optimizer</code>	The argument to <code>gam</code> defining the numerical optimization method to use.
<code>criterion</code>	Which smoothness selection criterion to use. One of "UBRE", "GCV", "GACV", "REML" or "P-REML".
<code>scale</code>	Supplied scale parameter. Positive indicates known.
<code>gamma</code>	The degree of freedom inflation factor for the GCV/UBRE/AIC score.

- G List produced by `mgcv::gam.setup`, containing most of what's needed to actually fit a GAM.
- ... other arguments, typically for passing on to `gam.fit3` (ultimately).

### Details

See Wood (2008) for full details on 'outer iteration'.

### Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

### References

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. *J.R.Statist.Soc.B* 70(3):495-518

<http://www.maths.bath.ac.uk/~sw283/>

### See Also

[gam.fit3](#), [gam](#), [mgcv](#), [magic](#)

---

gam.selection

*Generalized Additive Model Selection*

---

### Description

This page is intended to provide some more information on how to select GAMs. In particular, it gives a brief overview of smoothness selection, and then discusses how this can be extended to select inclusion/exclusion of terms. Hypothesis testing approaches to the latter problem are also discussed.

### Smoothness selection criteria

Given a model structure specified by a gam model formula, `gam()` attempts to find the appropriate smoothness for each applicable model term using prediction error criteria or likelihood based methods. The prediction error criteria used are Generalized (Approximate) Cross Validation (GCV or GACV) when the scale parameter is unknown or an Un-Biased Risk Estimator (UBRE) when it is known. UBRE is essentially scaled AIC (Generalized case) or Mallows'  $C_p$  (additive model case). GCV and UBRE are covered in Craven and Wahba (1979) and Wahba (1990). Alternatively REML of maximum likelihood (ML) may be used for smoothness selection, by viewing the smooth components as random effects (in this case the variance component for each smooth random effect will be given by the scale parameter divided by the smoothing parameter — for smooths with multiple penalties, there will be multiple variance components). The `method` argument to `gam` selects the smoothness selection criterion.

Automatic smoothness selection is unlikely to be successful with few data, particularly with multiple terms to be selected. In addition GCV and UBRE/AIC score can occasionally display local minima that can trap the minimisation algorithms. GCV/UBRE/AIC scores become constant with changing smoothing parameters at very low or very high smoothing parameters, and on occasion these 'flat' regions can be separated from regions of lower score by a small 'lip'. This seems to be the most common form of local minimum, but is usually avoidable by avoiding extreme smoothing

parameters as starting values in optimization, and by avoiding big jumps in smoothing parameters while optimizing. Never the less, if you are suspicious of smoothing parameter estimates, try changing fit method (see `gam` arguments `method` and `optimizer`) and see if the estimates change, or try changing some or all of the smoothing parameters ‘manually’ (argument `sp` of `gam`, or `sp` arguments to `s` or `te`).

REML and ML are less prone to local minima than the other criteria, and may therefore be preferable.

### Automatic term selection

Unmodified smoothness selection by GCV, AIC, REML etc. will not usually remove a smooth from a model. This is because most smoothing penalties view some space of (non-zero) functions as ‘completely smooth’ and once a term is penalized heavily enough that it is in this space, further penalization does not change it.

However it is straightforward to modify smooths so that under heavy penalization they are penalized to the zero function and thereby ‘selected out’ of the model. There are two approaches.

The first approach is to modify the smoothing penalty with an additional shrinkage term. Smooth classes `cs.smooth` and `tps.smooth` (specified by “`cs`” and “`ts`” respectively) have smoothness penalties which include a small shrinkage component, so that for large enough smoothing parameters the smooth becomes identically zero. This allows automatic smoothing parameter selection methods to effectively remove the term from the model altogether. The shrinkage component of the penalty is set at a level that usually makes negligible contribution to the penalization of the model, only becoming effective when the term is effectively ‘completely smooth’ according to the conventional penalty.

The second approach leaves the original smoothing penalty unchanged, but constructs an additional penalty for each smooth, which penalizes only functions in the null space of the original penalty (the ‘completely smooth’ functions). Hence, if all the smoothing parameters for a term tend to infinity, the term will be selected out of the model. This latter approach is more expensive computationally, but has the advantage that it can be applied automatically to any smooth term. The `select` argument to `gam` turns on this method.

In fact, as implemented, both approaches operate by eigen-decomposing the original penalty matrix. A new penalty is created on the null space: it is the matrix with the same eigenvectors as the original penalty, but with the originally positive eigenvalues set to zero, and the originally zero eigenvalues set to something positive. The first approach just adds a multiple of this penalty to the original penalty, where the multiple is chosen so that the new penalty can not dominate the original. The second approach treats the new penalty as an extra penalty, with its own smoothing parameter.

Of course, as with all model selection methods, some care must be taken to ensure that the automatic selection is sensible, and a decision about the effective degrees of freedom at which to declare a term ‘negligible’ has to be made.

### Interactive term selection

In general the most logically consistent method to use for deciding which terms to include in the model is to compare GCV/UBRE/ML scores for models with and without the term (REML scores should not be used to compare models with different fixed effects structures). When UBRE is the smoothness selection method this will give the same result as comparing by AIC (the AIC in this case uses the model EDF in place of the usual model DF). Similarly, comparison via GCV score and via AIC seldom yields different answers. Note that the negative binomial with estimated `theta` parameter is a special case: the GCV score is not informative, because of the `theta` estimation scheme used. More generally the score for the model with a smooth term can be compared to the score for the model with the smooth term replaced by appropriate parametric terms. Candidates for

replacement by parametric terms are smooth terms with estimated degrees of freedom close to their minimum possible.

Candidates for removal can also be identified by reference to the approximate p-values provided by `summary.gam`, and by looking at the extent to which the confidence band for an estimated term includes the zero function. It is perfectly possible to perform backwards selection using p-values in the usual way: that is by sequentially dropping the single term with the highest non-significant p-value from the model and re-fitting, until all terms are significant. This suffers from the same problems as stepwise procedures for any GLM/LM, with the additional caveat that the p-values are only approximate. If adopting this approach, it is probably best to use ML smoothness selection.

Note that GCV and UBRE are not appropriate for comparing models using different families: in that case AIC should be used.

### Caveats/platitudes

Formal model selection methods are only appropriate for selecting between reasonable models. If formal model selection is attempted starting from a model that simply doesn't fit the data, then it is unlikely to provide meaningful results.

The more thought is given to appropriate model structure up front, the more successful model selection is likely to be. Simply starting with a hugely flexible model with 'everything in' and hoping that automatic selection will find the right structure is not often successful.

### Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

### References

- Craven and Wahba (1979) Smoothing Noisy Data with Spline Functions. *Numer. Math.* 31:377-403
- Venables and Ripley (1999) *Modern Applied Statistics with S-PLUS*
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- Wood, S.N. (2003) Thin plate regression splines. *J.R.Statist.Soc.B* 65(1):95-114
- Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. *J.R.Statist. Soc. B* 70(3):495-518
- <http://www.maths.bath.ac.uk/~sw283/>

### See Also

[gam](#), [step.gam](#)

### Examples

```
## an example of automatic model selection via null space penalization
library(mgcv)
set.seed(3); n<-200
dat <- gamSim(1, n=n, scale=.15, dist="poisson") ## simulate data
dat$x4 <- runif(n, 0, 1); dat$x5 <- runif(n, 0, 1) ## spurious

b<-gam(y~s(x0)+s(x1)+s(x2)+s(x3)+s(x4)+s(x5), data=dat,
       family=poisson, select=TRUE, method="REML")
summary(b)
plot(b, pages=1)
```

---

`gam.side`*Identifiability side conditions for a GAM*

---

### Description

GAM formulae with repeated variables only correspond to identifiable models given some side conditions. This routine works out appropriate side conditions, based on zeroing redundant parameters. It is called from `mgcv:::gam.setup` and is not intended to be called by users.

The method identifies nested and repeated variables by their names, but numerically evaluates which constraints need to be imposed. Constraints are always applied to smooths of more variables in preference to smooths of fewer variables. The numerical approach allows appropriate constraints to be applied to models constructed using any smooths, including user defined smooths.

### Usage

```
gam.side(sm, Xp, tol=.Machine$double.eps^.5)
```

### Arguments

<code>sm</code>	A list of smooth objects as returned by <code>smooth.construct</code> .
<code>Xp</code>	The model matrix for the strictly parametric model components.
<code>tol</code>	The tolerance to use when assessing linear dependence of smooths.

### Details

Models such as  $y \sim s(x) + s(z) + s(x, z)$  can be estimated by `gam`, but require identifiability constraints to be applied, to make them identifiable. This routine does this, effectively setting redundant parameters to zero. When the redundancy is between smooths of lower and higher numbers of variables, the constraint is always applied to the smooth of the higher number of variables.

Dependent smooths are identified symbolically, but which constraints are needed to ensure identifiability of these smooths is determined numerically, using `fixDependence`. This makes the routine rather general, and not dependent on any particular basis.

`Xp` is used to check whether there is a constant term in the model (or columns that can be linearly combined to give a constant). This is because centred smooths can appear independent, when they would be dependent if there is a constant in the model, so dependence testing needs to take account of this.

### Value

A list of smooths, with model matrices and penalty matrices adjusted to automatically impose the required constraints. Any smooth that has been modified will have an attribute `"del.index"`, listing the columns of its model matrix that were deleted. This index is used in the creation of prediction matrices for the term.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>

**Examples**

```

set.seed(7)
dat <- gamSim(n=400,scale=2) ## simulate data
## estimate model with redundant smooth interaction...
b<-gam(y~s(x0)+s(x1)+s(x0,x1)+s(x2),data=dat)
plot(b,pages=1)

## Simulate data with real interaction...
dat <- gamSim(2,n=500,scale=.1)
old.par<-par(mfrow=c(2,2))
## a fully nested tensor product example
b<-gam(y~s(x,bs="cr",k=6)+s(z,bs="cr",k=6)+te(x,z,k=6),
       data=dat$data)
plot(b)

par(old.par)
rm(dat)

```

gam.vcomp

*Report gam smoothness estimates as variance components***Description**

GAMs can be viewed as mixed models, where the smoothing parameters are related to variance components. This routine extracts the estimated variance components associated with each smooth term, and if possible returns confidence intervals on the standard deviation scale.

**Usage**

```
gam.vcomp(x, rescale=TRUE, conf.lev=.95)
```

**Arguments**

<code>x</code>	a fitted model object of class <code>gam</code> as produced by <code>gam()</code> .
<code>rescale</code>	the penalty matrices for smooths are rescaled before fitting, for numerical stability reasons, if <code>rescale</code> this rescaling is reversed, so that the variance components are on the original scale.
<code>conf.lev</code>	when the smothing parameters are estimated by REML or ML, then confidence intervals for the variance components can be obtained from large sample likelihood results. This gives the confidence level to work at.

**Details**

The (pseudo) inverse of the penalty matrix penalizing a term is proportional to the covariance matrix of the term's coefficients, when these are viewed as random. For single penalty smooths, it is possible to compute the variance component for the smooth (which multiplies the inverse penalty matrix to obtain the covariance matrix of the smooth's coefficients). This variance component is given by the scale parameter divided by the smoothing parameter.

This routine computes such variance components, for `gam` models, and associated confidence intervals, if smoothing parameter estimation was likelihood based. Note that variance components are also returned for tensor product smooths, but that their interpretation is not so straightforward.

The routine is particularly useful for model fitted by `gam` in which random effects have been incorporated.

### Value

Either a vector of variance components for each smooth term (as standard deviations), or a matrix. The first column of the matrix gives standard deviations for each term, while the subsequent columns give lower and upper confidence bounds, on the same scale.

The routine prints a table of estimated standard deviations and confidence limits, if these can be computed, and reports the numerical rank of the covariance matrix.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>

### References

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. *Journal of the Royal Statistical Society (B)* 70(3):495-518

### See Also

[smooth.construct.re.smooth.spec](#)

### Examples

```
set.seed(3)

## simulate some data, consisting of a smooth truth + random effects

dat <- gamSim(1,n=400,dist="normal",scale=2)
a <- factor(sample(1:10,400,replace=TRUE))
b <- factor(sample(1:7,400,replace=TRUE))
Xa <- model.matrix(~a-1) ## random main effects
Xb <- model.matrix(~b-1)
Xab <- model.matrix(~a:b-1) ## random interaction
dat$y <- dat$y + Xa%%rnorm(10)*.5 +
          Xb%%rnorm(7)*.3 + Xab%%rnorm(70)*.7
dat$a <- a;dat$b <- b

## Fit the model using "re" terms, and smoother linkage

mod <- gam(y~s(a,bs="re")+s(b,bs="re")+s(a,b,bs="re")+s(x0,id=1)+s(x1,id=1)+
          s(x2,k=15)+s(x3),data=dat,method="ML")

gam.vcomp(mod)
```



---

`gam2objective`*Objective functions for GAM smoothing parameter estimation*

---

**Description**

Estimation of GAM smoothing parameters is most stable if optimization of the UBRE/AIC or GCV score is outer to the penalized iteratively re-weighted least squares scheme used to estimate the model given smoothing parameters. These functions evaluate the GCV/UBRE/AIC score of a GAM model, given smoothing parameters, in a manner suitable for use by `optim` or `nlm`. Not normally called directly, but rather service routines for `gam.outer`.

**Usage**

```
gam2objective(lsp, args, ...)  
gam2derivative(lsp, args, ...)
```

**Arguments**

<code>lsp</code>	The log smoothing parameters.
<code>args</code>	List of arguments required to call <code>gam.fit3</code> .
<code>...</code>	Other arguments for passing to <code>gam.fit3</code> .

**Details**

`gam2objective` and `gam2derivative` are functions suitable for calling by `optim`, to evaluate the GCV/UBRE/AIC score and its derivatives w.r.t. log smoothing parameters.

`gam4objective` is an equivalent to `gam2objective`, suitable for optimization by `nlm` - derivatives of the GCV/UBRE/AIC function are calculated and returned as attributes.

The basic idea of optimizing smoothing parameters ‘outer’ to the P-IRLS loop was first proposed in O’Sullivan et al. (1986).

**Author(s)**

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

**References**

O’Sullivan, Yandall & Raynor (1986) Automatic smoothing of regression functions in generalized linear models. *J. Amer. Statist. Assoc.* 81:96-103.

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. *J.R.Statist.Soc.B* 70(3):495-518

<http://www.maths.bath.ac.uk/~sw283/>

**See Also**

`gam.fit3`, `gam`, `mgcv`, `magic`

## Description

Fits the specified generalized additive mixed model (GAMM) to data, by a call to `lme` in the normal errors identity link case, or by a call to `gammPQL` (a modification of `glmPQL` from the MASS library) otherwise. In the latter case estimates are only approximately MLEs. The routine is typically slower than `gam`, and not quite as numerically robust.

To use `lme4` in place of `nlme` as the underlying fitting engine, see `gamm4` from package `gamm4`.

Smooths are specified as in a call to `gam` as part of the fixed effects model formula, but the wiggly components of the smooth are treated as random effects. The random effects structures and correlation structures available for `lme` are used to specify other random effects and correlations.

It is assumed that the random effects and correlation structures are employed primarily to model residual correlation in the data and that the prime interest is in inference about the terms in the fixed effects model formula including the smooths. For this reason the routine calculates a posterior covariance matrix for the coefficients of all the terms in the fixed effects formula, including the smooths.

To use this function effectively it helps to be quite familiar with the use of `gam` and `lme`.

## Usage

```
gamm(formula, random=NULL, correlation=NULL, family=gaussian(),
      data=list(), weights=NULL, subset=NULL, na.action, knots=NULL,
      control=nlme::lmeControl(niterEM=0, optimMethod="L-BFGS-B"),
      niterPQL=20, verbosePQL=TRUE, method="ML", ...)
```

## Arguments

<code>formula</code>	A GAM formula (see also <code>formula.gam</code> and <code>gam.models</code> ). This is like the formula for a <code>glm</code> except that smooth terms ( <code>s</code> and <code>te</code> ) can be added to the right hand side of the formula. Note that <code>ids</code> for smooths and fixed smoothing parameters are not supported.
<code>random</code>	The (optional) random effects structure as specified in a call to <code>lme</code> : only the <code>list</code> form is allowed, to facilitate manipulation of the random effects structure within <code>gamm</code> in order to deal with smooth terms. See example below.
<code>correlation</code>	An optional <code>corStruct</code> object (see <code>corClasses</code> ) as used to define correlation structures in <code>lme</code> . Any grouping factors in the formula for this object are assumed to be nested within any random effect grouping factors, without the need to make this explicit in the formula (this is slightly different to the behaviour of <code>lme</code> ). See examples below.
<code>family</code>	A family as used in a call to <code>glm</code> or <code>gam</code> . The default <code>gaussian</code> with identity link causes <code>gamm</code> to fit by a direct call to <code>lme</code> provided there is no offset term, otherwise <code>gammPQL</code> is used.
<code>data</code>	A data frame or list containing the model response variable and covariates required by the formula. By default the variables are taken from <code>environment(formula)</code> , typically the environment from which <code>gamm</code> is called.

<code>weights</code>	In the generalized case, weights with the same meaning as <code>glm</code> weights. An <code>lme</code> type weights argument may only be used in the identity link gaussian case, with no offset (see documentation for <code>lme</code> for details of how to use such an argument).
<code>subset</code>	an optional vector specifying a subset of observations to be used in the fitting process.
<code>na.action</code>	a function which indicates what should happen when the data contain 'NA's. The default is set by the 'na.action' setting of 'options', and is 'na.fail' if that is unset. The "factory-fresh" default is 'na.omit'.
<code>knots</code>	this is an optional list containing user specified knot values to be used for basis construction. Different terms can use different numbers of knots, unless they share a covariate.
<code>control</code>	A list of fit control parameters for <code>lme</code> returned by <code>lmeControl</code> . Note the default setting for the number of EM iterations used by <code>lme</code> : smooths are set up using custom <code>pdMat</code> classes, which are currently not supported by the EM iteration code. Only increase this number if you want to perturb the starting values used in model fitting (usually to worse values!). The <code>optimMethod</code> option is only used if your version of R does not have the <code>nlminb</code> optimizer function.
<code>niterPQL</code>	Maximum number of PQL iterations (if any).
<code>verbosePQL</code>	Should PQL report its progress as it goes along?
<code>method</code>	Which of "ML" or "REML" to use in the Gaussian additive mixed model case when <code>lme</code> is called directly. Ignored in the generalized case (or if the model has an offset), in which case <code>gammPQL</code> is used.
<code>...</code>	further arguments for passing on e.g. to <code>lme</code>

## Details

The Bayesian model of spline smoothing introduced by Wahba (1983) and Silverman (1985) opens up the possibility of estimating the degree of smoothness of terms in a generalized additive model as variances of the wiggly components of the smooth terms treated as random effects. Several authors have recognised this (see Wang 1998; Ruppert, Wand and Carroll, 2003) and in the normal errors, identity link case estimation can be performed using general linear mixed effects modelling software such as `lme`. In the generalized case only approximate inference is so far available, for example using the Penalized Quasi-Likelihood approach of Breslow and Clayton (1993) as implemented in `glmPQL` by Venables and Ripley (2002). One advantage of this approach is that it allows correlated errors to be dealt with via random effects or the correlation structures available in the `nlme` library.

Some details of how GAMs are represented as mixed models and estimated using `lme` or `gammPQL` in `gamm` can be found in Wood (2004, 2006a,b). In addition `gamm` obtains a posterior covariance matrix for the parameters of all the fixed effects and the smooth terms. The approach is similar to that described in Lin & Zhang (1999) - the covariance matrix of the data (or pseudodata in the generalized case) implied by the weights, correlation and random effects structure is obtained, based on the estimates of the parameters of these terms and this is used to obtain the posterior covariance matrix of the fixed and smooth effects.

The bases used to represent smooth terms are the same as those used in `gam`, although adaptive smoothing bases are not available.

In the event of `lme` convergence failures, consider modifying `option(mgcv.vc.logrange)`: reducing it helps to remove indefiniteness in the likelihood, if that is the problem, but too large a

reduction can force over or undersmoothing. See [notExp2](#) for more information on this option. Failing that, you can try increasing the `niterEM` option in `control`: this will perturb the starting values used in fitting, but usually to values with lower likelihood! Note that this version of `gamm` works best with R 2.2.0 or above and `nlme`, 3.1-62 and above, since these use an improved optimizer.

## Value

Returns a list with two items:

<code>gam</code>	an object of class <code>gam</code> , less information relating to GCV/UBRE model selection. At present this contains enough information to use <code>predict</code> , <code>summary</code> and <code>print</code> methods and <code>vis.gam</code> , but not to use e.g. the <code>anova</code> method function to compare models.
<code>lme</code>	the fitted model object returned by <code>lme</code> or <code>gammPQL</code> . Note that the model formulae and grouping structures may appear to be rather bizarre, because of the manner in which the GAMM is split up and the calls to <code>lme</code> and <code>gammPQL</code> are constructed.

## WARNINGS

`gamm` assumes that you know what you are doing! For example, unlike `glmPQL` from `MASS` it will return the complete `lme` object from the working model at convergence of the PQL iteration, including the ‘log likelihood’, even though this is not the likelihood of the fitted GAMM.

The routine will be very slow and memory intensive if correlation structures are used for the very large groups of data. e.g. attempting to run the spatial example in the examples section with many 1000’s of data is definitely not recommended: often the correlations should only apply within clusters that can be defined by a grouping factor, and provided these clusters do not get too huge then fitting is usually possible.

Models must contain at least one random effect: either a smooth with non-zero smoothing parameter, or a random effect specified in argument `random`.

`gamm` is not as numerically stable as `gam`: an `lme` call will occasionally fail. See details section for suggestions, or try the ‘`gamm4`’ package.

`gamm` is usually much slower than `gam`, and on some platforms you may need to increase the memory available to R in order to use it with large data sets (see [mem.limits](#)).

Note that the weights returned in the fitted GAM object are dummy, and not those used by the PQL iteration: this makes partial residual plots look odd.

Note that the `gam` object part of the returned object is not complete in the sense of having all the elements defined in [gamObject](#) and does not inherit from `glm`: hence e.g. multi-model `anova` calls will not work.

The parameterization used for the smoothing parameters in `gamm`, bounds them above and below by an effective infinity and effective zero. See [notExp2](#) for details of how to change this.

Linked smoothing parameters and adaptive smoothing are not supported.

## Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

## References

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- Wang, Y. (1998) Mixed effects smoothing spline analysis of variance. *J.R. Statist. Soc. B* 60, 159-174
- <http://www.maths.bath.ac.uk/~sw283/>

## See Also

[magic](#) for an alternative for correlated data, [te](#), [s](#), [predict.gam](#), [plot.gam](#), [summary.gam](#), [negbin](#), [vis.gam](#), [pdTens](#), [gamm4](#) (<http://cran.r-project.org/package=gamm4>)

## Examples

```
library(mgcv)
## simple examples using gamm as alternative to gam
set.seed(0)
dat <- gamSim(1, n=400, scale=2)
b <- gamm(y~s(x0)+s(x1)+s(x2)+s(x3), data=dat)
plot(b$gam, pages=1)
summary(b$lme) # details of underlying lme fit
summary(b$gam) # gam style summary of fitted model
anova(b$gam)

b <- gamm(y~te(x0, x1)+s(x2)+s(x3), data=dat)
op <- par(mfrow=c(2, 2))
plot(b$gam)
par(op)
rm(dat)

## Add a factor to the linear predictor, to be modelled as random
dat <- gamSim(6, n=400, scale=.2, dist="poisson")
```

```

b2<-gamm(y~s(x0)+s(x1)+s(x2)+s(x3),family=poisson,
         data=dat,random=list(fac=~1))
plot(b2$gam,pages=1)
fac <- dat$fac
rm(dat)
vis.gam(b2$gam)

## now an example with autocorrelated errors....
n <- 400;sig <- 2
x <- 0:(n-1)/(n-1)
f <- 0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10
e <- rnorm(n,0,sig)
for (i in 2:n) e[i] <- 0.6*e[i-1] + e[i]
y <- f + e
op <- par(mfrow=c(2,2))
b <- gamm(y~s(x,k=20),correlation=corAR1())
plot(b$gam);lines(x,f-mean(f),col=2)
b <- gamm(y~s(x,k=20))
plot(b$gam);lines(x,f-mean(f),col=2)
b <- gam(y~s(x,k=20))
plot(b);lines(x,f-mean(f),col=2)

## more complicated autocorrelation example - AR errors
## only within groups defined by `fac'
e <- rnorm(n,0,sig)
for (i in 2:n) e[i] <- 0.6*e[i-1]*(fac[i-1]==fac[i]) + e[i]
y <- f + e
b <- gamm(y~s(x,k=20),correlation=corAR1(form=~1|fac))
plot(b$gam);lines(x,f-mean(f),col=2)
par(op)

## more complex situation with nested random effects and within
## group correlation

set.seed(0)
n.g <- 10
n<-n.g*10*4
## simulate smooth part...
dat <- gamSim(1,n=n,scale=2)
f <- dat$f
## simulate nested random effects....
fa <- as.factor(rep(1:10,rep(4*n.g,10)))
ra <- rep(rnorm(10),rep(4*n.g,10))
fb <- as.factor(rep(rep(1:4,rep(n.g,4)),10))
rb <- rep(rnorm(4),rep(n.g,4))
for (i in 1:9) rb <- c(rb,rep(rnorm(4),rep(n.g,4)))
## simulate auto-correlated errors within groups
e<-array(0,0)
for (i in 1:40) {
eg <- rnorm(n.g, 0, sig)
for (j in 2:n.g) eg[j] <- eg[j-1]*0.6+ eg[j]
e<-c(e,eg)
}
dat$y <- f + ra + rb + e
dat$fa <- fa;dat$fb <- fb
## fit model ....

```

```

b <- gamm(y~s(x0,bs="cr")+s(x1,bs="cr")+s(x2,bs="cr")+
  s(x3,bs="cr"),data=dat,random=list(fa=~1,fb=~1),
  correlation=corAR1())
plot(b$gam,pages=1)
vis.gam(b$gam)
## and a "spatial" example...
library(nlme);set.seed(1);n <- 200
dat <- gamSim(2,n=n,scale=0) ## standard example
attach(dat)
old.par<-par(mfrow=c(2,2))
contour(truth$x,truth$z,truth$f) ## true function
f <- data$f ## true expected response
## Now simulate correlated errors...
cstr <- corGaus(.1,form = ~x+z)
cstr <- Initialize(cstr,data.frame(x=data$x,z=data$z))
V <- corMatrix(cstr) ## correlation matrix for data
Cv <- chol(V)
e <- t(Cv) %*% rnorm(n)*0.05 # correlated errors
## next add correlated simulated errors to expected values
data$y <- f + e ## ... to produce response
b<- gamm(y~s(x,z,k=50),correlation=corGaus(.1,form=~x+z),
  data=data)
plot(b$gam) # gamm fit accounting for correlation
# overfits when correlation ignored.....
b1 <- gamm(y~s(x,z,k=50),data=data);plot(b1$gam)
b2 <- gam(y~s(x,z,k=50),data=data);plot(b2)
par(old.par)

```

gamObject

*Fitted gam object***Description**

A fitted GAM object returned by function `gam` and of class "gam" inheriting from classes "glm" and "lm". Method functions `anova`, `logLik`, `influence`, `plot`, `predict`, `print`, `residuals` and `summary` exist for this class.

All compulsory elements of "glm" and "lm" objects are present, but the fitting method for a GAM is different to a linear model or GLM, so that the elements relating to the QR decomposition of the model matrix are absent.

**Value**

A gam object has the following elements:

<code>aic</code>	AIC of the fitted model: bear in mind that the degrees of freedom used to calculate this are the effective degrees of freedom of the model, and the likelihood is evaluated at the maximum of the penalized likelihood in most cases, not at the MLE.
<code>assign</code>	Array whose elements indicate which model term (listed in <code>pterms</code> ) each parameter relates to: applies only to non-smooth terms.
<code>boundary</code>	did parameters end up at boundary of parameter space?

<code>call</code>	the matched call (allows <code>update</code> to be used with <code>gam</code> objects, for example).
<code>cmX</code>	column means of the model matrix (with elements corresponding to smooths set to zero) — useful for componentwise CI calculation.
<code>coefficients</code>	the coefficients of the fitted model. Parametric coefficients are first, followed by coefficients for each spline term in turn.
<code>control</code>	the <code>gam</code> control list used in the fit.
<code>converged</code>	indicates whether or not the iterative fitting method converged.
<code>data</code>	the original supplied data argument (for class "glm" compatibility). Only included if <code>gam</code> control argument element <code>keepData</code> is set to <code>TRUE</code> (default is <code>FALSE</code> ).
<code>deviance</code>	model deviance (not penalized deviance).
<code>df.null</code>	null degrees of freedom.
<code>df.residual</code>	effective residual degrees of freedom of the model.
<code>edf</code>	estimated degrees of freedom for each model parameter. Penalization means that many of these are less than 1.
<code>edf1</code>	similar, but using alternative estimate of EDF. Useful for testing.
<code>family</code>	family object specifying distribution and link used.
<code>fitted.values</code>	fitted model predictions of expected value for each datum.
<code>formula</code>	the model formula.
<code>full.sp</code>	full array of smoothing parameters multiplying penalties (excluding any contribution from <code>min.sp</code> argument to <code>gam</code> ). May be larger than <code>sp</code> if some terms share smoothing parameters, and/or some smoothing parameter values were supplied in the <code>sp</code> argument of <code>gam</code> .
<code>gcv.ubre</code>	The minimized smoothing parameter selection score: GCV, UBRE(AIC), GACV, negative log marginal likelihood or negative log restricted likelihood.
<code>hat</code>	array of elements from the leading diagonal of the 'hat' (or 'influence') matrix. Same length as response data vector.
<code>iter</code>	number of iterations of P-IRLS taken to get convergence.
<code>linear.predictors</code>	fitted model prediction of link function of expected value for each datum.
<code>method</code>	One of "GCV" or "UBRE", "REML", "P-REML", "ML", "P-ML", "PQL", "lme.ML" or "lme.REML", depending on the fitting criterion used.
<code>mgcv.conv</code>	A list of convergence diagnostics relating to the "magic" parts of smoothing parameter estimation - this will not be very meaningful for pure "outer" estimation of smoothing parameters. The items are: <code>full.rank</code> , The apparent rank of the problem given the model matrix and constraints; <code>rank</code> , The numerical rank of the problem; <code>fully.converged</code> , TRUE is multiple GCV/UBRE converged by meeting convergence criteria and FALSE if method stopped with a steepest descent step failure; <code>hess.pos.def</code> Was the hessian of the GCV/UBRE score positive definite at smoothing parameter estimation convergence?; <code>iter</code> How many iterations were required to find the smoothing parameters? <code>score.calls</code> , and how many times did the GCV/UBRE score have to be evaluated?; <code>rms.grad</code> , root mean square of the gradient of the GCV/UBRE score at convergence.
<code>min.edf</code>	Minimum possible degrees of freedom for whole model.



<code>model</code>	model frame containing all variables needed in original model fit.
<code>na.action</code>	The <code>na.action</code> used in fitting.
<code>nsdf</code>	number of parametric, non-smooth, model terms including the intercept.
<code>null.deviance</code>	deviance for single parameter model.
<code>offset</code>	model offset.
<code>optimizer</code>	optimizer argument to <code>gam</code> , or "magic" if it's a pure additive model.
<code>outer.info</code>	If 'outer' iteration has been used to fit the model (see <code>gam</code> argument <code>optimizer</code> ) then this is present and contains whatever was returned by the optimization routine used (currently <code>nlm</code> or <code>optim</code> ).
<code>prior.weights</code>	prior weights on observations.
<code>pterms</code>	terms object for strictly parametric part of model.
<code>rank</code>	apparent rank of fitted model.
<code>reml.scale</code>	The scale (RE)ML scale parameter estimate, if (P-)(RE)ML used for smoothness estimation.
<code>residuals</code>	the working residuals for the fitted model.
<code>scale</code>	when present, the scale (as <code>sig2</code> )
<code>scale.estimated</code>	TRUE if the scale parameter was estimated, FALSE otherwise.
<code>sig2</code>	estimated or supplied variance/scale parameter.
<code>smooth</code>	list of smooth objects, containing the basis information for each term in the model formula in the order in which they appear. These smooth objects are what gets returned by the <code>smooth.construct</code> objects.
<code>sp</code>	estimated smoothing parameters for the model. These are the underlying smoothing parameters, subject to optimization. For the full set of smoothing parameters multiplying the penalties see <code>full.sp</code> . Divide the scale parameter by the smoothing parameters to get, variance components, but note that this is not valid for smooths that have used rescaling to improve conditioning.
<code>terms</code>	terms object of model model frame.
<code>var.summary</code>	A named list of summary information on the predictor variables. If a parametric variable is a matrix, then the summary is a one row matrix, containing the observed data value closest to the column median, for each matrix column. If the variable is a factor then the summary is the modal factor level, returned as a factor, with levels corresponding to those of the data. For numerics and matrix arguments of smooths, the summary is the mean, nearest observed value to median and maximum, as a numeric vector. Used by <code>vis.gam</code> , in particular.
<code>Ve</code>	frequentist estimated covariance matrix for the parameter estimators. Particularly useful for testing whether terms are zero. Not so useful for CI's as smooths are usually biased.
<code>Vp</code>	estimated covariance matrix for the parameters. This is a Bayesian posterior covariance matrix that results from adopting a particular Bayesian model of the smoothing process. Particularly useful for creating credible/confidence intervals.
<code>weights</code>	final weights used in IRLS iteration.
<code>y</code>	response data.

## WARNINGS

This model object is different to that described in Chambers and Hastie (1993) in order to allow smoothing parameter estimation etc.

## Author(s)

Simon N. Wood <simon.wood@r-project.org>

## References

A Key Reference on this implementation:

Wood, S.N. (2006) Generalized Additive Models: An Introduction with R. Chapman & Hall/ CRC, Boca Raton, Florida

Key Reference on GAMs generally:

Hastie (1993) in Chambers and Hastie (1993) Statistical Models in S. Chapman and Hall.

Hastie and Tibshirani (1990) Generalized Additive Models. Chapman and Hall.

## See Also

[gam](#)

---

gamSim

*Simulate example data for GAMs*

---

## Description

Function used to simulate data sets to illustrate the use of [gam](#) and [gamm](#). Mostly used in help files to keep down the length of the example code sections.

## Usage

```
gamSim(eg=1, n=400, dist="normal", scale=2)
```

## Arguments

eg	numeric value specifying the example required.
n	number of data to simulate.
dist	character string which may be used to specify the distribution of the response.
scale	Used to set noise level.

## Details

See the source code for exactly what is simulated in each case.

1. Gu and Wahba 4 univariate term example.
2. A smooth function of 2 variables.
3. Example with continuous by variable.
4. Example with factor by variable.
5. An additive example plus a factor variable.
6. Additive + random effect.
7. As 1 but with correlated covariates.

**Value**

Depends on `eg`, but usually a dataframe, which may also contain some information on the underlying truth. Sometimes a list with more items, including a data frame for model fitting. See source code or helpfile examples where the function is used for further information.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**See Also**

[gam](#), [gamm](#)

**Examples**

```
## see ?gam
```

---

`get.var`

*Get named variable or evaluate expression from list or data.frame*

---

**Description**

This routine takes a text string and a data frame or list. It first sees if the string is the name of a variable in the data frame/ list. If it is then the value of this variable is returned. Otherwise the routine tries to evaluate the expression within the data.frame/list (but nowhere else) and if successful returns the result. If neither step works then `NULL` is returned. The routine is useful for processing gam formulae. If the variable is a matrix then it is coerced to a numeric vector, by default.

**Usage**

```
get.var(txt, data, vecMat=TRUE)
```

**Arguments**

<code>txt</code>	a text string which is either the name of a variable in <code>data</code> or when parsed is an expression that can be evaluated in <code>data</code> . It can also be neither in which case the function returns <code>NULL</code> .
<code>data</code>	A data frame or list.
<code>vecMat</code>	Should matrices be coerced to numeric vectors?

**Value**

The evaluated variable or `NULL`. May be coerced to a numeric vector if it's a matrix.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

<http://www.maths.bath.ac.uk/~sw283/>

**See Also**[gam](#)**Examples**

```
y <- 1:4; dat<-data.frame(x=5:10)
get.var("x", dat)
get.var("y", dat)
get.var("x==6", dat)
dat <- list(X=matrix(1:6,3,2))
get.var("X", dat)
```

---

`influence.gam`*Extract the diagonal of the influence/hat matrix for a GAM*

---

**Description**

Extracts the leading diagonal of the influence matrix (hat matrix) of a fitted `gam` object.

**Usage**

```
## S3 method for class 'gam':
influence(model, ...)
```

**Arguments**

<code>model</code>	fitted model objects of class <code>gam</code> as produced by <code>gam()</code> .
<code>...</code>	un-used in this case

**Details**

Simply extracts `hat` array from fitted model. (More may follow!)

**Value**

An array (see above).

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**See Also**[gam](#)

---

`initial.sp`*Starting values for multiple smoothing parameter estimation*

---

### Description

Finds initial smoothing parameter guesses for multiple smoothing parameter estimation. The idea is to find values such that the estimated degrees of freedom per penalized parameter should be well away from 0 and 1 for each penalized parameter, thus ensuring that the values are in a region of parameter space where the smoothing parameter estimation criterion is varying substantially with smoothing parameter value.

### Usage

```
initial.sp(X, S, off, expensive=FALSE)
```

### Arguments

<code>X</code>	is the model matrix.
<code>S</code>	is a list of of penalty matrices. <code>S[[i]]</code> is the <i>i</i> th penalty matrix, but note that it is not stored as a full matrix, but rather as the smallest square matrix including all the non-zero elements of the penalty matrix. Element 1,1 of <code>S[[i]]</code> occupies element <code>off[i], off[i]</code> of the <i>i</i> th penalty matrix. Each <code>S[[i]]</code> must be positive semi-definite.
<code>off</code>	is an array indicating the first parameter in the parameter vector that is penalized by the penalty involving <code>S[[i]]</code> .
<code>expensive</code>	if <code>TRUE</code> then the overall amount of smoothing is adjusted so that the average degrees of freedom per penalized parameter is exactly 0.5: this is numerically costly.

### Details

Basically uses a crude approximation to the estimated degrees of freedom per model coefficient, to try and find smoothing parameters which bound these e.d.f.'s away from 0 and 1.

Usually only called by `magic` and `gam`.

### Value

An array of initial smoothing parameter estimates.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>

### See Also

`magic`, `gam.outer`, `gam`,

---

interpret.gam      *Interpret a GAM formula*

---

### Description

This is an internal function of package `mgcv`. It is a service routine for `gam` which splits off the strictly parametric part of the model formula, returning it as a formula, and interprets the smooth parts of the model formula.

Not normally called directly.

### Usage

```
interpret.gam(gf)
```

### Arguments

`gf`                    A GAM formula as supplied to `gam` or `gamm`.

### Value

An object of class `split.gam.formula` with the following items:

`pf`                    A model formula for the strictly parametric part of the model.

`pfok`                 TRUE if there is a `pf` formula.

`smooth.spec`        A list of class `xx.smooth.spec` objects where `xx` depends on the basis specified for the term. (These can be passed to smooth constructor method functions to actually set up penalties and bases.)

`full.formula`        An expanded version of the model formula in which the options are fully expanded, and the options do not depend on variables which might not be available later.

`fake.formula`        A formula suitable for use in evaluating a model frame.

`response`            Name of the response variable.

### Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

### References

<http://www.maths.bath.ac.uk/~sw283/>

### See Also

[gam](#) [gamm](#)

ldTweedie

*Log Tweedie density evaluation***Description**

A function to evaluate the log of the Tweedie density for variance powers between 1 and 2, inclusive. Also evaluates first and second derivatives of log density w.r.t. its scale parameter.

**Usage**

```
ldTweedie(y, mu=y, p=1.5, phi=1)
```

**Arguments**

y	values at which to evaluate density.
mu	corresponding means (either of same length as y or a single value).
p	the variance of y is proportional to its mean to the power p. p must be between 1 and 2. 1 is Poisson like (exactly Poisson if phi=1), 2 is gamma.
phi	The scale parameter. Variance of y is phi*mu^p.

**Details**

A Tweedie random variable with  $1 < p < 2$  is a sum of  $N$  gamma random variables where  $N$  has a Poisson distribution. The  $p=1$  case is a generalization of a Poisson distribution and is a discrete distribution supported on integer multiples of the scale parameter. For  $1 < p < 2$  the distribution is supported on the positive reals with a point mass at zero.  $p=2$  is a gamma distribution. As  $p$  gets very close to 1 the continuous distribution begins to converge on the discretely supported limit at  $p=1$ .

ldTweedie is based on the series evaluation method of Dunn and Smyth (2005). Without the restriction on  $p$  the calculation of Tweedie densities is less straightforward. If you really need this case then the `tweedie` package is the place to start.

**Value**

A matrix with 3 columns. The first is the log density of y (log probability if  $p=1$ ). The second and third are the first and second derivatives of the log density w.r.t. phi.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org> modified from Venables and Ripley's `negative.binomial` family.

**References**

Dunn, P.K. and G.K. Smith (2005) Series evaluation of Tweedie exponential dispersion model densities. *Statistics and Computing* 15:267-280

Tweedie, M. C. K. (1984). An index which distinguishes between some important exponential families. *Statistics: Applications and New Directions. Proceedings of the Indian Statistical Institute Golden Jubilee International Conference* (Eds. J. K. Ghosh and J. Roy), pp. 579-604. Calcutta: Indian Statistical Institute.

**Examples**

```

library(mgcv)
## convergence to Poisson illustrated
## notice how p>1.1 is OK
y <- seq(1e-10,10,length=1000)
p <- c(1.0001,1.001,1.01,1.1,1.2,1.5,1.8,2)
phi <- .5
fy <- exp(ldTweedie(y,mu=2,p=p[1],phi=phi)[,1])
plot(y,fy,type="l",ylim=c(0,3),main="Tweedie density as p changes")
for (i in 2:length(p)) {
  fy <- exp(ldTweedie(y,mu=2,p=p[i],phi=phi)[,1])
  lines(y,fy,col=i)
}

```

---

```
linear.functional.terms
```

*Linear functionals of a smooth in GAMs*

---

**Description**

`gam` allows the response variable to depend on linear functionals of smooth terms. Specifically dependencies of the form

$$g(\mu_i) = \dots + \sum_j L_{ij} f(x_{ij}) + \dots$$

are allowed, where the  $x_{ij}$  are covariate values and the  $L_{ij}$  are fixed weights. i.e. the response can depend on the weighted sum of the same smooth evaluated at different covariate values. This allows, for example, for the response to depend on the derivatives or integrals of a smooth (approximated by finite differencing or quadrature, respectively). It also allows dependence on predictor functions (sometimes called ‘signal regression’).

The mechanism by which this is achieved is to supply matrices of covariate values to the model smooth terms specified by `s` or `te` terms in the model formula. Each column of the covariate matrix gives rise to a corresponding column of predictions from the smooth. Let the resulting matrix of evaluated smooth values be  $F$  ( $F$  will have the same dimension as the covariate matrices). In the absence of a `by` variable then these columns are simply summed and added to the linear predictor. i.e. the contribution of the term to the linear predictor is `rowSums(F)`. If a `by` variable is present then it must be a matrix,  $L$ , say, of the same dimension as  $F$  (and the covariate matrices), and it contains the weights  $L_{ij}$  in the summation given above. So in this case the contribution to the linear predictor is `rowSums(L*F)`.

Note that if a  $L\mathbf{1}$  (i.e. `rowSums(L)`) is a constant vector, or there is no `by` variable then the smooth will automatically be centred in order to ensure identifiability. Otherwise it will not be. Note also that for centred smooths it can be worth replacing the constant term in the model with `rowSums(L)` in order to ensure that predictions are automatically on the right scale.

When predicting from the model it is not necessary to provide matrix covariate and `by` variable values. For example to simply examine the underlying smooth function one would use vectors of covariate values and vector `by` variables, with the `by` variable and equivalent of  $L\mathbf{1}$ , above, set to vectors of ones.



**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**Examples**

```
### matrix argument `linear operator' smoothing
library(mgcv)
set.seed(0)

#####
## simple summation example...#
#####

n<-400
sig<-2
x <- runif(n, 0, .9)
f2 <- function(x) 0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10
x1 <- x + .1

f <- f2(x) + f2(x1) ## response is sum of f at two adjacent x values
y <- f + rnorm(n)*sig

X <- matrix(c(x,x1),n,2) ## matrix covariate contains both x values
b <- gam(y~s(X))

plot(b) ## reconstruction of f
plot(f,fitted(b))

#####
## multivariate integral example. Function `test1' will be integrated#
## (by midpoint quadrature) over 100 equal area sub-squares covering #
## the unit square. Noise is added to the resulting simulated data. #
## `test1' is estimated from the resulting data using two alternative#
## smooths. #
#####

test1 <- function(x,z,sx=0.3,sz=0.4)
{ (pi*sx*sz)*(1.2*exp(-(x-0.2)^2/sx^2-(z-0.3)^2/sz^2)+
  0.8*exp(-(x-0.7)^2/sx^2-(z-0.8)^2/sz^2))
}

## create quadrature (integration) grid, in useful order
ig <- 5 ## integration grid within square
mx <- mz <- (1:ig-.5)/ig
ix <- rep(mx,ig);iz <- rep(mz,rep(ig,ig))

og <- 10 ## observation grid
mx <- mz <- (1:og-1)/og
ox <- rep(mx,og);ox <- rep(ox,rep(ig^2,og^2))
oz <- rep(mz,rep(og,og));oz <- rep(oz,rep(ig^2,og^2))

x <- ox + ix/og;z <- oz + iz/og ## full grid, subsquare by subsquare

## create matrix covariates...
X <- matrix(x,og^2,ig^2,byrow=TRUE)
Z <- matrix(z,og^2,ig^2,byrow=TRUE)
```

```

## create simulated test data...
dA <- 1/(og*ig)^2 ## quadrature square area
F <- test1(X,Z) ## evaluate on grid
f <- rowSums(F)*dA ## integrate by midpoint quadrature
y <- f + rnorm(og^2)*5e-4 ## add noise
## ... so each y is a noisy observation of the integral of `test1'
## over a 0.1 by 0.1 sub-square from the unit square

## Now fit model to simulated data...

L <- X*0 + dA

## ... let F be the matrix of the smooth evaluated at the x,z values
## in matrices X and Z. rowSums(L*F) gives the model predicted
## integrals of `test1' corresponding to the observed `y'

L1 <- rowSums(L) ## smooths are centred --- need to add in L%*%1

## fit models to reconstruct `test1'....

b <- gam(y~s(X,Z,by=L)+L1-1) ## (L1 and const are confounded here)
b1 <- gam(y~te(X,Z,by=L)+L1-1) ## tensor product alternative

## plot results...

old.par<-par(mfrow=c(2,2))
x<-runif(n);z<-runif(n);
xs<-seq(0,1,length=30);zs<-seq(0,1,length=30)
pr<-data.frame(x=rep(xs,30),z=rep(zs,rep(30,30)))
truth<-matrix(test1(pr$x,pr$z),30,30)
contour(xs,zs,truth)
plot(b)
vis.gam(b,view=c("X","Z"),cond=list(L1=1,L=1),plot.type="contour")
vis.gam(b1,view=c("X","Z"),cond=list(L1=1,L=1),plot.type="contour")

#####
## A "signal" regression example...#
#####

rf <- function(x=seq(0,1,length=100)) {
## generates random functions...
  m <- ceiling(runif(1)*5) ## number of components
  f <- x*0;
  mu <- runif(m,min(x),max(x));sig <- (runif(m)+.5)*(max(x)-min(x))/10
  for (i in 1:m) f <- f+ dnorm(x,mu[i],sig[i])
  f
}

x <- seq(0,1,length=100) ## evaluation points

## example functional predictors...
par(mfrow=c(3,3));for (i in 1:9) plot(x,rf(x),type="l",xlab="x")

## simulate 200 functions and store in rows of L...
L <- matrix(NA,200,100)
for (i in 1:200) L[i,] <- rf() ## simulate the functional predictors

```

```

f2 <- function(x) { ## the coefficient function
  (0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10)/10
}

f <- f2(x) ## the true coefficient function

y <- L%*%f + rnorm(200)*20 ## simulated response data

## Now fit the model E(y) = L%*%f(x) where f is a smooth function.
## The summation convention is used to evaluate smooth at each value
## in matrix X to get matrix F, say. Then rowSum(L*F) gives E(y).

## create matrix of eval points for each function. Note that
## `smoothCon' is smart and will recognize the duplication...
X <- matrix(x,200,100,byrow=TRUE)

b <- gam(y~s(X,by=L,k=20))
par(mfrow=c(1,1))
plot(b,shade=TRUE);lines(x,f,col=2)

```

---

logLik.gam

---

*Extract the log likelihood for a fitted GAM*


---

## Description

Function to extract the log-likelihood for a fitted `gam` model (note that the models are usually fitted by penalized likelihood maximization).

## Usage

```
## S3 method for class 'gam':
logLik(object, ...)
```

## Arguments

<code>object</code>	fitted model objects of class <code>gam</code> as produced by <code>gam()</code> .
<code>...</code>	un-used in this case

## Details

Modification of `logLik.glm` which corrects the degrees of freedom for use with `gam` objects.

The function is provided so that [AIC](#) functions correctly with `gam` objects, and uses the appropriate degrees of freedom (accounting for penalization). Note, when using [AIC](#) for penalized models, that the degrees of freedom are the effective degrees of freedom and not the number of parameters, and the model maximizes the penalized likelihood, not the actual likelihood! This seems to be reasonably well founded for the known scale parameter case (see Hastie and Tibshirani, 1990, section 6.8.3 and also Wood 2008), and in fact in this case the default smoothing parameter estimation criterion is effectively this modified [AIC](#).

**Value**

Standard logLik object: see [logLik](#).

**Author(s)**

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)> based directly on logLik.glm

**References**

Hastie and Tibshirani, 1990, Generalized Additive Models.

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. J.R.Statist.Soc.B 70(3):495-518

**See Also**

[AIC](#)

---

ls.size

*Size of list elements*

---

**Description**

Produces a named array giving the size, in bytes, of the elements of a list.

**Usage**

```
ls.size(x)
```

**Arguments**

x                    A list.

**Details**

A numeric vector giving the size in bytes of each element of the list x. The elements of the array have the same names as the elements of the list. If x is not a list then its size in bytes is returned, un-named.

**Value**

An object of class "gam" as described in [gamObject](#).

**Author(s)**

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

**References**

<http://www.maths.bath.ac.uk/~sw283/>

**Examples**

```
library(mgcv)
b <- list(M=matrix(runif(100),10,10),quote=
"The world is ruled by idiots because only an idiot would want to rule the world.",
fam=binomial())
ls.size(b)
```

magic

*Stable Multiple Smoothing Parameter Estimation by GCV or UBRE,  
with optional fixed penalty*

**Description**

Function to efficiently estimate smoothing parameters in generalized ridge regression problems with multiple (quadratic) penalties, by GCV or UBRE. The function uses Newton's method in multi-dimensions, backed up by steepest descent to iteratively adjust the smoothing parameters for each penalty (one penalty may have a smoothing parameter fixed at 1).

For maximal numerical stability the method is based on orthogonal decomposition methods, and attempts to deal with numerical rank deficiency gracefully using a truncated singular value decomposition approach.

**Usage**

```
magic(y, X, sp, S, off, L=NULL, lsp0=NULL, rank=NULL, H=NULL, C=NULL,
w=NULL, gamma=1, scale=1, gcv=TRUE, ridge.parameter=NULL,
control=list(maxit=50, tol=1e-6, step.half=25,
rank.tol=.Machine$double.eps^0.5), extra.rss=0, n.score=length(y))
```

**Arguments**

- |     |   |
|-----|---|
| y   | is the response data vector.  |
| X   | is the model matrix.  |
| sp  | is the array of smoothing parameters. The vector $L \times \log(sp) + lsp0$ contains the logs of the smoothing parameters that actually multiply the penalty matrices stored in S (L is taken as the identity if NULL). Any sp values that are negative are autoinitialized, otherwise they are taken as supplying starting values. A supplied starting value will be reset to a default starting value if the gradient of the GCV/UBRE score is too small at the supplied value. |
| S   | is a list of of penalty matrices. $S[[i]]$ is the <i>i</i> th penalty matrix, but note that it is not stored as a full matrix, but rather as the smallest square matrix including all the non-zero elements of the penalty matrix. Element 1,1 of $S[[i]]$ occupies element $off[i], off[i]$ of the <i>i</i> th penalty matrix. Each $S[[i]]$ must be positive semi-definite. Set to <code>list()</code> if there are no smoothing parameters to be estimated.                    |
| off | is an array indicating the first parameter in the parameter vector that is penalized by the penalty involving $S[[i]]$ .  |
| L   | is a matrix mapping $\log(sp)$ to the log smoothing parameters that actually multiply the penalties defined by the elems of S. Taken as the identity, if NULL. See above under sp.  |

<code>lsp0</code>	If <code>L</code> is not <code>NULL</code> this is a vector of constants in the linear transformation from <code>log(sp)</code> to the actual log smoothing parameters. So the logs of the smoothing parameters multiplying the <code>S[[i]]</code> are given by <code>L%%log(sp) + lsp0</code> . Taken as 0 if <code>NULL</code> .
<code>rank</code>	is an array specifying the ranks of the penalties. This is useful, but not essential, for forming square roots of the penalty matrices.
<code>H</code>	is the optional offset penalty - i.e. a penalty with a smoothing parameter fixed at 1. This is useful for allowing regularization of the estimation process, fixed smoothing penalties etc.
<code>C</code>	is the optional matrix specifying any linear equality constraints on the fitting problem. If <code>b</code> is the parameter vector then the parameters are forced to satisfy $\mathbf{Cb} = \mathbf{0}$ .
<code>w</code>	the regression weights. If this is a matrix then it is taken as being the square root of the inverse of the covariance matrix of $\mathbf{y}$ , specifically $\mathbf{V}_y^{-1} = \mathbf{w}'\mathbf{w}$ . If <code>w</code> is an array then it is taken as the diagonal of this matrix, or simply the weight for each element of $\mathbf{y}$ . See below for an example using this.
<code>gamma</code>	is an inflation factor for the model degrees of freedom in the GCV or UBRE score.
<code>scale</code>	is the scale parameter for use with UBRE.
<code>gcv</code>	should be set to <code>TRUE</code> if GCV is to be used, <code>FALSE</code> for UBRE.
<code>ridge.parameter</code>	It is sometimes useful to apply a ridge penalty to the fitting problem, penalizing the parameters in the constrained space directly. Setting this parameter to a value greater than zero will cause such a penalty to be used, with the magnitude given by the parameter value.
<code>control</code>	is a list of iteration control constants with the following elements: <b>maxit</b> The maximum number of iterations of the magic algorithm to allow. <b>tol</b> The tolerance to use in judging convergence. <b>step.half</b> If a trial step fails then the method tries halving it up to a maximum of <code>step.half</code> times. <b>rank.tol</b> is a constant used to test for numerical rank deficiency of the problem. Basically any singular value less than <code>rank_tol</code> multiplied by the largest singular value of the problem is set to zero.
<code>extra.rss</code>	is a constant to be added to the residual sum of squares (squared norm) term in the calculation of the GCV, UBRE and scale parameter estimate. In conjunction with <code>n.score</code> , this is useful for certain methods for dealing with very large data sets.
<code>n.score</code>	number to use as the number of data in GCV/UBRE score calculation: usually the actual number of data, but there are methods for dealing with very large datasets that change this.

## Details

The method is a computationally efficient means of applying GCV or UBRE (often approximately AIC) to the problem of smoothing parameter selection in generalized ridge regression problems of the form:

$$\text{minimise } \|\mathbf{W}(\mathbf{Xb} - \mathbf{y})\|^2 + \mathbf{b}'\mathbf{Hb} + \sum_{i=1}^m \theta_i \mathbf{b}'\mathbf{S}_i \mathbf{b}$$

possibly subject to constraints  $\mathbf{Cb} = \mathbf{0}$ .  $\mathbf{X}$  is a design matrix,  $\mathbf{b}$  a parameter vector,  $\mathbf{y}$  a data vector,  $\mathbf{W}$  a weight matrix,  $\mathbf{S}_i$  a positive semi-definite matrix of coefficients defining the  $i$ th penalty with associated smoothing parameter  $\theta_i$ ,  $\mathbf{H}$  is the positive semi-definite offset penalty matrix and  $\mathbf{C}$  a matrix of coefficients defining any linear equality constraints on the problem.  $\mathbf{X}$  need not be of full column rank.

The  $\theta_i$  are chosen to minimize either the GCV score:

$$V_g = \frac{n \|\mathbf{W}(\mathbf{y} - \mathbf{A}\mathbf{y})\|^2}{[\text{tr}(\mathbf{I} - \gamma\mathbf{A})]^2}$$

or the UBRE score:

$$V_u = \|\mathbf{W}(\mathbf{y} - \mathbf{A}\mathbf{y})\|^2/n - 2\phi \text{tr}(\mathbf{I} - \gamma\mathbf{A})/n + \phi$$

where  $\gamma$  is gamma the inflation factor for degrees of freedom (usually set to 1) and  $\phi$  is `scale`, the scale parameter.  $\mathbf{A}$  is the hat matrix (influence matrix) for the fitting problem (i.e the matrix mapping data to fitted values). Dependence of the scores on the smoothing parameters is through  $\mathbf{A}$ .

The method operates by Newton or steepest descent updates of the logs of the  $\theta_i$ . A key aspect of the method is stable and economical calculation of the first and second derivatives of the scores w.r.t. the log smoothing parameters. Because the GCV/UBRE scores are flat w.r.t. very large or very small  $\theta_i$ , it's important to get good starting parameters, and to be careful not to step into a flat region of the smoothing parameter space. For this reason the algorithm rescales any Newton step that would result in a  $\log(\theta_i)$  change of more than 5. Newton steps are only used if the Hessian of the GCV/UBRE is positive definite, otherwise steepest descent is used. Similarly steepest descent is used if the Newton step has to be contracted too far (indicating that the quadratic model underlying Newton is poor). All initial steepest descent steps are scaled so that their largest component is 1. However a step is calculated, it is never expanded if it is successful (to avoid flat portions of the objective), but steps are successively halved if they do not decrease the GCV/UBRE score, until they do, or the direction is deemed to have failed. (Given the smoothing parameters the optimal  $\mathbf{b}$  parameters are easily found.)

The method is coded in C with matrix factorizations performed using LINPACK and LAPACK routines.

## Value

The function returns a list with the following items:

<code>b</code>	The best fit parameters given the estimated smoothing parameters.
<code>scale</code>	the estimated (GCV) or supplied (UBRE) scale parameter.
<code>score</code>	the minimized GCV or UBRE score.
<code>sp</code>	an array of the estimated smoothing parameters.
<code>sp.full</code>	an array of the smoothing parameters that actually multiply the elements of <code>S</code> (same as <code>sp</code> if <code>L</code> was <code>NULL</code> ). This is $\exp(L \cdot \log(sp))$ .
<code>rV</code>	a factored form of the parameter covariance matrix. The (Bayesian) covariance matrix of the parameters <code>b</code> is given by $rV \%*\%t(rV) * scale$ .
<code>gcv.info</code>	is a list of information about the performance of the method with the following elements: <b>full.rank</b> The apparent rank of the problem: number of parameters less number of equality constraints.

**rank** The estimated actual rank of the problem (at the final iteration of the method).

**fully.converged** is TRUE if the method converged by satisfying the convergence criteria, and FALSE if it covered by failing to decrease the score along the search direction.

**hess.pos.def** is TRUE if the hessian of the UBRE or GCV score was positive definite at convergence.

**iter** is the number of Newton/Steepest descent iterations taken.

**score.calls** is the number of times that the GCV/UBRE score had to be evaluated.

**rms.grad** is the root mean square of the gradient of the UBRE/GCV score w.r.t. the smoothing parameters.

Note that some further useful quantities can be obtained using [magic.post.proc](#).

### Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

### References

Wood, S.N. (2004) Stable and efficient multiple smoothing parameter estimation for generalized additive models. *J. Amer. Statist. Ass.* 99:673-686

<http://www.maths.bath.ac.uk/~sw283/>

### See Also

[magic.post.proc](#), [mgcv](#), [gam](#)

### Examples

```
## Use 'magic' for a standard additive model fit ...
library(mgcv)
set.seed(1); n <- 400; sig <- 2
dat <- gamSim(1, n=n, scale=sig)
## set up additive model
G <- gam(y~s(x0)+s(x1)+s(x2)+s(x3), fit=FALSE, data=dat)
## fit using magic
mgfit <- magic(G$y, G$X, G$sp, G$S, G$off, rank=G$rank, C=G$C)
## and fit using gam as consistency check
b <- gam(G=G)
mgfit$sp; b$sp # compare smoothing parameter estimates
edf <- magic.post.proc(G$X, mgfit, G$w)$edf # get e.d.f. per param
range(edf-b$edf) # compare

## constrain first two smooths to have identical smoothing parameters
L <- diag(3); L <- rbind(L[,1], L)
mgfit <- magic(G$y, G$X, rep(-1, 3), G$S, G$off, L=L, rank=G$rank, C=G$C)

## Now a correlated data example ...
library(nlme)
## simulate truth
set.seed(1); n<-400; sig<-2
x <- 0:(n-1)/(n-1)
f <- 0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10
```



```

## produce scaled covariance matrix for AR1 errors...
V <- corMatrix(Initialize(corAR1(.6),data.frame(x=x)))
Cv <- chol(V) # t(Cv)%*%Cv=V
## Simulate AR1 errors ...
e <- t(Cv)%*%rnorm(n,0,sig) # so cov(e) = V * sig^2
## Observe truth + AR1 errors
y <- f + e
## GAM ignoring correlation
par(mfrow=c(1,2))
b <- gam(y~s(x,k=20))
plot(b);lines(x,f-mean(f),col=2);title("Ignoring correlation")
## Fit smooth, taking account of *known* correlation...
w <- solve(t(Cv)) # V^{-1} = w'w
## Use `gam` to set up model for fitting...
G <- gam(y~s(x,k=20),fit=FALSE)
## fit using magic, with weight *matrix*
mgfit <- magic(G$y,G$X,G$sp,G$S,G$off,rank=G$rank,C=G$C,w=w)
## Modify previous gam object using new fit, for plotting...
mg.stuff <- magic.post.proc(G$X,mgfit,w)
b$edf <- mg.stuff$edf;b$Vp <- mg.stuff$Vb
b$coefficients <- mgfit$b
plot(b);lines(x,f-mean(f),col=2);title("Known correlation")

```

---

magic.post.proc      *Auxilliary information from magic fit*

---

## Description

Obtains Bayesian parameter covariance matrix, frequentist parameter estimator covariance matrix, estimated degrees of freedom for each parameter and leading diagonal of influence/hat matrix, for a penalized regression estimated by `magic`.

## Usage

```
magic.post.proc(X, object, w)
```

## Arguments

<code>X</code>	is the model matrix.
<code>object</code>	is the list returned by <code>magic</code> after fitting the model with model matrix <code>X</code> .
<code>w</code>	is the weight vector used in fitting, or the weight matrix used in fitting (i.e. supplied to <code>magic</code> , if one was.). If <code>w</code> is a vector then its elements are typically proportional to reciprocal variances (but could even be negative). If <code>w</code> is a matrix then <code>t(w) %*% w</code> should typically give the inverse of the covariance matrix of the response data supplied to <code>magic</code> .

## Details

`object` contains  $rV(\mathbf{V}, \text{say})$ , and  $\text{scale}(\phi, \text{say})$  which can be used to obtain the require quantities as follows. The Bayesian covariance matrix of the parameters is  $\mathbf{V}\mathbf{V}'\phi$ . The vector of estimated degrees of freedom for each parameter is the leading diagonal of  $\mathbf{V}\mathbf{V}'\mathbf{X}'\mathbf{W}'\mathbf{W}\mathbf{X}$  where  $\mathbf{W}$  is either the weight matrix `w` or the matrix `diag(w)`. The hat/influence matrix is given by  $\mathbf{W}\mathbf{X}\mathbf{V}\mathbf{V}'\mathbf{X}'\mathbf{W}'$ .

The frequentist parameter estimator covariance matrix is  $\mathbf{V}\mathbf{V}'\mathbf{X}'\mathbf{W}'\mathbf{W}\mathbf{X}\mathbf{V}\mathbf{V}'\phi$ : it is sometimes useful for testing terms for equality to zero.

### Value

A list with three items:

<code>Vb</code>	the Bayesian covariance matrix of the model parameters.
<code>Ve</code>	the frequentist covariance matrix for the parameter estimators.
<code>hat</code>	the leading diagonal of the hat (influence) matrix.
<code>edf</code>	the array giving the estimated degrees of freedom associated with each parameter.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>

### See Also

[magic](#)

---

mgcv

*Multiple Smoothing Parameter Estimation by GCV or UBRE*

---

### Description

Function to efficiently estimate smoothing parameters in Generalized Ridge Regression Problem with multiple (quadratic) penalties, by GCV or UBRE. The function uses Newton's method in multi-dimensions, backed up by steepest descent to iteratively adjust a set of relative smoothing parameters for each penalty. To ensure that the overall level of smoothing is optimal, and to guard against trapping by local minima, a highly efficient global minimisation with respect to one overall smoothing parameter is also made at each iteration. This is the original Wood (2000) method. It has now been superceded by the methods in [magic](#) (Wood, 2004) and [gam.fit3](#) (Wood, 2008).

For a listing of all routines in the `mgcv` package type:

```
library(help="mgcv"). For an overview of the mgcv package see mgcv-package.
```

### Usage

```
mgcv(y, X, sp, S, off, C=NULL, w=rep(1, length(y)), H=NULL,
      scale=1, gcv=TRUE, control=mgcv.control())
```

### Arguments

<code>y</code>	The response data vector.
<code>X</code>	The design matrix for the problem, note that <code>ncol(X)</code> must give the number of model parameters, while <code>nrow(X)</code> should give the number of data.
<code>sp</code>	An array of smoothing parameters. If <code>control\$fixed==TRUE</code> then these are taken as being the smoothing parameters. Otherwise any positive values are assumed to be initial estimates and negative values to signal auto-initialization.

<code>S</code>	A list of penalty matrices. Only the smallest square block containing all non-zero matrix elements is actually stored, and <code>off[i]</code> indicates the element of the parameter vector that <code>S[[i]][1,1]</code> relates to.
<code>off</code>	Offset values indicating where in the overall parameter a particular stored penalty starts operating. For example if <code>p</code> is the model parameter vector and <code>k=nrow(S[[i]])-1</code> , then the <i>i</i> th penalty is given by <code>t(p[off[i]:(off[i]+k)])%*%S[[i]]%*%p[off[i]:(off[i]+k)]</code> .
<code>C</code>	Matrix containing any linear equality constraints on the problem (i.e. $\mathbf{C}\mathbf{p} = \mathbf{0}$ ).
<code>w</code>	A vector of weights for the data (often proportional to the reciprocal of the standard deviation of $\bar{y}$ ).
<code>H</code>	A single fixed penalty matrix to be used in place of the multiple penalty matrices in <code>S</code> . <code>mgcv</code> cannot mix fixed and estimated penalties.
<code>scale</code>	This is the known scale parameter/error variance to use with UBRE. Note that it is assumed that the variance of $y_i$ is given by $\sigma^2/w_i$ .
<code>gcv</code>	If <code>gcv</code> is TRUE then smoothing parameters are estimated by GCV, otherwise UBRE is used.
<code>control</code>	A list of control options returned by <code>mgcv.control</code> .

## Details

This is documentation for the code implementing the method described in section 4 of Wood (2000). The method is a computationally efficient means of applying GCV to the problem of smoothing parameter selection in generalized ridge regression problems of the form:

$$\text{minimise } \|\mathbf{W}(\mathbf{X}\mathbf{p} - \mathbf{y})\|^2 \rho + \sum_{i=1}^m \lambda_i \mathbf{p}' \mathbf{S}_i \mathbf{p}$$

possibly subject to constraints  $\mathbf{C}\mathbf{p} = \mathbf{0}$ .  $\mathbf{X}$  is a design matrix,  $\mathbf{p}$  a parameter vector,  $\mathbf{y}$  a data vector,  $\mathbf{W}$  a diagonal weight matrix,  $\mathbf{S}_i$  a positive semi-definite matrix of coefficients defining the *i*th penalty and  $\mathbf{C}$  a matrix of coefficients defining any linear equality constraints on the problem. The smoothing parameters are the  $\lambda_i$  but there is an overall smoothing parameter  $\rho$  as well. Note that  $\mathbf{X}$  must be of full column rank, at least when projected into the null space of any equality constraints.

The method operates by alternating very efficient direct searches for  $\rho$  with Newton or steepest descent updates of the logs of the  $\lambda_i$ . Because the GCV/UBRE scores are flat w.r.t. very large or very small  $\lambda_i$ , it's important to get good starting parameters, and to be careful not to step into a flat region of the smoothing parameter space. For this reason the algorithm rescales any Newton step that would result in a  $\log(\lambda_i)$  change of more than 5. Newton steps are only used if the Hessian of the GCV/UBRE is positive definite, otherwise steepest descent is used. Similarly steepest descent is used if the Newton step has to be contracted too far (indicating that the quadratic model underlying Newton is poor). All initial steepest descent steps are scaled so that their largest component is 1. However a step is calculated, it is never expanded if it is successful (to avoid flat portions of the objective), but steps are successively halved if they do not decrease the GCV/UBRE score, until they do, or the direction is deemed to have failed. `M$conv` provides some convergence diagnostics.

The method is coded in C and is intended to be portable. It should be noted that seriously ill conditioned problems (i.e. with close to column rank deficiency in the design matrix) may cause problems, especially if weights vary wildly between observations.

**Value**

An object is returned with the following elements:

<code>b</code>	The best fit parameters given the estimated smoothing parameters.
<code>scale</code>	The estimated or supplied scale parameter/error variance.
<code>score</code>	The UBRE or GCV score.
<code>sp</code>	The estimated (or supplied) smoothing parameters ( $\lambda_i/\rho$ )
<code>Vb</code>	Estimated covariance matrix of model parameters.
<code>hat</code>	diagonal of the hat/influence matrix.
<code>edf</code>	array of estimated degrees of freedom for each parameter.
<code>info</code>	A list of convergence diagnostics, with the following elements: <b>edf</b> Array of whole model estimated degrees of freedom. <b>score</b> Array of ubre/gcv scores at the edfs for the final set of relative smoothing parameters. <b>g</b> the gradient of the GCV/UBRE score w.r.t. the smoothing parameters at termination. <b>h</b> the second derivatives corresponding to <code>g</code> above - i.e. the leading diagonal of the Hessian. <b>e</b> the eigenvalues of the Hessian. These should all be non-negative! <b>iter</b> the number of iterations taken. <b>in.ok</b> TRUE if the second smoothing parameter guess improved the GCV/UBRE score. (Please report examples where this is FALSE) <b>step.fail</b> TRUE if the algorithm terminated by failing to improve the GCV/UBRE score rather than by "converging". Not necessarily a problem, but check the above derivative information quite carefully.

**WARNING**

The method may not behave well with near column rank deficient **X** especially in contexts where the weights vary wildly.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

- Gu and Wahba (1991) Minimizing GCV/GML scores with multiple smoothing parameters via the Newton method. *SIAM J. Sci. Statist. Comput.* 12:383-398
- Wood, S.N. (2000) Modelling and Smoothing Parameter Estimation with Multiple Quadratic Penalties. *J.R.Statist.Soc.B* 62(2):413-428
- Wood, S.N. (2004) Stable and efficient multiple smoothing parameter estimation for generalized additive models. *J. Amer. Statist. Ass.* 99:673-686
- Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. *J.R.Statist.Soc.B* 70(3):495-518
- <http://www.maths.bath.ac.uk/~sw283/>

**See Also**

[gam](#), [magic](#)

**Examples**

```
library(help="mgcv") # listing of all routines

set.seed(1);n<-400;sig2<-4
x0 <- runif(n, 0, 1);x1 <- runif(n, 0, 1)
x2 <- runif(n, 0, 1);x3 <- runif(n, 0, 1)
f <- 2 * sin(pi * x0)
f <- f + exp(2 * x1) - 3.75887
f <- f+0.2*x2^11*(10*(1-x2))^6+10*(10*x2)^3*(1-x2)^10-1.396
e <- rnorm(n, 0, sqrt(sig2))
y <- f + e
# set up additive model
G<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),fit=FALSE)
# fit using mgcv
mgfit<-mgcv(G$y,G$X,G$sp,G$S,G$off,C=G$C)
```

---

mgcv.control

*Setting mgcv defaults*


---

**Description**

This is an internal function of package `mgcv` which allows control of the numerical options for fitting a generalized ridge regression problem using routine `mgcv`.

**Usage**

```
mgcv.control(conv.tol=1e-7,max.half=20,target.edf=NULL,min.edf=-1)
```

**Arguments**

<code>conv.tol</code>	The convergence tolerance.
<code>max.half</code>	successive step halvings are employed if the Newton method and then the steepest descent backup fail to improve the UBRE/GCV score. This is how many to use before giving up.
<code>target.edf</code>	If this is non-null it indicates that cautious optimization should be used, which opts for the local minimum closest to the target model edf if there are multiple local minima in the GCV/UBRE score.
<code>min.edf</code>	Lower bound on the model edf. Useful for avoiding numerical problems at high smoothing parameter values. Negative for none.

**Author(s)**

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

## References

Gu and Wahba (1991) Minimizing GCV/GML scores with multiple smoothing parameters via the Newton method. *SIAM J. Sci. Statist. Comput.* 12:383-398

Wood, S.N. (2000) Modelling and Smoothing Parameter Estimation with Multiple Quadratic Penalties. *J.R.Statist.Soc.B* 62(2):413-428

<http://www.maths.bath.ac.uk/~sw283/>

## See Also

[mgcv](#)

---

model.matrix.gam    *Extract model matrix from GAM fit*

---

## Description

Obtains the model matrix from a fitted gam object.

## Usage

```
## S3 method for class 'gam':  
model.matrix(object, ...)
```

## Arguments

object            fitted model object of class gam as produced by gam().  
...                other arguments, passed to [predict.gam](#).

## Details

Calls [predict.gam](#) with no newdata argument and type="lpmatrix" in order to obtain the model matrix of object.

## Value

A model matrix.

## Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

## References

Wood S.N. (2006b) *Generalized Additive Models: An Introduction with R*. Chapman and Hall/CRC Press.

## See Also

[gam](#)

**Examples**

```
n <- 15
x <- runif(n)
y <- sin(x*2*pi) + rnorm(n)*.2
mod <- gam(y~s(x,bs="cc",k=6),knots=list(x=seq(0,1,length=6)))
model.matrix(mod)
```

mono.con

*Monotonicity constraints for a cubic regression spline***Description**

Finds linear constraints sufficient for monotonicity (and optionally upper and/or lower boundedness) of a cubic regression spline. The basis representation assumed is that given by the `gam`, "cr" basis: that is the spline has a set of knots, which have fixed x values, but the y values of which constitute the parameters of the spline.

**Usage**

```
mono.con(x, up=TRUE, lower=NA, upper=NA)
```

**Arguments**

x	The array of knot locations.
up	If TRUE then the constraints imply increase, if FALSE then decrease.
lower	This specifies the lower bound on the spline unless it is NA in which case no lower bound is imposed.
upper	This specifies the upper bound on the spline unless it is NA in which case no upper bound is imposed.

**Details**

Consider the natural cubic spline passing through the points:  $\{x_i, p_i : i = 1 \dots n\}$ . Then it is possible to find a relatively small set of linear constraints on  $\mathbf{p}$  sufficient to ensure monotonicity (and bounds if required):  $\mathbf{A}\mathbf{p} \geq \mathbf{b}$ . Details are given in Wood (1994). This function returns a list containing  $\mathbf{A}$  and  $\mathbf{b}$ .

**Value**

The function returns a list containing constraint matrix  $\mathbf{A}$  and constraint vector  $\mathbf{b}$ .

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

Gill, P.E., Murray, W. and Wright, M.H. (1981) Practical Optimization. Academic Press, London.  
 Wood, S.N. (1994) Monotonic smoothing splines fitted by cross validation SIAM Journal on Scientific Computing 15(5):1126-1133

<http://www.maths.bath.ac.uk/~sw283/>

**See Also**

`mgcv` `pcls`

**Examples**

```
## see ?pcls
```

---

mroot	<i>Smallest square root of matrix</i>
-------	---------------------------------------

---

**Description**

Find a square root of a positive semi-definite matrix, having as few columns as possible. Uses either pivoted choleski decomposition or singular value decomposition to do this.

**Usage**

```
mroot(A, rank=NULL, method="chol")
```

**Arguments**

A	The positive semi-definite matrix, a square root of which is to be found.
rank	if the rank of the matrix A is known then it should be supplied.
method	"chol" to use pivoted choleski decompositon, which is fast but tends to over-estimate rank. "svd" to use singular value decomposition, which is slow, but is the most accurate way to estimate rank.

**Details**

The routine uses an LAPACK SVD routine, or the LINPACK pivoted Choleski routine. It is primarily of use for turning penalized regression problems into ordinary regression problems.

**Value**

A matrix, **B** with as many columns as the rank of **A**, and such that  $A = BB'$ .

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**Examples**

```
set.seed(0)
a <- matrix(runif(24), 6, 4)
A <- a%*%t(a) ## A is +ve semi-definite, rank 4
B <- mroot(A) ## default pivoted choleski method
tol <- 100*.Machine$double.eps
chol.err <- max(abs(A-B%*%t(B)));chol.err
if (chol.err>tol) warning("mroot (chol) suspect")
B <- mroot(A,method="svd") ## svd method
svd.err <- max(abs(A-B%*%t(B)));svd.err
if (svd.err>tol) warning("mroot (svd) suspect")
```



negbin

*GAM negative binomial family***Description**

The `gam` modelling function is designed to be able to use the `negbin` family (a modification of MASS library `negative.binomial` family by Venables and Ripley), with or without a known  $\theta$  parameter. Two approaches to estimating the `theta` parameter are available:

- If ‘performance iteration’ is used for smoothing parameter estimation (see `gam`), then smoothing parameters are chosen by GCV and `theta` is chosen in order to ensure that the Pearson estimate of the scale parameter is as close as possible to 1, the value that the scale parameter should have.
- If ‘outer iteration’ is used for smoothing parameter selection, and smoothing parameters are chosen by UBRE/AIC (with scale parameter set to 1) then a value of `theta` is searched for which minimizes the AIC of the model. Alternatively If (RE)ML is used for smoothing parameter estimation then a value of `theta` is searched for which maximizes the (restricted) likelihood.

The second option is much slower than the first, but the first can sometimes fail to converge. To use the first option, set the `optimizer` argument of `gam` to "perf".

**Usage**

```
negbin(theta = stop("'theta' must be specified"), link = "log")
```

**Arguments**

<code>theta</code>	Either i) a single value known value of $\theta$ , ii) two values of $\theta$ specifying the endpoints of an interval over which to search for $\theta$ or iii) an array of values of $\theta$ , specifying the set of $\theta$ values to search. (iii) is only available with AIC based $\theta$ estimation.
<code>link</code>	The link function: one of "log", "identity" or "sqrt"

**Details**

If a single value of `theta` is supplied then it is always taken as the known fixed value, and estimation of smoothing parameters is then by UBRE/AIC. If `theta` is two numbers (`theta[2]>theta[1]`) then they are taken as specifying the range of values over which to search for the optimal  $\theta$ . If `theta` is any other array of numbers then they are taken as the discrete set of values of  $\theta$  over which to search for  $\theta$ . The latter option only works with AIC based outer iteration, if performance iteration is used then an array will only be used to define a search range.

If performance iteration is used (see `gam` argument `optimizer`) then the method of estimation is to choose  $\hat{\theta}$  so that the GCV (Pearson) estimate of the scale parameter is one (since the scale parameter is one for the negative binomial). In this case  $\theta$  estimation is nested within the IRLS loop used for GAM fitting. After each call to fit an iteratively weighted additive model to the IRLS pseudodata, the  $\theta$  estimate is updated. This is done by conditioning on all components of the current GCV/Pearson estimator of the scale parameter except  $\theta$  and then searching for the  $\hat{\theta}$  which equates this conditional estimator to one. The search is a simple bisection search after an initial crude line

search to bracket one. The search will terminate at the upper boundary of the search region is a Poisson fit would have yielded an estimated scale parameter  $<1$ .

If outer iteration is used then  $\theta$  is estimated by searching for the value yielding the lowest AIC. The search is either over the supplied array of values, or is a grid search over the supplied range, followed by a golden section search. A full fit is required for each trial  $\theta$ , so the process is slow, but speed is enhanced by making the changes in  $\theta$  as small as possible, from one step to the next, and using the previous smoothing parameter and fitted values to start the new fit.

In a simulation test based on 800 replicates of the first example data, given below, the GCV based (performance iteration) method yielded models with, on average 6% better MSE performance than the AIC based (outer iteration) method. `theta` had a 0.86 correlation coefficient between the two methods. `theta` estimates averaged 3.36 with a standard deviation of 0.44 for the AIC based method and 3.22 with a standard deviation of 0.43 for the GCV based method. However the GCV based method is less computationally reliable, failing in around 4% of replicates.

### Value

An object inheriting from class `family`, with additional elements

<code>dvar</code>	the function giving the first derivative of the variance function w.r.t. <code>mu</code> .
<code>d2var</code>	the function giving the second derivative of the variance function w.r.t. <code>mu</code> .
<code>getTheta</code>	A function for retrieving the value(s) of <code>theta</code> . This also useful for retrieving the estimate of <code>theta</code> after fitting (see example).

### WARNINGS

`gamm` does not support `theta` estimation

The negative binomial functions from the MASS library are no longer supported.

### Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)> modified from Venables and Ripley's `negative.binomial` family.

### References

Venables, B. and B.R. Ripley (2002) *Modern Applied Statistics in S*, Springer.

### Examples

```
library(mgcv)
set.seed(3)
n<-400
dat <- gamSim(1,n=n)
g <- exp(dat$f/5)

# negative binomial data
dat$y <- rnbinom(g, size=3, mu=g)
# known theta ...
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3), family=negbin(3), data=dat)
plot(b, pages=1)
print(b)

## unknown theta via performance iteration...
b1 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3), family=negbin(c(1,10)),
```

```

        optimizer="perf",data=dat)
plot(b1,pages=1)
print(b1)

## unknown theta via outer iteration and AIC search...
b2<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=negbin(c(1,10)),
        data=dat)
plot(b2,pages=1)
print(b2)

## Same again all by REML...
b2a <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=negbin(c(1,10)),
        data=dat,method="REML")
plot(b2a,pages=1)
print(b2a)

## how to retrieve Theta...
b2a$family$getTheta()

## unknown theta via outer iteration and AIC search
## over a discrete set of values...
b3<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=negbin(2:10/2),
        data=dat)
plot(b3,pages=1)
print(b3)

## another example...
set.seed(1)
f <- dat$f
f <- f - min(f);g <- f^2
dat$y <- rnbino(m,g,size=3,mu=g)
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=negbin(1:10,link="sqrt"),
        data=dat)
plot(b,pages=1)
print(b)
rm(dat)

```

---

new.name

---

*Obtain a name for a new variable that is not already in use*


---

## Description

`gamm` works by transforming a GAMM into something that can be estimated by `lme`, but this involves creating new variables, the names of which should not clash with the names of other variables on which the model depends. This simple service routine checks a suggested name against a list of those in use, and if necessary modifies it so that there is no clash.

## Usage

```
new.name(proposed, old.names)
```

**Arguments**

proposed      a suggested name  
old.names      An array of names that must not be duplicated

**Value**

A name that is not in old.names.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

<http://www.maths.bath.ac.uk/~sw283/>

**See Also**

[gamm](#)

**Examples**

```
old <- c("a", "tuba", "is", "tubby")  
new.name("tubby", old)
```

---

notExp

*Functions for better-than-log positive parameterization*

---

**Description**

It is common practice in statistical optimization to use log-parameterizations when a parameter ought to be positive. i.e. if an optimization parameter  $a$  should be non-negative then we use  $a = \exp(b)$  and optimize with respect to the unconstrained parameter  $b$ . This often works well, but it does imply a rather limited working range for  $b$ : using 8 byte doubles, for example, if  $b$ 's magnitude gets much above 700 then  $a$  overflows or underflows. This can cause problems for numerical optimization methods.

notExp is a monotonic function for mapping the real line into the positive real line with much less extreme underflow and overflow behaviour than `exp`. It is a piece-wise function, but is continuous to second derivative: see the source code for the exact definition, and the example below to see what it looks like.

notLog is the inverse function of notExp.

The major use of these functions was originally to provide more robust `pdMat` classes for `lme` for use by `gamm`. Currently the `notExp2` and `notLog2` functions are used in their place, as a result of changes to the `nlme` optimization routines.

**Usage**

```
notExp(x)
```

```
notLog(x)
```

**Arguments**

`x` Argument array of real numbers (`notExp`) or positive real numbers (`notLog`).

**Value**

An array of function values evaluated at the supplied argument values.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

<http://www.maths.bath.ac.uk/~sw283/>

**See Also**

[pdTens](#), [pdIdnot](#), [gamm](#)

**Examples**

```
## Illustrate the notExp function:
## less steep than exp, but still monotonic.
x <- -100:100/10
op <- par(mfrow=c(2,2))
plot(x,notExp(x),type="l")
lines(x,exp(x),col=2)
plot(x,log(notExp(x)),type="l")
lines(x,log(exp(x)),col=2) # redundancy intended
x <- x/4
plot(x,notExp(x),type="l")
lines(x,exp(x),col=2)
plot(x,log(notExp(x)),type="l")
lines(x,log(exp(x)),col=2) # redundancy intended
par(op)
range(notLog(notExp(x))-x) # show that inverse works!
```

---

notExp2

*Alternative to log parameterization for variance components*

---

**Description**

`notLog2` and `notExp2` are alternatives to `log` and `exp` or `notLog` and `notExp` for re-parameterization of variance parameters. They are used by the `pdTens` and `pdIdnot` classes which in turn implement smooths for `gamm`.

The functions are typically used to ensure that smoothing parameters are positive, but the `notExp2` is not monotonic: rather it cycles between ‘effective zero’ and ‘effective infinity’ as its argument changes. The `notLog2` is the inverse function of the `notExp2` only over an interval centered on zero.

Parameterizations using these functions ensure that estimated smoothing parameters remain positive, but also help to ensure that the likelihood is never indefinite: once a working parameter pushes

a smoothing parameter below ‘effective zero’ or above ‘effective infinity’ the cyclic nature of the `notExp2` causes the likelihood to decrease, where otherwise it might simply have flattened.

This parameterization is really just a numerical trick, in order to get `lme` to fit `gamm` models, without failing due to indefiniteness. Note in particular that asymptotic results on the likelihood/REML criterion are not invalidated by the trick, unless parameter estimates end up close to the effective zero or effective infinity: but if this is the case then the asymptotics would also have been invalid for a conventional monotonic parameterization.

This reparameterization was made necessary by some modifications to the underlying optimization method in `lme` introduced in `nlme` 3.1-62. It is possible that future releases will return to the `notExp` parameterization.

Note that you can reset ‘effective zero’ and ‘effective infinity’: see below.

### Usage

```
notExp2(x, d=.Options$mgcv.vc.logrange, b=1/d)
```

```
notLog2(x, d=.Options$mgcv.vc.logrange, b=1/d)
```

### Arguments

<code>x</code>	Argument array of real numbers ( <code>notExp</code> ) or positive real numbers ( <code>notLog</code> ).
<code>d</code>	the range of <code>notExp2</code> runs from $\exp(-d)$ to $\exp(d)$ . To change the range used by <code>gamm</code> reset <code>mgcv.vc.logrange</code> using <code>options</code> .
<code>b</code>	determines the period of the cycle of <code>notExp2</code> .

### Value

An array of function values evaluated at the supplied argument values.

### Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

### References

<http://www.maths.bath.ac.uk/~sw283/>

### See Also

[pdTens](#), [pdIdnot](#), [gamm](#)

### Examples

```
## Illustrate the notExp2 function:
x <- seq(-50, 50, length=1000)
op <- par(mfrow=c(2, 2))
plot(x, notExp2(x), type="l")
lines(x, exp(x), col=2)
plot(x, log(notExp2(x)), type="l")
lines(x, log(exp(x)), col=2) # redundancy intended
x <- x/4
plot(x, notExp2(x), type="l")
lines(x, exp(x), col=2)
```

```
plot(x, log(notExp2(x)), type="l")
lines(x, log(exp(x)), col=2) # redundancy intended
par(op)
```

---

```
null.space.dimension
```

*The basis of the space of un-penalized functions for a TPRS*

---

## Description

The thin plate spline penalties give zero penalty to some functions. The space of these functions is spanned by a set of polynomial terms. `null.space.dimension` finds the dimension of this space,  $M$ , given the number of covariates that the smoother is a function of,  $d$ , and the order of the smoothing penalty,  $m$ . If  $m$  does not satisfy  $2m > d$  then the smallest possible dimension for the null space is found given  $d$  and the requirement that the smooth should be visually smooth.

## Usage

```
null.space.dimension(d, m)
```

## Arguments

`d` is a positive integer - the number of variables of which the t.p.s. is a function.  
`m` a non-negative integer giving the order of the penalty functional, or signalling that the default order should be used.

## Details

Thin plate splines are only visually smooth if the order of the wiggleness penalty,  $m$ , satisfies  $2m > d + 1$ . If  $2m < d + 1$  then this routine finds the smallest  $m$  giving visual smoothness for the given  $d$ , otherwise the supplied  $m$  is used. The null space dimension is given by:

$$M = (m + d - 1)! / (d!(m - 1)!)$$

which is the value returned.

## Value

An integer (array), the null space dimension  $M$ .

## Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

## References

Wood, S.N. (2003) Thin plate regression splines. *J.R.Statist.Soc.B* 65(1):95-114  
<http://www.maths.bath.ac.uk/~sw283/>

## See Also

[tprs](#)

**Examples**

```
null.space.dimension(2,0)
```

pcls

*Penalized Constrained Least Squares Fitting***Description**

Solves least squares problems with quadratic penalties subject to linear equality and inequality constraints using quadratic programming.

**Usage**

```
pcls(M)
```

**Arguments**

- M** is the single list argument to `pcls`. It should have the following elements:
- y** The response data vector.
  - w** A vector of weights for the data (often proportional to the reciprocal of the variance).
  - X** The design matrix for the problem, note that `ncol(M$X)` must give the number of model parameters, while `nrow(M$X)` should give the number of data.
  - C** Matrix containing any linear equality constraints on the problem (e.g.  $\mathbf{C}\mathbf{p} = \mathbf{c}$ ). If you have no equality constraints initialize this to a zero by zero matrix. Note that there is no need to supply the vector  $\mathbf{c}$ , it is defined implicitly by the initial parameter estimates  $\mathbf{p}$ .
  - S** A list of penalty matrices. `S[[i]]` is the smallest contiguous matrix including all the non-zero elements of the  $i$ th penalty matrix. The first parameter it penalizes is given by `off[i]+1` (starting counting at 1).
  - off** Offset values locating the elements of `M$S` in the correct location within each penalty coefficient matrix. (Zero offset implies starting in first location)
  - sp** An array of smoothing parameter estimates.
  - p** An array of feasible initial parameter estimates - these must satisfy the constraints, but should avoid satisfying the inequality constraints as equality constraints.
  - Ain** Matrix for the inequality constraints  $\mathbf{A}_{in}\mathbf{p} > \mathbf{b}_{in}$ .
  - bin** vector in the inequality constraints.

**Details**

This solves the problem:

$$\text{minimise } \|\mathbf{W}^{1/2}(\mathbf{X}\mathbf{p} - \mathbf{y})\|^2 + \sum_{i=1}^m \lambda_i \mathbf{p}' \mathbf{S}_i \mathbf{p}$$

subject to constraints  $\mathbf{C}\mathbf{p} = \mathbf{c}$  and  $\mathbf{A}_{in}\mathbf{p} > \mathbf{b}_{in}$ , w.r.t.  $\mathbf{p}$  given the smoothing parameters  $\lambda_i$ .  $\mathbf{X}$  is a design matrix,  $\mathbf{p}$  a parameter vector,  $\mathbf{y}$  a data vector,  $\mathbf{W}$  a diagonal weight matrix,  $\mathbf{S}_i$  a positive



semi-definite matrix of coefficients defining the  $i$ th penalty and  $\mathbf{C}$  a matrix of coefficients defining the linear equality constraints on the problem. The smoothing parameters are the  $\lambda_i$ . Note that  $\mathbf{X}$  must be of full column rank, at least when projected into the null space of any equality constraints.  $\mathbf{A}_{in}$  is a matrix of coefficients defining the inequality constraints, while  $\mathbf{b}_{in}$  is a vector involved in defining the inequality constraints.

Quadratic programming is used to perform the solution. The method used is designed for maximum stability with least squares problems: i.e.  $\mathbf{X}'\mathbf{X}$  is not formed explicitly. See Gill et al. 1981.

### Value

The function returns an array containing the estimated parameter vector.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>

### References

- Gill, P.E., Murray, W. and Wright, M.H. (1981) Practical Optimization. Academic Press, London.
- Wood, S.N. (1994) Monotonic smoothing splines fitted by cross validation SIAM Journal on Scientific Computing 15(5):1126-1133
- <http://www.maths.bath.ac.uk/~sw283/>

### See Also

[mgcv.mono.con](http://mgcv.mono.con)

### Examples

```
# first an un-penalized example - fit E(y)=a+bx subject to a>0
set.seed(0)
n<-100
x<-runif(n);y<-x-0.2+rnorm(n)*0.1
M<-list(X=matrix(0,n,2),p=c(0.1,0.5),off=array(0,0),S=list(),
Ain=matrix(0,1,2),bin=0,C=matrix(0,0,0),sp=array(0,0),y=y,w=y*0+1)
M$X[,1]<-1;M$X[,2]<-x;M$Ain[1,]<-c(1,0)
pcls(M)->M$p
plot(x,y);abline(M$p,col=2);abline(coef(lm(y~x)),col=3)

# Penalized example: monotonic penalized regression spline .....

# Generate data from a monotonic truth.
x<-runif(100)*4-1;x<-sort(x);
f<-exp(4*x)/(1+exp(4*x));y<-f+rnorm(100)*0.1;plot(x,y)
dat<-data.frame(x=x,y=y)
# Show regular spline fit (and save fitted object)
f.ug<-gam(y~s(x,k=10,bs="cr"));lines(x,fitted(f.ug))
# Create Design matrix, constraints etc. for monotonic spline....
sm<-smoothCon(s(x,k=10,bs="cr"),dat,knots=NULL)[[1]]
F<-mono.con(sm$xp); # get constraints
G<-list(X=sm$X,C=matrix(0,0,0),sp=f.ug$sp,p=sm$xp,y=y,w=y*0+1)
G$Ain<-F$A;G$bin<-F$b;G$S<-sm$S;G$off<-0

p<-pcls(G); # fit spline (using s.p. from unconstrained fit)
```

```

fv<-Predict.matrix(sm,data.frame(x=x))%*%p
lines(x,fv,col=2)

# now a tprs example of the same thing...

f.ug<-gam(y~s(x,k=10));lines(x,fitted(f.ug))
# Create Design matrix, constraints etc. for monotonic spline....
sm<-smoothCon(s(x,k=10,bs="tp"),dat,knots=NULL)[[1]]
xc<-0:39/39 # points on [0,1]
nc<-length(xc) # number of constraints
xc<-xc*4-1 # points at which to impose constraints
A0<-Predict.matrix(sm,data.frame(x=xc))
# ... A0%*%p evaluates spline at xc points
A1<-Predict.matrix(sm,data.frame(x=xc+1e-6))
A<-(A1-A0)/1e-6
## ... approx. constraint matrix (A%*%p is -ve
## spline gradient at points xc)
G<-list(X=sm$X,C=matrix(0,0,0),sp=f.ug$sp,y=y,w=y*0+1,S=sm$S,off=0)
G$Ain<-A; # constraint matrix
G$bin<-rep(0,nc); # constraint vector
G$p<-rep(0,10);G$p[10]<-0.1
# ... monotonic start params, got by setting coefs of polynomial part
p<-pcls(G); # fit spline (using s.p. from unconstrained fit)

fv2<-Predict.matrix(sm,data.frame(x=x))%*%p
lines(x,fv2,col=3)

#####
## monotonic additive model example...
#####

## First simulate data...

set.seed(10)
f1 <- function(x) 5*exp(4*x)/(1+exp(4*x));
f2 <- function(x) {
  ind <- x > .5
  f <- x*0
  f[ind] <- (x[ind] - .5)^2*10
  f
}
f3 <- function(x) 0.2 * x^11 * (10 * (1 - x))^6 +
  10 * (10 * x)^3 * (1 - x)^10
n <- 200
x <- runif(n); z <- runif(n); v <- runif(n)
mu <- f1(x) + f2(z) + f3(v)
y <- mu + rnorm(n)

## Preliminary unconstrained gam fit...
G <- gam(y~s(x)+s(z)+s(v,k=20),fit=FALSE)
b <- gam(G=G)

## generate constraints, by finite differencing
## using predict.gam ....
eps <- 1e-7
pd0 <- data.frame(x=seq(0,1,length=100),z=rep(.5,100),
  v=rep(.5,100))

```

```

pd1 <- data.frame(x=seq(0,1,length=100)+eps,z=rep(.5,100),
                 v=rep(.5,100))
X0 <- predict(b,newdata=pd0,type="lpmatrix")
X1 <- predict(b,newdata=pd1,type="lpmatrix")
Xx <- (X1 - X0)/eps ## Xx %*% coef(b) must be positive
pd0 <- data.frame(z=seq(0,1,length=100),x=rep(.5,100),
                 v=rep(.5,100))
pd1 <- data.frame(z=seq(0,1,length=100)+eps,x=rep(.5,100),
                 v=rep(.5,100))
X0 <- predict(b,newdata=pd0,type="lpmatrix")
X1 <- predict(b,newdata=pd1,type="lpmatrix")
Xz <- (X1-X0)/eps
G$Ain <- rbind(Xx,Xz) ## inequality constraint matrix
G$bin <- rep(0,nrow(G$Ain))
G$sp <- b$sp
G$p <- coef(b)
## force initial parameters to meet constraint
G$p[11:18] <- G$p[2:9] <- 0
p <- pcls(G) ## constrained fit
par(mfrow=c(2,3))
plot(b) ## original fit
b$coefficients <- p
plot(b) ## constrained fit
## note that standard errors in preceding plot are obtained from
## unconstrained fit

```

---

pdIdnot

*Overflow proof pdMat class for multiples of the identity matrix*


---

## Description

This set of functions is a modification of the `pdMat` class `pdIdent` from library `nlme`. The modification is to replace the log parameterization used in `pdMat` with a `notLog2` parameterization, since the latter avoids indefiniteness in the likelihood and associated convergence problems: the parameters also relate to variances rather than standard deviations, for consistency with the `pdTens` class. The functions are particularly useful for working with Generalized Additive Mixed Models where variance parameters/smoothing parameters can be very large or very small, so that overflow or underflow can be a problem.

These functions would not normally be called directly, although unlike the `pdTens` class it is easy to do so.

## Usage

```

pdIdnot(value = numeric(0), form = NULL,
        nam = NULL, data = sys.frame(sys.parent()))

```

## Arguments

<code>value</code>	Initialization values for parameters. Not normally used.
<code>form</code>	A one sided formula specifying the random effects structure.
<code>nam</code>	a names argument, not normally used with this class.
<code>data</code>	data frame in which to evaluate formula.

**Details**

The following functions are provided: `Dim.pdIndot`, `coef.pdIdnot`, `corMatrix.pdIdnot`, `logDet.pdIdnot`, `pdConstruct.pdIdnot`, `pdFactor.pdIdnot`, `pdMatrix.pdIdnot`, `solve.pdIdnot`, `summary.pdIdnot`. (e.g. `mgcv:::coef.pdIdnot` to access.)

Note that while the `pdFactor` and `pdMatrix` functions return the inverse of the scaled random effect covariance matrix or its factor, the `pdConstruct` function is initialised with estimates of the scaled covariance matrix itself.

**Value**

A class `pdIdnot` object, or related quantities. See the `nlme` documentation for further details.

**Author(s)**

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

**References**

Pinheiro J.C. and Bates, D.M. (2000) *Mixed effects Models in S and S-PLUS*. Springer

The `nlme` source code.

<http://www.maths.bath.ac.uk/~sw283/>

**See Also**

[te](#), [pdTens](#), [notLog2](#), [gamm](#)

**Examples**

```
# see gamm
```

---

pdTens

*Functions implementing a pdMat class for tensor product smooths*

---

**Description**

This set of functions implements an `nlme` library `pdMat` class to allow tensor product smooths to be estimated by `lme` as called by `gamm`. Tensor product smooths have a penalty matrix made up of a weighted sum of penalty matrices, where the weights are the smoothing parameters. In the mixed model formulation the penalty matrix is the inverse of the covariance matrix for the random effects of a term, and the smoothing parameters (times a half) are variance parameters to be estimated. It's not possible to transform the problem to make the required random effects covariance matrix look like one of the standard `pdMat` classes: hence the need for the `pdTens` class. A `notLog2` parameterization ensures that the parameters are positive.

These functions (`pdTens`, `pdConstruct.pdTens`, `pdFactor.pdTens`, `pdMatrix.pdTens`, `coef.pdTens` and `summary.pdTens`) would not normally be called directly.

**Usage**

```
pdTens(value = numeric(0), form = NULL,
       nam = NULL, data = sys.frame(sys.parent()))
```

**Arguments**

value	Initialization values for parameters. Not normally used.
form	A one sided formula specifying the random effects structure. The formula should have an attribute <code>S</code> which is a list of the penalty matrices the weighted sum of which gives the inverse of the covariance matrix for these random effects.
nam	a names argument, not normally used with this class.
data	data frame in which to evaluate formula.

**Details**

If using this class directly note that it is worthwhile scaling the `S` matrices to be of ‘moderate size’, for example by dividing each matrix by its largest singular value: this avoids problems with `lme` defaults (`smooth.construct.tensor.smooth.spec` does this automatically).

This appears to be the minimum set of functions required to implement a new `pdMat` class.

Note that while the `pdFactor` and `pdMatrix` functions return the inverse of the scaled random effect covariance matrix or its factor, the `pdConstruct` function is sometimes initialised with estimates of the scaled covariance matrix, and sometimes intialized with its inverse.

**Value**

A class `pdTens` object, or its coefficients or the matrix it represents or the factor of that matrix. `pdFactor` returns the factor as a vector (packed column-wise) (`pdMatrix` always returns a matrix).

**Author(s)**

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

**References**

Pinheiro J.C. and Bates, D.M. (2000) Mixed effects Models in S and S-PLUS. Springer

The `nlme` source code.

<http://www.maths.bath.ac.uk/~sw283/>

**See Also**

[te gamm](#)

**Examples**

```
# see gamm
```

---

`place.knots`*Automatically place a set of knots evenly through covariate values*

---

**Description**

Given a univariate array of covariate values, places a set of knots for a regression spline evenly through the covariate values.

**Usage**

```
place.knots(x, nk)
```

**Arguments**

`x`                array of covariate values (need not be sorted).  
`nk`                integer indicating the required number of knots.

**Details**

Places knots evenly throughout a set of covariates. For example, if you had 11 covariate values and wanted 6 knots then a knot would be placed at the first (sorted) covariate value and every second (sorted) value thereafter. With less convenient numbers of data and knots the knots are placed within intervals between data in order to achieve even coverage, where even means having approximately the same number of data between each pair of knots.

**Value**

An array of knot locations.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

<http://www.maths.bath.ac.uk/~sw283/>

**See Also**

[smooth.construct.cc.smooth.spec](http://smooth.construct.cc.smooth.spec)

**Examples**

```
x<-runif(30)
place.knots(x, 7)
rm(x)
```

plot.gam

*Default GAM plotting***Description**

Takes a fitted `gam` object produced by `gam()` and plots the component smooth functions that make it up, on the scale of the linear predictor. Optionally produces term plots for parametric model components as well.

**Usage**

```
## S3 method for class 'gam':
plot(x, residuals=FALSE, rug=TRUE, se=TRUE, pages=0, select=NULL, scale=-1,
      n=100, n2=40, pers=FALSE, theta=30, phi=30, jit=FALSE, xlab=NULL,
      ylab=NULL, main=NULL, ylim=NULL, xlim=NULL, too.far=0.1,
      all.terms=FALSE, shade=FALSE, shade.col="gray80",
      shift=0, trans=I, seWithMean=FALSE, by.resids=FALSE, ...)
```

**Arguments**

<code>x</code>	a fitted <code>gam</code> object as produced by <code>gam()</code> .
<code>residuals</code>	If <code>TRUE</code> then partial residuals are added to plots of 1-D smooths. If <code>FALSE</code> then no residuals are added. If this is an array of the correct length then it is used as the array of residuals to be used for producing partial residuals. If <code>TRUE</code> then the residuals are the working residuals from the IRLS iteration weighted by the IRLS weights. Partial residuals for a smooth term are the residuals that would be obtained by dropping the term concerned from the model, while leaving all other estimates fixed (i.e. the estimates for the term plus the residuals).
<code>rug</code>	when <code>TRUE</code> (default) then the covariate to which the plot applies is displayed as a rug plot at the foot of each plot of a 1-d smooth, and the locations of the covariates are plotted as points on the contour plot representing a 2-d smooth.
<code>se</code>	when <code>TRUE</code> (default) upper and lower lines are added to the 1-d plots at 2 standard errors above and below the estimate of the smooth being plotted while for 2-d plots, surfaces at +1 and -1 standard errors are contoured and overlaid on the contour plot for the estimate. If a positive number is supplied then this number is multiplied by the standard errors when calculating standard error curves or surfaces. See also <code>shade</code> , below.
<code>pages</code>	(default 0) the number of pages over which to spread the output. For example, if <code>pages=1</code> then all terms will be plotted on one page with the layout performed automatically. Set to 0 to have the routine leave all graphics settings as they are.
<code>select</code>	Allows the plot for a single model term to be selected for printing. e.g. if you just want the plot for the second smooth term set <code>select=2</code> .
<code>scale</code>	set to -1 (default) to have the same y-axis scale for each plot, and to 0 for a different y axis for each plot. Ignored if <code>ylim</code> supplied.
<code>n</code>	number of points used for each 1-d plot - for a nice smooth plot this needs to be several times the estimated degrees of freedom for the smooth. Default value 100.
<code>n2</code>	Square root of number of points used to grid estimates of 2-d functions for contouring.

<code>pers</code>	Set to TRUE if you want perspective plots for 2-d terms.
<code>theta</code>	One of the perspective plot angles.
<code>phi</code>	The other perspective plot angle.
<code>jit</code>	Set to TRUE if you want rug plots for 1-d terms to be jittered.
<code>xlab</code>	If supplied then this will be used as the x label for all plots.
<code>ylab</code>	If supplied then this will be used as the y label for all plots.
<code>main</code>	Used as title (or z axis label) for plots if supplied.
<code>ylim</code>	If supplied then this pair of numbers are used as the y limits for each plot.
<code>xlim</code>	If supplied then this pair of numbers are used as the x limits for each plot.
<code>too.far</code>	If greater than 0 then this is used to determine when a location is too far from data to be plotted when plotting 2-D smooths. This is useful since smooths tend to go wild away from data. The data are scaled into the unit square before deciding what to exclude, and <code>too.far</code> is a distance within the unit square.
<code>all.terms</code>	if set to TRUE then the partial effects of parametric model components are also plotted, via a call to <code>termplot</code> . Only terms of order 1 can be plotted in this way.
<code>shade</code>	Set to TRUE to produce shaded regions as confidence bands for smooths (not available for parametric terms, which are plotted using <code>termplot</code> ).
<code>shade.col</code>	define the color used for shading confidence bands.
<code>shift</code>	constant to add to each smooth (on the scale of the linear predictor) before plotting. Can be useful for some diagnostics, or with <code>trans</code> .
<code>trans</code>	function to apply to each smooth (after any shift), before plotting. <code>shift</code> and <code>trans</code> are occasionally useful as a means for getting plots on the response scale, when the model consists only of a single smooth.
<code>seWithMean</code>	if TRUE the component smooths are shown with confidence intervals that include the uncertainty about the overall mean. If FALSE then the uncertainty relates purely to the centred smooth itself. An extension of the argument presented in Nychka (1988) suggests that TRUE results in better coverage performance, and this is also suggested by simulation.
<code>by.resids</code>	Should partial residuals be plotted for terms with <code>by</code> variables? Usually the answer is no, they would be meaningless.
<code>...</code>	other graphics parameters to pass on to plotting commands.

## Details

Produces default plot showing the smooth components of a fitted GAM, and optionally parametric terms as well, when these can be handled by `termplot`.

For plots of 1-d smooths, the x axis of each plot is labelled with the covariate name, while the y axis is labelled `s(cov, edf)` where `cov` is the covariate name, and `edf` the estimated (or user defined for regression splines) degrees of freedom of the smooth.

Contour plots are produced for 2-d smooths with the x-axes labelled with the first covariate name and the y axis with the second covariate name. The main title of the plot is something like `s(var1, var2, edf)`, indicating the variables of which the term is a function, and the estimated degrees of freedom for the term. When `se=TRUE`, estimator variability is shown by overlaying contour plots at plus and minus 1 s.e. relative to the main estimate. If `se` is a positive number then contour plots are at plus or minus `se` multiplied by the s.e. Contour levels are chosen to try and



ensure reasonable separation of the contours of the different plots, but this is not always easy to achieve. Note that these plots can not be modified to the same extent as the other plot.

Smooths of more than 2 variables are not currently dealt with, but simply generate a warning, but see [vis.gam](#).

Fine control of plots for parametric terms can be obtained by calling `termplot` directly, taking care to use its `terms` argument.

Note that, if `seWithMean=TRUE`, the confidence bands include the uncertainty about the overall mean. In other words although each smooth is shown centred, the confidence bands are obtained as if every other term in the model was constrained to have average 0, (average taken over the covariate values), except for the smooth concerned. This seems to correspond more closely to how most users interpret componentwise intervals in practice, and also results in intervals with close to nominal (frequentist) coverage probabilities by an extension of Nychka's (1988) results.

### Value

The function simply generates plots.

### WARNING

Note that the behaviour of this function is not identical to `plot.gam()` in S-PLUS.

Plots of 2-D smooths with standard error contours shown can not easily be customized.

The function can not deal with smooths of more than 2 variables!

### Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

Henric Nilsson <[henric.nilsson@statisticon.se](mailto:henric.nilsson@statisticon.se)> donated the code for the `shade` option.

The design is inspired by the S function of the same name described in Chambers and Hastie (1993) (but is not a clone).

### References

Chambers and Hastie (1993) *Statistical Models in S*. Chapman & Hall.

Nychka (1988) Bayesian Confidence Intervals for Smoothing Splines. *Journal of the American Statistical Association* 83:1134-1143.

Wood S.N. (2006) *Generalized Additive Models: An Introduction with R*. Chapman and Hall/CRC Press.

### See Also

[gam](#), [predict.gam](#), [vis.gam](#)

### Examples

```
library(mgcv)
set.seed(0)
## fake some data...
f1 <- function(x) {exp(2 * x)}
f2 <- function(x) {
  0.2*x^11*(10*(1-x))^6+10*(10*x)^3*(1-x)^10
```

```

}
f3 <- function(x) {x*0}

n<-200
sig2<-4
x0 <- rep(1:4,50)
x1 <- runif(n, 0, 1)
x2 <- runif(n, 0, 1)
x3 <- runif(n, 0, 1)
e <- rnorm(n, 0, sqrt(sig2))
y <- 2*x0 + f1(x1) + f2(x2) + f3(x3) + e
x0 <- factor(x0)

## fit and plot...
b<-gam(y~x0+s(x1)+s(x2)+s(x3))
plot(b,pages=1,residuals=TRUE,all.terms=TRUE,shade=TRUE,shade.col=2)
plot(b,pages=1,seWithMean=TRUE) ## better coverage intervals

## just parametric term alone...
termplot(b,terms="x0",se=TRUE)

## more use of color...
op <- par(mfrow=c(2,2),bg="blue")
x <- 0:1000/1000
for (i in 1:3) {
  plot(b,select=i,rug=FALSE,col="green",
       col.axis="white",col.lab="white",all.terms=TRUE)
  for (j in 1:2) axis(j,col="white",labels=FALSE)
  box(col="white")
  eval(parse(text=paste("fx <- f",i,"(x)",sep="")))
  fx <- fx-mean(fx)
  lines(x,fx,col=2) ## overlay `truth' in red
}
par(op)

## example with 2-d plots...
b1<-gam(y~x0+s(x1,x2)+s(x3))
op<-par(mfrow=c(2,2))
plot(b1,all.terms=TRUE)
par(op)

```

---

predict.gam

*Prediction from fitted GAM model*


---

## Description

Takes a fitted `gam` object produced by `gam()` and produces predictions given a new set of values for the model covariates or the original values used for the model fit. Predictions can be accompanied by standard errors, based on the posterior distribution of the model coefficients. The routine can optionally return the matrix by which the model coefficients must be pre-multiplied in order to yield the values of the linear predictor at the supplied covariate values: this is useful for obtaining credible regions for quantities derived from the model (e.g. derivatives of smooths), and for lookup table prediction outside R (see example code below).

**Usage**

```
## S3 method for class 'gam':
predict(object, newdata, type="link", se.fit=FALSE, terms=NULL,
        block.size=1000, newdata.guaranteed=FALSE, na.action=na.pass, ...)
```

**Arguments**

<code>object</code>	a fitted <code>gam</code> object as produced by <code>gam()</code> .
<code>newdata</code>	A data frame or list containing the values of the model covariates at which predictions are required. If this is not provided then predictions corresponding to the original data are returned. If <code>newdata</code> is provided then it should contain all the variables needed for prediction: a warning is generated if not.
<code>type</code>	When this has the value "link" (default) the linear predictor (possibly with associated standard errors) is returned. When <code>type="terms"</code> each component of the linear predictor is returned separately (possibly with standard errors): this includes parametric model components, followed by each smooth component, but excludes any offset and any intercept. <code>type="iterms"</code> is the same, except that any standard errors returned for smooth components will include the uncertainty about the intercept/overall mean. When <code>type="response"</code> predictions on the scale of the response are returned (possibly with approximate standard errors). When <code>type="lpmatrix"</code> then a matrix is returned which yields the values of the linear predictor (minus any offset) when postmultiplied by the parameter vector (in this case <code>se.fit</code> is ignored). The latter option is most useful for getting variance estimates for quantities derived from the model: for example integrated quantities, or derivatives of smooths. A linear predictor matrix can also be used to implement approximate prediction outside R (see example code, below).
<code>se.fit</code>	when this is TRUE (not default) standard error estimates are returned for each prediction.
<code>terms</code>	if <code>type=="terms"</code> then only results for the terms given in this array will be returned.
<code>block.size</code>	maximum number of predictions to process per call to underlying code: larger is quicker, but more memory intensive. Set to < 1 to use total number of predictions as this.
<code>newdata.guaranteed</code>	Set to TRUE to turn off all checking of <code>newdata</code> except for sanity of factor levels: this can speed things up for large prediction tasks, but <code>newdata</code> must be complete, with no NA values for predictors required in the model.
<code>na.action</code>	what to do about NA values in <code>newdata</code> . With the default <code>na.pass</code> , any row of <code>newdata</code> containing NA values for required predictors, gives rise to NA predictions (even if the term concerned has no NA predictors). <code>na.exclude</code> or <code>na.omit</code> result in the dropping of <code>newdata</code> rows, if they contain any NA values for required predictors. If <code>newdata</code> is missing then NA handling is determined from <code>object\$na.action</code> .
<code>...</code>	other arguments.

**Details**

The standard errors produced by `predict.gam` are based on the Bayesian posterior covariance matrix of the parameters  $V_p$  in the fitted `gam` object.

To facilitate plotting with `termplot`, if object possesses an attribute "para.only" and `type=="terms"` then only parametric terms of order 1 are returned (i.e. those that `termplot` can handle).

Note that, in common with other prediction functions, any offset supplied to `gam` as an argument is always ignored when predicting, unlike offsets specified in the gam model formula.

See the examples for how to use the `lpmatrix` for obtaining credible regions for quantities derived from the model.

### Value

If `type=="lpmatrix"` then a matrix is returned which will give a vector of linear predictor values (minus any offset) at the supplied covariate values, when applied to the model coefficient vector. Otherwise, if `se.fit` is TRUE then a 2 item list is returned with items (both arrays) `fit` and `se.fit` containing predictions and associated standard error estimates, otherwise an array of predictions is returned. The dimensions of the returned arrays depends on whether `type` is "terms" or not: if it is then the array is 2 dimensional with each term in the linear predictor separate, otherwise the array is 1 dimensional and contains the linear predictor/predicted values (or corresponding s.e.s). The linear predictor returned termwise will not include the offset or the intercept.

`newdata` can be a data frame, list or model.frame: if it's a model frame then all variables must be supplied.

### WARNING

Note that the behaviour of this function is not identical to `predict.gam()` in `Splus`.

`type=="terms"` does not exactly match what `predict.lm` does for parametric model components.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>

The design is inspired by the `S` function of the same name described in Chambers and Hastie (1993) (but is not a clone).

### References

Chambers and Hastie (1993) Statistical Models in *S*. Chapman & Hall.

Wood S.N. (2006b) Generalized Additive Models: An Introduction with *R*. Chapman and Hall/CRC Press.

### See Also

`gam`, `gamm`, `plot.gam`

### Examples

```
library(mgcv)
n<-200
sig <- 2
dat <- gamSim(1,n=n,scale=sig)

b<-gam(y~s(x0)+s(I(x1^2))+s(x2)+offset(x3),data=dat)
```

```

newd <- data.frame(x0=(0:30)/30,x1=(0:30)/30,x2=(0:30)/30,x3=(0:30)/30)
pred <- predict.gam(b,newd)

#####
## difference between "terms" and "iterms"
#####
nd2 <- data.frame(x0=c(.25,.5),x1=c(.25,.5),x2=c(.25,.5),x3=c(.25,.5))
predict(b,nd2,type="terms",se=TRUE)
predict(b,nd2,type="iterms",se=TRUE)

#####
## now get variance of sum of predictions using lpmatrix
#####

Xp <- predict(b,newd,type="lpmatrix")

## Xp %*% coef(b) yields vector of predictions

a <- rep(1,31)
Xs <- t(a) %*% Xp ## Xs %*% coef(b) gives sum of predictions
var.sum <- Xs %*% b$Vp %*% t(Xs)

#####
## Now get the variance of non-linear function of predictions
## by simulation from posterior distribution of the params
#####

library(MASS)
br<-mvrnorm(1000,coef(b),b$Vp) ## 1000 replicate param. vectors
res <- rep(0,1000)
for (i in 1:1000)
{ pr <- Xp %*% br[i,] ## replicate predictions
  res[i] <- sum(log(abs(pr))) ## example non-linear function
}
mean(res);var(res)

## loop is replace-able by following ....

res <- colSums(log(abs(Xp %*% t(br))))

#####
## The following shows how to use use an "lpmatrix" as a lookup
## table for approximate prediction. The idea is to create
## approximate prediction matrix rows by appropriate linear
## interpolation of an existing prediction matrix. The additivity
## of a GAM makes this possible.
## There is no reason to ever do this in R, but the following
## code provides a useful template for predicting from a fitted
## gam *outside* R: all that is needed is the coefficient vector
## and the prediction matrix. Use larger `Xp`/ smaller `dx` and/or
## higher order interpolation for higher accuracy.
#####

xn <- c(.341,.122,.476,.981) ## want prediction at these values
x0 <- 1 ## intercept column

```

```

dx <- 1/30      ## covariate spacing in `newd`
for (j in 0:2) { ## loop through smooth terms
  cols <- 1+j*9 +1:9      ## relevant cols of Xp
  i <- floor(xn[j+1]*30)  ## find relevant rows of Xp
  w1 <- (xn[j+1]-i*dx)/dx ## interpolation weights
  ## find approx. predict matrix row portion, by interpolation
  x0 <- c(x0,Xp[i+2,cols]*w1 + Xp[i+1,cols]*(1-w1))
}
dim(x0)<-c(1,28)
fv <- x0%%coef(b) + xn[4];fv      ## evaluate and add offset
se <- sqrt(x0%%b$Vp%%t(x0));se ## get standard error
## compare to normal prediction
predict(b,newdata=data.frame(x0=xn[1],x1=xn[2],
                             x2=xn[3],x3=xn[4]),se=TRUE)

#####
## Differentiating the smooths in a model (with CIs for derivatives)
#####

## simulate data and fit model...
dat <- gamSim(1,n=300,scale=sig)
b<-gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat)
plot(b,pages=1)

## now evaluate derivatives of smooths with associated standard
## errors, by finite differencing...
x.mesh <- seq(0,1,length=200) ## where to evaluate derivatives
newd <- data.frame(x0 = x.mesh,x1 = x.mesh, x2=x.mesh,x3=x.mesh)
X0 <- predict(b,newd,type="lpmatrix")

eps <- 1e-7 ## finite difference interval
x.mesh <- x.mesh + eps ## shift the evaluation mesh
newd <- data.frame(x0 = x.mesh,x1 = x.mesh, x2=x.mesh,x3=x.mesh)
X1 <- predict(b,newd,type="lpmatrix")

Xp <- (X1-X0)/eps ## maps coefficients to (fd approx.) derivatives
colnames(Xp)      ## can check which cols relate to which smooth

par(mfrow=c(2,2))
for (i in 1:4) { ## plot derivatives and corresponding CIs
  Xi <- Xp*0
  Xi[, (i-1)*9+1:9+1] <- Xp[, (i-1)*9+1:9+1] ## Xi%%coef(b) = smooth deriv i
  df <- Xi%%coef(b)      ## ith smooth derivative
  df.sd <- rowSums(Xi%%b$Vp*Xi)^.5 ## cheap diag(Xi%%b$Vp%%t(Xi))^.5
  plot(x.mesh,df,type="l",ylim=range(c(df+2*df.sd,df-2*df.sd)))
  lines(x.mesh,df+2*df.sd,lty=2);lines(x.mesh,df-2*df.sd,lty=2)
}

```

## Description

Takes smooth objects produced by `smooth.construct` methods and obtains the matrix mapping the parameters associated with such a smooth to the predicted values of the smooth at a set of new covariate values.

In practice this method is often called via the wrapper function `PredictMat`.

## Usage

```
Predict.matrix(object, data)
Predict.matrix2(object, data)
```

## Arguments

<code>object</code>	is a smooth object produced by a <code>smooth.construct</code> method function. The object contains all the information required to specify the basis for a term of its class, and this information is used by the appropriate <code>Predict.matrix</code> function to produce a prediction matrix for new covariate values. Further details are given in <code>smooth.construct</code> .
<code>data</code>	A data frame containing the values of the (named) covariates at which the smooth term is to be evaluated. Exact requirements are as for <code>smooth.construct</code> and <code>smooth.construct2</code> .

## Details

Smooth terms in a GAM formula are turned into smooth specification objects of class `xx.smooth.spec` during processing of the formula. Each of these objects is converted to a smooth object using an appropriate `smooth.construct` function. The `Predict.matrix` functions are used to obtain the matrix that will map the parameters associated with a smooth term to the predicted values for the term at new covariate values.

Note that new smooth classes can be added by writing a new `smooth.construct` method function and a corresponding `Predict.matrix` method function: see the example code provided for `smooth.construct` for details.

## Value

A matrix which will map the parameters associated with the smooth to the vector of values of the smooth evaluated at the covariate values given in `object`. If the smooth class is one which generates offsets the corresponding offset is returned as attribute `"offset"` of the matrix.

## Author(s)

Simon N. Wood <simon.wood@r-project.org>

## References

Wood S.N. (2006) Generalized Additive Models: An Introduction with R. Chapman and Hall/CRC Press.

## See Also

`gam`, `gamm`, `smooth.construct`, `PredictMat`

**Examples**

```
# See smooth.construct examples
```

---

```
Predict.matrix.cr.smooth
```

*Predict matrix method functions*

---

**Description**

The various built in smooth classes for use with `gam` have associate `Predict.matrix` method functions to enable prediction from the fitted model.

**Usage**

```
## S3 method for class 'cr.smooth':
Predict.matrix(object, data)
## S3 method for class 'cs.smooth':
Predict.matrix(object, data)
## S3 method for class 'cyclic.smooth':
Predict.matrix(object, data)
## S3 method for class 'pspline.smooth':
Predict.matrix(object, data)
## S3 method for class 'tensor.smooth':
Predict.matrix(object, data)
## S3 method for class 'tprs.smooth':
Predict.matrix(object, data)
## S3 method for class 'ts.smooth':
Predict.matrix(object, data)
```

**Arguments**

object	a smooth object, usually generated by a <code>smooth.construct</code> method having processed a smooth specification object generated by an <code>s</code> or <code>te</code> term in a <code>gam</code> formula.
data	A data frame containing the values of the (named) covariates at which the smooth term is to be evaluated. Exact requirements are as for <code>smooth.construct</code> and <code>smooth.construct2</code> .

**Details**

The `Predict` matrix function is not normally called directly, but is rather used internally by `predict.gam` etc. to predict from a fitted `gam` model. See `Predict.matrix` for more details, or the specific `smooth.construct` pages for details on a particular smooth class.

**Value**

A matrix mapping the coefficients for the smooth term to its values at the supplied data values.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>



## References

Wood S.N. (2006) Generalized Additive Models: An Introduction with R. Chapman and Hall/CRC Press.

## Examples

```
## see smooth.construct
```

---

print.gam

*Print a Generalized Additive Model object.*

---

## Description

The default print method for a gam object.

## Usage

```
## S3 method for class 'gam':  
print(x, ...)
```

## Arguments

x, ... fitted model objects of class gam as produced by gam().

## Details

Prints out the family, model formula, effective degrees of freedom for each smooth term, and optimized value of the smoothness selection criterion used. See [gamObject](#) (or `names(x)`) for a listing of what the object contains. [summary.gam](#) provides more detail.

Note that the optimized smoothing parameter selection criterion reported is one of GCV, UBRE(AIC), GACV, negative log marginal likelihood (ML), or negative log restricted likelihood (REML).

## Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

## References

Wood, S.N. (2006) Generalized Additive Models: An Introduction with R. CRC/ Chapman and Hall, Boca Raton, Florida.

<http://www.maths.bath.ac.uk/~sw283/>

## See Also

[gam](#), [summary.gam](#)

## Description

The smooth components of GAMs can be viewed as random effects for estimation purposes. This means that more conventional random effects terms can be incorporated into GAMs in two ways. The first method converts all the smooths into fixed and random components suitable for estimation by standard mixed modelling software. Once the GAM is in this form then conventional random effects are easily added, and the whole model is estimated as a general mixed model. `gamm` and `gamm4` from the `gamm4` package operate in this way.

The second method represents the conventional random effects in a GAM in the same way that the smooths are represented — as penalized regression terms. This method can be used with `gam` by making use of `s(..., "re")` terms in a model: see `smooth.construct.re.smooth.spec`. Alternatively, but less straightforwardly, the `paraPen` argument to `gam` can be used: see `gam.models`. If smoothing parameter estimation is by ML or REML (e.g. `gam(..., method="REML")`) then this approach is a completely conventional likelihood based treatment of random effects.

`gam` can be slow for fitting models with large numbers of random effects, because it does not exploit the sparsity that is often a feature of parametric random effects. It can not be used for models with more coefficients than data. However `gam` is often faster and more reliable than `gamm` or `gamm4`, when the number of random effects is modest.

To facilitate the use of random effects with `gam`, `gam.vcomp` is a utility routine for converting smoothing parameters to variance components. It also provides confidence intervals, if smoothness estimation is by ML or REML.

## Author(s)

Simon Wood <simon.wood@r-project.org>

## References

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. *Journal of the Royal Statistical Society (B)* 70(3):495-518

Wood, S.N. (2006) Low rank scale invariant tensor product smooths for generalized additive mixed models. *Biometrics* 62(4):1025-1036

## See Also

`gam.vcomp`, `gam.models`, `smooth.terms`, `smooth.construct.re.smooth.spec`, `gamm`

## Examples

```
## see also examples for gam.models, gam.vcomp and gamm

## simple comparison of lme and gam

require(nlme)
b0 <- lme(travel~1, data=Rail, ~1|Rail, method="REML")
```

```
b <- gam(travel~s(Rail,bs="re"),data=Rail,method="REML")

intervals(b0)
gam.vcomp(b)
```

---

residuals.gam

*Generalized Additive Model residuals*


---

### Description

Returns residuals for a fitted `gam` model object. Pearson, deviance, working and response residuals are available.

### Usage

```
## S3 method for class 'gam':
residuals(object, type = c("deviance", "pearson", "scaled.pearson",
                           "working", "response"), ...)
```

### Arguments

<code>object</code>	a <code>gam</code> fitted model object.
<code>type</code>	the type of residuals wanted.
<code>...</code>	other arguments.

### Details

Response residuals are the raw residuals (data minus fitted values). Scaled Pearson residuals are raw residuals divided by the standard deviation of the data according to the model mean variance relationship and estimated scale parameter. Pearson residuals are the same, but multiplied by the square root of the scale parameter (so they are independent of the scale parameter):  $((y-\mu)/\sqrt{V(\mu)})$ , where  $y$  is data  $\mu$  is model fitted value and  $V$  is model mean-variance relationship.). Both are provided since not all texts agree on the definition of Pearson residuals. Deviance residuals simply return the deviance residuals defined by the model family. Working residuals are the residuals returned from model fitting at convergence.

There is a special function for `gam` objects because of a bug in the calculation of Pearson residuals in some earlier versions of `residual.glm`.

### Value

An array of residuals.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>

### See Also

[gam](#)

rig

*Generate inverse Gaussian random deviates***Description**

Generates inverse Gaussian random deviates.

**Usage**

```
rig(n, mean, scale)
```

**Arguments**

n	the number of deviates required. If this has length > 1 then the length is taken as the number of deviates required.
mean	vector of mean values.
scale	vector of scale parameter values (lambda, see below)

**Details**

If  $x$  is the returned vector, then  $E(x) = \text{mean}$  while  $\text{var}(x) = \text{scale} * \text{mean}^3$ . For density and distribution functions see the `statmod` package. The algorithm used is Algorithm 5.7 of Gentle (2003), based on Michael et al. (1976). Note that `scale` here is the scale parameter in the GLM sense, which is the reciprocal of the usual 'lambda' parameter.

**Value**

A vector of inverse Gaussian random deviates.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

Gentle, J.E. (2003) Random Number Generation and Monte Carlo Methods (2nd ed.) Springer.  
 Michael, J.R., W.R. Schucany & R.W. Hass (1976) Generating random variates using transformations with multiple roots. *The American Statistician* 30, 88-90.  
<http://www.maths.bath.ac.uk/~sw283/>

**Examples**

```
set.seed(7)
## An inverse.gaussian GAM example, by modify `gamSim' output...
dat <- gamSim(1, n=400, dist="normal", scale=1)
dat$f <- dat$f/4 ## true linear predictor
Ey <- exp(dat$f); scale <- .5 ## mean and GLM scale parameter
## Note that `shape' and `scale' in `rgamma' are almost
## opposite terminology to that used with GLM/GAM...
dat$y <- rig(Ey, mean=Ey, scale=.2)
big <- gam(y ~ s(x0) + s(x1) + s(x2) + s(x3), family=inverse.gaussian(link=log),
          data=dat, method="REML")
```

```
plot(big, pages=1)
gam.check(big)
summary(big)
```

s

---

*Defining smooths in GAM formulae*


---

**Description**

Function used in definition of smooth terms within `gam` model formulae. The function does not evaluate a (spline) smooth - it exists purely to help set up a model using spline based smooths.

**Usage**

```
s(..., k=-1, fx=FALSE, bs="tp", m=NA, by=NA, xt=NULL, id=NULL, sp=NULL)
```

**Arguments**

- `...` a list of variables that are the covariates that this smooth is a function of.
- `k` the dimension of the basis used to represent the smooth term. The default depends on the number of variables that the smooth is a function of. `k` should not be less than the dimension of the null space of the penalty for the term (see [null.space.dimension](#)), but will be reset if it is. See [choose.k](#) for further information.
- `fx` indicates whether the term is a fixed d.f. regression spline (TRUE) or a penalized regression spline (FALSE).
- `bs` a two letter character string indicating the (penalized) smoothing basis to use. (eg "tp" for thin plate regression spline, "cr" for cubic regression spline). see [smooth.terms](#) for an over view of what is available.
- `m` The order of the penalty for this term (e.g. 2 for normal cubic spline penalty with 2nd derivatives when using default t.p.r.s basis). NA signals autoinitialization. Only some smooth classes use this. The "ps" class can use a 2 item array giving the basis and penalty order separately.
- `by` a numeric or factor variable of the same dimension as each covariate. In the numeric vector case the elements multiply the smooth, evaluated at the corresponding covariate values (a 'varying coefficient model' results). For the numeric `by` variable case the resulting smooth is not usually subject to a centering constraint (so the `by` variable should not be added as an additional main effect). In the factor `by` variable case a replicate of the smooth is produced for each factor level (these smooths will be centered, so the factor usually needs to be added as a main effect as well). See [gam.models](#) for further details. A `by` variable may also be a matrix if covariates are matrices: in this case implements linear functional of a smooth (see [gam.models](#) and [linear.functional.terms](#) for details).
- `xt` Any extra information required to set up a particular basis. Used e.g. to set large data set handling behaviour for "tp" basis.

<code>id</code>	A label or integer identifying this term in order to link its smoothing parameters to others of the same type. If two or more terms have the same <code>id</code> then they will have the same smoothing parameters, and, by default, the same bases (first occurrence defines basis type, but data from all terms used in basis construction). An <code>id</code> with a factor <code>by</code> variable causes the smooths at each factor level to have the same smoothing parameter.
<code>sp</code>	any supplied smoothing parameters for this term. Must be an array of the same length as the number of penalties for this smooth. Positive or zero elements are taken as fixed smoothing parameters. Negative elements signal auto-initialization. Over-rides values supplied in <code>sp</code> argument to <code>gam</code> . Ignored by <code>gamm</code> .

### Details

The function does not evaluate the variable arguments. To use this function to specify use of your own smooths, note the relationships between the inputs and the output object and see the example in `smooth.construct`.

### Value

A class `xx.smooth.spec` object, where `xx` is a basis identifying code given by the `bs` argument of `s`. These `smooth.spec` objects define smooths and are turned into bases and penalties by `smooth.construct` method functions.

The returned object contains the following items:

<code>term</code>	An array of text strings giving the names of the covariates that the term is a function of.
<code>bs.dim</code>	The dimension of the basis used to represent the smooth.
<code>fixed</code>	TRUE if the term is to be treated as a pure regression spline (with fixed degrees of freedom); FALSE if it is to be treated as a penalized regression spline
<code>dim</code>	The dimension of the smoother - i.e. the number of covariates that it is a function of.
<code>p.order</code>	The order of the t.p.r.s. penalty, or 0 for auto-selection of the penalty order.
<code>by</code>	is the name of any <code>by</code> variable as text ("NA" for none).
<code>label</code>	A suitable text label for this smooth term.
<code>xt</code>	The object passed in as argument <code>xt</code> .
<code>id</code>	An identifying label or number for the smooth, linking it to other smooths. Defaults to <code>NULL</code> for no linkage.
<code>sp</code>	array of smoothing parameters for the term (negative for auto-estimation). Defaults to <code>NULL</code> .

### Author(s)

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### References

- Wood, S.N. (2003) Thin plate regression splines. *J.R.Statist.Soc.B* 65(1):95-114
- Wood S.N. (2006) *Generalized Additive Models: An Introduction with R*. Chapman and Hall/CRC Press.
- <http://www.maths.bath.ac.uk/~sw283/>

**See Also**

[te](#), [gam](#), [gamm](#)

**Examples**

```
# example utilising `by' variables
library(mgcv)
set.seed(0)
n<-200;sig2<-4
x1 <- runif(n, 0, 1);x2 <- runif(n, 0, 1);x3 <- runif(n, 0, 1)
fac<-c(rep(1,n/2),rep(2,n/2)) # create factor
fac.1<-rep(0,n)+(fac==1);fac.2<-1-fac.1 # and dummy variables
fac<-as.factor(fac)
f1 <- exp(2 * x1) - 3.75887
f2 <- 0.2 * x1^11 * (10 * (1 - x1))^6 + 10 * (10 * x1)^3 * (1 - x1)^10
f<-f1*fac.1+f2*fac.2+x2
e <- rnorm(n, 0, sqrt(abs(sig2)))
y <- f + e
# NOTE: smooths will be centered, so need to include fac in model....
b<-gam(y~fac+s(x1,by=fac)+x2)
plot(b,pages=1)
```

---

smooth.construct     *Constructor functions for smooth terms in a GAM*

---

**Description**

Smooth terms in a GAM formula are turned into smooth specification objects of class `xx.smooth.spec` during processing of the formula. Each of these objects is converted to a smooth object using an appropriate `smooth.construct` function. New smooth classes can be added by writing a new `smooth.construct` method function and a corresponding `Predict.matrix` method function (see example code below).

In practice, `smooth.construct` is usually called via `smooth.construct2` and the wrapper function `smoothCon`, in order to handle `by` variables and centering constraints (see the `smoothCon` documentation if you need to handle these things directly, for a user defined smooth class).

**Usage**

```
smooth.construct(object, data, knots)
smooth.construct2(object, data, knots)
```

**Arguments**

`object` is a smooth specification object, generated by an `s` or `te` term in a GAM formula. Objects generated by `s` terms have class `xx.smooth.spec` where `xx` is given by the `bs` argument of `s` (this convention allows the user to add their own smoothers). If `object` is not class `tensor.smooth.spec` it will have the following elements:

**term** The names of the covariates for this smooth, in an array.

**bs.dim** Argument  $k$  of the  $s$  term generating the object. This is the dimension of the basis used to represent the term (or, arguably, 1 greater than the basis dimension for  $cc$  terms).  $bs.dim < 0$  indicates that the constructor should set this to the default value.

**fixed** TRUE if the term is to be unpenalized, otherwise FALSE.

**dim** the number covariates of which this smooth is a function.

**p.order** the order of the smoothness penalty or NA for autoselection of this. This is argument  $m$  of the  $s$  term that generated `object`.

**by** the name of any *by* variable to multiply this term as supplied as an argument to  $s$ . "NA" if there is no such term.

**label** A suitable label for use with this term.

**xt** An object containing information that may be needed for basis setup (used, e.g. by "tp" smooths to pass optional information on big dataset handling).

**id** Any identity associated with this term — used for linking bases and smoothing parameters. NULL by default, indicating no linkage.

**sp** Smoothing parameters for the term. Any negative are estimated, otherwise they are fixed at the supplied value. Unless NULL (default), over-rides `sp` argument to `gam`.

If `object` is of class `tensor.smooth.spec` then it was generated by a `te` term in the GAM formula, and specifies a smooth of several variables with a basis generated as a tensor product of lower dimensional bases. In this case the object will be different and will have the following elements:

**margin** is a list of smooth specification objects of the type listed above, defining the bases which have their tensor product formed in order to construct this term.

**term** is the array of names of the covariates that are arguments of the smooth.

**by** is the name of any *by* variable, or "NA".

**fx** is an array, the elements of which indicate whether (TRUE) any of the margins in the tensor product should be unpenalized.

**label** A suitable label for use with this term.

**dim** is the number of covariates of which this smooth is a function.

**mp** TRUE if multiple penalties are to be used.

**np** TRUE if 1-D marginal smooths are to be re-parameterized in terms of function values.

**id** Any identity associated with this term — used for linking bases and smoothing parameters. NULL by default, indicating no linkage.

**sp** Smoothing parameters for the term. Any negative are estimated, otherwise they are fixed at the supplied value. Unless NULL (default), over-rides `sp` argument to `gam`.

`data` For `smooth.construct` a data frame or list containing the evaluation of the elements of `object$term`, with names given by `object$term`. The last entry will be the *by* variable, if `object$by` is not "NA". For `smooth.construct2` data need only be an object within which `object$term` can be evaluated, the variables can be in any order, and there can be irrelevant variables present as well.

`knots` an optional data frame or list containing the knots relating to `object$term`. If it is NULL then the knot locations are generated automatically. The structure of `knots` should be as for `data`, depending on whether `smooth.construct` or `smooth.construct2` is used.



## Details

There are built in methods for objects with the following classes: `tp.smooth.spec` (thin plate regression splines: see [tprs](#)); `ts.smooth.spec` (thin plate regression splines with shrinkage-to-zero); `cr.smooth.spec` (cubic regression splines: see [cubic.regression.spline](#)); `cs.smooth.spec` (cubic regression splines with shrinkage-to-zero); `cc.smooth.spec` (cyclic cubic regression splines); `ps.smooth.spec` (Eilers and Marx (1986) style P-splines: see [p.spline](#)); `cp.smooth.spec` (cyclic P-splines) `ad.smooth.spec` (adaptive smooths of 1 or 2 variables: see [adaptive.smooth](#)); `tensor.smooth.spec` (tensor product smooths).

There is an implicit assumption that the basis only depends on the knots and/or the set of unique covariate combinations; i.e. that the basis is the same whether generated from the full set of covariates, or just the unique combinations of covariates.

## Value

The input argument `object`, assigned a new class to indicate what type of smooth it is and with at least the following items added:

<code>X</code>	The model matrix from this term. This may have an "offset" attribute: a vector of length <code>nrow(X)</code> containing any contribution of the smooth to the model offset term. <code>by</code> variables do not need to be dealt with here, but if they are then an item <code>by.done</code> must be added to the <code>object</code> .
<code>S</code>	A list of positive semi-definite penalty matrices that apply to this term. The list will be empty if the term is to be left un-penalized.
<code>rank</code>	An array giving the ranks of the penalties.
<code>null.space.dim</code>	The dimension of the penalty null space (before centering).

The following items may be added:

<code>C</code>	The matrix defining any constraints on the term. If this is <code>NULL</code> then <code>smoothCon</code> will add an identifiability constraint that each term should sum to zero over the covariate values. Set to a zero row matrix if no constraints are required. Note that a supplied <code>C</code> is never ignored, even if any <code>by</code> variables of a smooth imply that no constraint is actually needed.
<code>no.rescale</code>	if this is non- <code>NULL</code> then the penalty coefficient matrix of the smooth will not be rescaled for enhanced numerical stability (rescaling is the default, because <a href="#">gamm</a> requires it). Turning off rescaling is useful if the values of the smoothing parameters should be interpretable in a model, for example because they are inverse variance components.
<code>df</code>	the degrees of freedom associated with this term (when unpenalized and unconstrained). If this is <code>null</code> then <code>smoothCon</code> will set it to the basis dimension. <code>smoothCon</code> will reduce this by the number of constraints.
<code>te.ok</code>	<code>FALSE</code> if this term should not be used as a tensor product marginal. Set to <code>TRUE</code> if <code>NULL</code> .
<code>plot.me</code>	Set to <code>FALSE</code> if this smooth should not be plotted by <code>plot.gam</code> . Set to <code>TRUE</code> if <code>NULL</code> .
<code>L</code>	smooths may depend on fewer 'underlying' smoothing parameters than there are elements of <code>S</code> . In this case <code>L</code> is the matrix mapping the vector of underlying log smoothing parameters to the vector of logs of the smoothing parameters actually multiplying the <code>S[[i]]</code> . <code>L=NULL</code> signifies that there is one smoothing parameter per <code>S[[i]]</code> .

Usually the returned object will also include extra information required to define the basis, and used by `Predict.matrix` methods to make predictions using the basis. See the `Details` section for links to the information included for the built in smooth classes.

`tensor.smooth` returned objects will additionally have each element of the `margin` list updated in the same way. `tensor.smooths` also have a list, `XP`, containing re-parameterization matrices for any 1-D marginal terms re-parameterized in terms of function values. This list will have `NULL` entries for marginal smooths that are not re-parameterized, and is only long enough to reach the last re-parameterized marginal in the list.

## WARNING

User defined smooth objects should avoid having attributes names "qrc" or "nCons" as these are used internally to provide constraint free parameterizations.

## Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

## References

Wood, S.N. (2003) Thin plate regression splines. *J.R.Statist.Soc.B* 65(1):95-114

Wood, S.N. (2006) Low rank scale invariant tensor product smooths for generalized additive mixed models. *Biometrics* 62(4):1025-1036

The P-spline code given in the example is based on those advocated in:

Ruppert, D., M.P. Wand and R.J. Carroll (2003) *Semiparametric Regression*. Cambridge University Press.

However if you want p-splines, rather than splines with derivative based penalties, then the built in "ps" class is probably a better bet. It's based on

Eilers, P.H.C. and B.D. Marx (1996) Flexible Smoothing with B-splines and Penalties. *Statistical Science*, 11(2):89-121

<http://www.maths.bath.ac.uk/~sw283/>

## See Also

`s.get.var`, `gamm`, `gam`, `Predict.matrix`, `smoothCon`, `PredictMat`

## Examples

```
# adding "p-spline" classes and methods

smooth.construct.tr.smooth.spec<-function(object,data,knots)
## a truncated power spline constructor method function
## object$p.order = null space dimension
{ m <- object$p.order[1]
  if (is.na(m)) m <- 2 ## default
  if (m<1) stop("silly m supplied")
  if (object$bs.dim<0) object$bs.dim <- 10 ## default
  nk<-object$bs.dim-m-1 ## number of knots
  if (nk<=0) stop("k too small for m")
  x <- data[[object$term]] ## the data
  x.shift <- mean(x) # shift used to enhance stability
  k <- knots[[object$term]] ## will be NULL if none supplied
  if (is.null(k)) # space knots through data
```

```

{ n<-length(x)
  k<-quantile(x[2:(n-1)],seq(0,1,length=nk+2))[2:(nk+1)]
}
if (length(k)!=nk) # right number of knots?
stop(paste("there should be ",nk," supplied knots"))
x <- x - x.shift # basis stabilizing shift
k <- k - x.shift # knots treated the same!
X<-matrix(0,length(x),object$bs.dim)
for (i in 1:(m+1)) X[,i] <- x^(i-1)
for (i in 1:nk) X[,i+m+1]<-(x-k[i])^m*as.numeric(x>k[i])
object$X<-X # the finished model matrix
if (!object$fixed) # create the penalty matrix
{ object$S[[1]]<-diag(c(rep(0,m+1),rep(1,nk)))
}
object$rank<-nk # penalty rank
object$null.space.dim <- m+1 # dim. of unpenalized space
## store "tr" specific stuff ...
object$knots<-k;object$m<-m;object$x.shift <- x.shift

object$df<-ncol(object$X) # maximum DoF (if unconstrained)

class(object)<-"tr.smooth" # Give object a class
object
}

Predict.matrix.tr.smooth<-function(object,data)
## prediction method function for the `tr' smooth class
{ x <- data[[object$term]]
  x <- x - object$x.shift # stabilizing shift
  m <- object$m; # spline order (3=cubic)
  k<-object$knots # knot locations
  nk<-length(k) # number of knots
  X<-matrix(0,length(x),object$bs.dim)
  for (i in 1:(m+1)) X[,i] <- x^(i-1)
  for (i in 1:nk) X[,i+m+1] <- (x-k[i])^m*as.numeric(x>k[i])
  X # return the prediction matrix
}

# an example, using the new class....
set.seed(100)
dat <- gamSim(1,n=400,scale=2)
b<-gam(y~s(x0,bs="tr",m=2)+s(x1,bs="ps",m=c(1,3))+
      s(x2,bs="tr",m=3)+s(x3,bs="tr",m=2),data=dat)
plot(b,pages=1)
b<-gam(y~s(x0,bs="tr",m=2)+s(x1,bs="ps",m=c(1,3))+
      s(x2,bs="tr",m=3)+s(x3,bs="tr",m=2),data=dat)
plot(b$gam,pages=1)
# another example using tensor products of the new class
dat <- gamSim(2,n=400,scale=.1)$data
b <- gam(y~te(x,z,bs=c("tr","tr"),m=c(2,2)),data=dat)
vis.gam(b)

```

---

smooth.construct.ad.smooth.spec  
*Adaptive smooths in GAMs*

---

## Description

`gam` can use adaptive smooths of one or two variables, specified via terms like `s(..., bs="ad", ...)`. (`gam` can not use such terms — check out package `AdaptFit` if this is a problem.) The basis for such a term is a (tensor product of) p-spline(s) or cubic regression spline(s). Discrete P-spline type penalties are applied directly to the coefficients of the basis, but the penalties themselves have a basis representation, allowing the strength of the penalty to vary with the covariates. The coefficients of the penalty basis are the smoothing parameters.

When invoking an adaptive smoother the `k` argument specifies the dimension of the smoothing basis, while the `m` argument specifies the dimension of the penalty basis. For an adaptive smooth of two variables `k` is taken as the dimension of both marginal bases: different marginal basis dimensions can be specified by making `k` a two element vector. Similarly, in the two dimensional case `m` is the dimension of both marginal bases for the penalties, unless it is a two element vector, which specifies different basis dimensions for each marginal (If the penalty basis is based on a thin plate spline then `m` specifies its dimension directly).

By default, P-splines are used for the smoothing and penalty bases, but this can be modified by supplying a list as argument `xt` with a character vector `xt$bs` specifying the smoothing basis type. Only "ps", "cp", "cc" and "cr" may be used for the smoothing basis. The penalty basis is always a B-spline, or a cyclic B-spline for cyclic bases.

The total number of smoothing parameters to be estimated for the term will be the dimension of the penalty basis. Bear in mind that adaptive smoothing places quite severe demands on the data. For example, setting `m=10` for a univariate smooth of 200 data is rather like estimating 10 smoothing parameters, each from a data series of length 20. The problem is particularly serious for smooths of 2 variables, where the number of smoothing parameters required to get reasonable flexibility in the penalty can grow rather fast, but it often requires a very large smoothing basis dimension to make good use of this flexibility. In short, adaptive smooths should be used sparingly and with care.

In practice it is often as effective to simply transform the smoothing covariate as it is to use an adaptive smooth.

## Usage

```
## S3 method for class 'ad.smooth.spec':
smooth.construct(object, data, knots)
```

## Arguments

<code>object</code>	a smooth specification object, usually generated by a term <code>s(..., bs="ad", ...)</code>
<code>data</code>	a list containing just the data (including any <code>by</code> variable) required by this term, with names corresponding to <code>object\$term</code> (and <code>object\$by</code> ). The <code>by</code> variable is the last element.
<code>knots</code>	a list containing any knots supplied for basis setup — in same order and with same names as <code>data</code> . Can be <code>NULL</code>

**Details**

The constructor is not normally called directly, but is rather used internally by `gam`. To use for basis setup it is recommended to use `smooth.construct2`.

This class can not be used as a marginal basis in a tensor product smooth, nor by `gamm`.

**Value**

An object of class `"pspline.smooth"` in the 1D case or `"tensor.smooth"` in the 2D case.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**Examples**

```
## Comparison using an example taken from AdaptFit
## library(AdaptFit)
set.seed(0)
x <- 1:1000/1000
mu <- exp(-400*(x-.6)^2)+5*exp(-500*(x-.75)^2)/3+2*exp(-500*(x-.9)^2)
y <- mu+0.5*rnorm(1000)

##fit with default knots
## y.fit <- asp(y~f(x))

par(mfrow=c(2,2))
## plot(y.fit,main=round(cor(fitted(y.fit),mu),digits=4))
## lines(x,mu,col=2)

b <- gam(y~s(x,bs="ad",k=40,m=5)) ## adaptive
plot(b,shade=TRUE,main=round(cor(fitted(b),mu),digits=4))
lines(x,mu-mean(mu),col=2)

b <- gam(y~s(x,k=40)) ## non-adaptive
plot(b,shade=TRUE,main=round(cor(fitted(b),mu),digits=4))
lines(x,mu-mean(mu),col=2)

b <- gam(y~s(x,bs="ad",k=40,m=5,xt=list(bs="cr")))
plot(b,shade=TRUE,main=round(cor(fitted(b),mu),digits=4))
lines(x,mu-mean(mu),col=2)

## A 2D example....
par(mfrow=c(2,2),mar=c(1,1,1,1))
x <- seq(-.5, 1.5, length= 60)
z <- x
f3 <- function(x,z,k=15) { r<-sqrt(x^2+z^2);f<-exp(-r^2*k);f}
f <- outer(x, z, f3)
op <- par(bg = "white")

## Plot truth....
persp(x,z,f,theta=30,phi=30,col="lightblue",ticktype="detailed")

n <- 2000
x <- runif(n)*2-.5
z <- runif(n)*2-.5
f <- f3(x,z)
```

```

y <- f + rnorm(n)*.1

## Try tprs for comparison...
b0 <- gam(y~s(x, z, k=150))
vis.gam(b0, theta=30, phi=30, ticktype="detailed")

## Tensor product with non-adaptive version of adaptive penalty
b1 <- gam(y~s(x, z, bs="ad", k=15, m=1), gamma=1.4)
vis.gam(b1, theta=30, phi=30, ticktype="detailed")

## Now adaptive...
b <- gam(y~s(x, z, bs="ad", k=15, m=3), gamma=1.4)
vis.gam(b, theta=30, phi=30, ticktype="detailed")
cor(fitted(b0), f); cor(fitted(b), f)

```

---

```
smooth.construct.cr.smooth.spec
```

*Penalized Cubic regression splines in GAMs*

---

## Description

`gam` can use univariate penalized cubic regression spline smooths, specified via terms like `s(x, bs="cr")`. `s(x, bs="cs")` specifies a penalized cubic regression spline which has had its penalty modified to shrink towards zero at high enough smoothing parameters (as the smoothing parameter goes to infinity a normal cubic spline tends to a straight line.) `s(x, bs="cc")` specifies a cyclic penalized cubic regression spline smooth.

‘Cardinal’ spline bases are used: Wood (2006) sections 4.1.2 and 4.1.3 gives full details. These bases have very low setup costs. For a given basis dimension, `k`, they typically perform a little less well than thin plate regression splines, but a little better than p-splines. See [te](#) to use these bases in tensor product smooths of several variables.

## Usage

```

## S3 method for class 'cr.smooth.spec':
smooth.construct(object, data, knots)
## S3 method for class 'cs.smooth.spec':
smooth.construct(object, data, knots)
## S3 method for class 'cc.smooth.spec':
smooth.construct(object, data, knots)

```

## Arguments

<code>object</code>	a smooth specification object, usually generated by a term <code>s(..., bs="cr", ...)</code> , <code>s(..., bs="cs", ...)</code> or <code>s(..., bs="cc", ...)</code>
<code>data</code>	a list containing just the data (including any <code>by</code> variable) required by this term, with names corresponding to <code>object\$term</code> (and <code>object\$by</code> ). The <code>by</code> variable is the last element.
<code>knots</code>	a list containing any knots supplied for basis setup — in same order and with same names as <code>data</code> . Can be <code>NULL</code> . See details.

## Details

The constructor is not normally called directly, but is rather used internally by `gam`. To use for basis setup it is recommended to use `smooth.construct2`.

If they are not supplied then the knots of the spline are placed evenly throughout the covariate values to which the term refers: For example, if fitting 101 data with an 11 knot spline of  $x$  then there would be a knot at every 10th (ordered)  $x$  value. The parameterization used represents the spline in terms of its values at the knots. The values at neighbouring knots are connected by sections of cubic polynomial constrained to be continuous up to and including second derivative at the knots. The resulting curve is a natural cubic spline through the values at the knots (given two extra conditions specifying that the second derivative of the curve should be zero at the two end knots).

The shrinkage version of the smooth, eigen-decomposes the wiggleness penalty matrix, and sets its 2 zero eigenvalues to small multiples of the smallest strictly positive eigenvalue. The penalty is then set to the matrix with eigenvectors corresponding to those of the original penalty, but eigenvalues set to the perturbed versions. This penalty matrix has full rank and shrinks the curve to zero at high enough smoothing parameters.

Note that the cyclic smoother will wrap at the smallest and largest covariate values, unless knots are supplied. If only two knots are supplied then they are taken as the end points of the smoother (provided all the data lie between them), and the remaining knots are generated automatically.

The cyclic smooth is not subject to the condition that second derivatives go to zero at the first and last knots.

## Value

An object of class `"cr.smooth"`, `"cs.smooth"` or `"cyclic.smooth"`. In addition to the usual elements of a smooth class documented under `smooth.construct`, this object will contain:

<code>xp</code>	giving the knot locations used to generate the basis.
<code>BD</code>	class <code>"cyclic.smooth"</code> objects include matrix <code>BD</code> which transforms function values at the knots to second derivatives at the knots.

## Author(s)

Simon N. Wood <simon.wood@r-project.org>

## References

Wood S.N. (2006) Generalized Additive Models: An Introduction with R. Chapman and Hall/CRC Press.

## Examples

```
## cyclic spline example...
set.seed(6)
x <- sort(runif(200)*10)
z <- runif(200)
f <- sin(x*2*pi/10)+.5
y <- rpois(exp(f), exp(f))

## finished simulating data, now fit model...
b <- gam(y ~ s(x,bs="cc",k=12) + s(z),family=poisson,
         knots=list(x=seq(0,10,length=12)))
```

```
## or more simply
b <- gam(y ~ s(x,bs="cc",k=12) + s(z),family=poisson,
         knots=list(x=c(0,10)))

## plot results...
par(mfrow=c(2,2))
plot(x,y);plot(b,select=1,shade=TRUE);lines(x,f-mean(f),col=2)
plot(b,select=2,shade=TRUE);plot(fitted(b),residuals(b))
```

---

smooth.construct.ps.smooth.spec  
*P-splines in GAMs*

---

## Description

`gam` can use univariate P-splines as proposed by Eilers and Marx (1996), specified via terms like `s(x,bs="ps")`. These terms use B-spline bases penalized by discrete penalties applied directly to the basis coefficients. Cyclic P-splines are specified by model terms like `s(x,bs="cp",...)`. These bases can be used in tensor product smooths (see [te](#)).

The advantage of P-splines is the flexible way that penalty and basis order can be mixed. This often provides a useful way of ‘taming’ an otherwise poorly behaved smooth. However, in regular use, splines with derivative based penalties (e.g. "tp" or "cr" bases) tend to result in slightly better MSE performance, presumably because the good approximation theoretic properties of splines are rather closely connected to the use of derivative penalties.

## Usage

```
## S3 method for class 'ps.smooth.spec':
smooth.construct(object, data, knots)
## S3 method for class 'cp.smooth.spec':
smooth.construct(object, data, knots)
```

## Arguments

<code>object</code>	a smooth specification object, usually generated by a term <code>s(x,bs="ps",...)</code> or <code>s(x,bs="cp",...)</code>
<code>data</code>	a list containing just the data (including any <code>by</code> variable) required by this term, with names corresponding to <code>object\$term</code> (and <code>object\$by</code> ). The <code>by</code> variable is the last element.
<code>knots</code>	a list containing any knots supplied for basis setup — in same order and with same names as <code>data</code> . Can be <code>NULL</code> . See details for further information.

## Details

A smooth term of the form `s(x,bs="ps",m=c(2,3))` specifies a 2nd order P-spline basis (cubic spline), with a third order difference penalty (0th order is a ridge penalty) on the coefficients. If `m` is a single number then it is taken as the basis order and penalty order. The default is the ‘cubic spline like’ `m=c(2,2)`.



The default basis dimension,  $k$ , is the larger of 10 and  $m[1]+1$  for a "ps" terms and the larger of 10 and  $m[1]$  for a "cp" term.  $m[1]+1$  and  $m[1]$  are the lower limits on basis dimension for the two types.

If knots are supplied, then the number of knots should be one more than the basis dimension (i.e.  $k+1$ ) for a "cp" smooth. For the "ps" basis the number of supplied knots should be  $k + m[1] + 2$ , and the range of the middle  $k-m[1]$  knots should include all the covariate values. See example.

Alternatively, for both types of smooth, 2 knots can be supplied, denoting the lower and upper limits between which the spline can be evaluated (Don't make this range too wide, however, or you can end up with no information about some basis coefficients, because the corresponding basis functions have a span that includes no data!). Note that P-splines don't make much sense with uneven knot spacing.

### Value

An object of class "ps.smooth" or "cp.smooth". See [smooth.construct](#), for the elements that this object will contain.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>

### References

Eilers, P.H.C. and B.D. Marx (1996) Flexible Smoothing with B-splines and Penalties. *Statistical Science*, 11(2):89-121

### See Also

[cSplineDes](#)

### Examples

```
## see ?gam
## cyclic example ...
set.seed(6)
x <- sort(runif(200)*10)
z <- runif(200)
f <- sin(x*2*pi/10)+.5
y <- rpois(exp(f), exp(f))

## finished simulating data, now fit model...
b <- gam(y ~ s(x,bs="cp") + s(z,bs="ps"),family=poisson)

## example with supplied knot ranges for x and z (can do just one)
b <- gam(y ~ s(x,bs="cp") + s(z,bs="ps"),family=poisson,
         knots=list(x=c(0,10),z=c(0,1)))

## example with supplied knots...
bk <- gam(y ~ s(x,bs="cp",k=12) + s(z,bs="ps",k=13),family=poisson,
         knots=list(x=seq(0,10,length=13),z=(-3):13/10))

## plot results...
par(mfrow=c(2,2))
plot(b,select=1,shade=TRUE);lines(x,f-mean(f),col=2)
```

```
plot(b, select=2, shade=TRUE); lines(z, 0*z, col=2)
plot(bk, select=1, shade=TRUE); lines(x, f-mean(f), col=2)
plot(bk, select=2, shade=TRUE); lines(z, 0*z, col=2)
```

---

```
smooth.construct.re.smooth.spec
```

*Simple random effects in GAMs*

---

## Description

`gam` can deal with simple independent random effects, by exploiting the link between smooths and random effects to treat random effects as smooths. `s(x, bs="re")` implements this. Such terms can have any number of predictors, which can be any mixture of numeric or factor variables. The terms produce a parametric interaction of the predictors, and penalize the corresponding coefficients with a multiple of the identity matrix, corresponding to an assumption of i.i.d. normality. See details.

## Usage

```
## S3 method for class 're.smooth.spec':
smooth.construct(object, data, knots)
## S3 method for class 'random.effect':
Predict.matrix(object, data)
```

## Arguments

object	For the <code>smooth.construct</code> method a smooth specification object, usually generated by a term <code>s(x, ..., bs="re", )</code> . For the <code>predict.Matrix</code> method and object of class "random.effect" produced by the <code>smooth.construct</code> method.
data	a list containing just the data (including any by variable) required by this term, with names corresponding to <code>object\$term</code> (and <code>object\$by</code> ). The by variable is the last element.
knots	generically a list containing any knots supplied for basis setup — unused at present.

## Details

Exactly how the random effects are implemented is best seen by example. Consider the model term `s(x, z, bs="re")`. This will result in the model matrix component corresponding to  $\sim x:z-1$  being added to the model matrix for the whole model. The coefficients associated with the model matrix component are assumed i.i.d. normal, with unknown variance (to be estimated). This assumption is equivalent to an identity penalty matrix (i.e. a ridge penalty) on the coefficients. Because such a penalty is full rank, random effects terms do not require centering constraints.

If the nature of the random effect specification is not clear, consider a couple more examples: `s(x, bs="re")` results in `model.matrix(~x-1)` being appended to the overall model matrix, while `s(x, v, w, bs="re")` would result in `model.matrix(~x:v:w-1)` being appended to the model matrix. In both cases the corresponding model coefficients are assumed i.i.d. normal, and are hence subject to ridge penalties.

Note that smooth `ids` are not supported for random effect terms, and that `"re"` terms are not suitable for use as marginal smooths in a tensor product smooth.

Random effects implemented in this way do not exploit the sparse structure of many random effects, and may therefore be relatively inefficient for models with large numbers of random effects, when `gamm4` or `gamm` may be better alternatives. Note also that `gam` will not support models with more coefficients than data.

### Value

An object of class `"random.effect"` or a matrix mapping the coefficients of the random effect to the random effects themselves.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>

### References

Wood, S.N. (2008) Fast stable direct fitting and smoothness selection for generalized additive models. *Journal of the Royal Statistical Society (B)* 70(3):495-518

### See Also

[gam.vcomp](#), [gamm](#)

### Examples

```
## see ?gam.vcomp
```

---

```
smooth.construct.tensor.smooth.spec
      Tensor product smoothing constructor
```

---

### Description

A special `smooth.construct` method function for creating tensor product smooths from any combination of single penalty marginal smooths.

### Usage

```
## S3 method for class 'tensor.smooth.spec':
smooth.construct(object, data, knots)
```

### Arguments

<code>object</code>	a smooth specification object of class <code>tensor.smooth.spec</code> , usually generated by a term like <code>te(x, z)</code> in a <code>gam</code> model formula
<code>data</code>	a list containing just the data (including any <code>by</code> variable) required by this term, with names corresponding to <code>object\$term</code> (and <code>object\$by</code> ). The <code>by</code> variable is the last element.
<code>knots</code>	a list containing any knots supplied for basis setup — in same order and with same names as <code>data</code> . Can be <code>NULL</code> . See details for further information.

**Details**

Tensor product smooths are smooths of several variables which allow the degree of smoothing to be different with respect to different variables. They are useful as smooth interaction terms, as they are invariant to linear rescaling of the covariates, which means, for example, that they are insensitive to the measurement units of the different covariates. They are also useful whenever isotropic smoothing is inappropriate. See [te](#), [smooth.construct](#) and [smooth.terms](#).

**Value**

An object of class "tensor.smooth". See [smooth.construct](#), for the elements that this object will contain.

**Author(s)**

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

**References**

Wood, S.N. (2006) Low rank scale invariant tensor product smooths for generalized additive mixed models. *Biometrics* 62(4):1025-1036

**See Also**

[cSplineDes](#)

**Examples**

```
## see ?gam
```

---

smooth.construct.tp.smooth.spec

*Penalized thin plate regression splines in GAMs*

---

**Description**

`gam` can use isotropic smooths of any number of variables, specified via terms like `s(x, z, bs="tp", m=3)` (or just `s(x, z)` as this is the default basis). These terms are based on thin plate regression splines. `m` specifies the order of the derivatives in the thin plate spline penalty.

Thin plate regression splines are constructed by starting with the basis and penalty for a full thin plate spline and then truncating this basis in an optimal manner, to obtain a low rank smoother. Details are given in Wood (2003). One key advantage of the approach is that it avoids the knot placement problems of conventional regression spline modelling, but it also has the advantage that smooths of lower rank are nested within smooths of higher rank, so that it is legitimate to use conventional hypothesis testing methods to compare models based on pure regression splines. Note that the basis truncation does not change the meaning of the thin plate spline penalty (it penalizes exactly what it would have penalized for a full thin plate spline).

The t.p.r.s. basis and penalties can become expensive to calculate for large datasets. For this reason the default behaviour is to randomly subsample `max.knots` unique data locations if there are more than `max.knots` such, and to use the sub-sample for basis construction. The sampling is always

done with the same random seed to ensure repeatability (does not reset R RNG). `max.knots` is 3000, by default. Both `seed` and `max.knots` can be modified using the `xt` argument to `s`. Alternatively the user can supply knots from which to construct a basis.

The "ts" smooths are t.p.r.s. with the penalty modified so that the term is shrunk to zero for high enough smoothing parameter, rather than being shrunk towards a function in the penalty null space (see details).

### Usage

```
## S3 method for class 'tp.smooth.spec':
smooth.construct(object, data, knots)
## S3 method for class 'ts.smooth.spec':
smooth.construct(object, data, knots)
```

### Arguments

<code>object</code>	a smooth specification object, usually generated by a term <code>s(...,bs="tp",...)</code> or <code>s(...,bs="ts",...)</code>
<code>data</code>	a list containing just the data (including any <code>by</code> variable) required by this term, with names corresponding to <code>object\$term</code> (and <code>object\$by</code> ). The <code>by</code> variable is the last element.
<code>knots</code>	a list containing any knots supplied for basis setup — in same order and with same names as <code>data</code> . Can be <code>NULL</code>

### Details

The default basis dimension for this class is  $k=10 \cdot 3^{(d-1)}$  where  $d$  is the number of covariates for the term. This is essentially arbitrary, and should be checked.

The default is to set  $m$  (the order of derivative in the thin plate spline penalty) to the smallest value satisfying  $2m > d+1$  where  $d$  is the number of covariates of the term: this yields ‘visually smooth’ functions. In any case  $2m > d$  must be satisfied.

The constructor is not normally called directly, but is rather used internally by `gam`. To use for basis setup it is recommended to use `smooth.construct2`.

For these classes the specification `object` will contain information on how to handle large datasets in their `xt` field. The default is to randomly subsample 3000 ‘knots’ from which to produce a tprs basis, if the number of unique predictor variable combinations in excess of 3000. The default can be modified via the `xt` argument to `s`. This is supplied as a list with elements `max.knots` and `seed` containing a number to use in place of 3000, and the random number seed to use (either can be missing).

For these bases `knots` has two uses. Firstly, as mentioned already, for large datasets the calculation of the `tp` basis can be time-consuming. The user can retain most of the advantages of the t.p.r.s. approach by supplying a reduced set of covariate values from which to obtain the basis - typically the number of covariate values used will be substantially smaller than the number of data, and substantially larger than the basis dimension,  $k$ . This approach is the one taken automatically if the number of unique covariate values (combinations) exceeds `max.knots`. The second possibility is to avoid the eigen-decomposition used to find the t.p.r.s. basis altogether and simply use the basis implied by the chosen knots: this will happen if the number of knots supplied matches the basis dimension,  $k$ . For a given basis dimension the second option is faster, but gives poorer results (and the user must be quite careful in choosing knot locations).

The shrinkage version of the smooth, eigen-decomposes the wiggleness penalty matrix, and sets its zero eigenvalues to small multiples of the smallest strictly positive eigenvalue. The penalty is then

set to the matrix with eigenvectors corresponding to those of the original penalty, but eigenvalues set to the perturbed versions. This penalty matrix has full rank and shrinks the curve to zero at high enough smoothing parameters.

### Value

An object of class "tprs.smooth" or "ts.smooth". In addition to the usual elements of a smooth class documented under [smooth.construct](#), this object will contain:

shift	A record of the shift applied to each covariate in order to center it around zero and avoid any co-linearity problems that might otherwise occur in the penalty null space basis of the term.
Xu	A matrix of the unique covariate combinations for this smooth (the basis is constructed by first stripping out duplicate locations).
UZ	The matrix mapping the t.p.r.s. parameters back to the parameters of a full thin plate spline.
null.space.dimension	The dimension of the space of functions that have zero wiggleness according to the wiggleness penalty for this term.

### Author(s)

Simon N. Wood <simon.wood@r-project.org>

### References

Wood, S.N. (2003) Thin plate regression splines. *J.R.Statist.Soc.B* 65(1):95-114

### Examples

```
## see ?gam
```

---

smooth.terms

*Smooth terms in GAM*

---

### Description

Smooth terms are specified in a `gam` formula using `s` and `te` terms. Various smooth classes are available, for different modelling tasks, and users can add smooth classes (see [user.defined.smooth](#)). What defines a smooth class is the basis used to represent the smooth function and quadratic penalty (or multiple penalties) used to penalize the basis coefficients in order to control the degree of smoothness. Smooth classes are invoked directly by `s` terms, or as building blocks for tensor product smoothing via `te` terms (only smooth classes with single penalties can be used in tensor products). The smooths built into the `mgcv` package are all based one way or another on low rank versions of splines. For the full rank versions see Wahba (1990).

Note that smooths can be used rather flexibly in `gam` models. In particular the linear predictor of the GAM can depend on (a discrete approximation to) any linear functional of a smooth term, using `by` variables and the 'summation convention' explained in [linear.functional.terms](#).

The single penalty built in smooth classes are summarized as follows

**Thin plate regression splines** `bs="tp"`. These are low rank isotropic smoothers of any number of covariates. By isotropic is meant that rotation of the covariate co-ordinate system will not change the result of smoothing. By low rank is meant that they have far fewer coefficients than there are data to smooth. They are reduced rank versions of the thin plate splines and use the thin plate spline penalty. They are the default smooth for `s` terms because there is a defined sense in which they are the optimal smoother of any given basis dimension/rank (Wood, 2003). Thin plate regression splines do not have ‘knots’ (at least not in any conventional sense): a truncated eigen-decomposition is used to achieve the rank reduction. See `tpres` for further details.

`bs="ts"` is as `"tp"` but with a small ridge penalty added to the smoothing penalty, so that the whole term can be shrunk to zero.

**Cubic regression splines** `bs="cr"`. These have a cubic spline basis defined by a modest sized set of knots spread evenly through the covariate values. They are penalized by the conventional integrated square second derivative cubic spline penalty. For details see `cubic.regression.spline` and e.g. Wood (2006a).

`bs="cs"` specifies a shrinkage version of `"cr"`.

`bs="cc"` specifies a cyclic cubic regression splines. i.e. a penalized cubic regression splines whose ends match, up to second derivative.

**P-splines** `bs="ps"`. These are P-splines as proposed by Eilers and Marx (1996). They combine a B-spline basis, with a discrete penalty on the basis coefficients, and any sane combination of penalty and basis order is allowed. Although this penalty has no exact interpretation in terms of function shape, in the way that the derivative penalties do, P-splines perform almost as well as conventional splines in many standard applications, and can perform better in particular cases where it is advantageous to mix different orders of basis and penalty.

`bs="cs"` gives a cyclic version of a P-spline.

**Random effects** `bs="re"`. These are parametric terms penalized by a ridge penalty (i.e. the identity matrix). When such a smooth has multiple arguments then it represents the parametric interaction of these arguments, with the coefficients penalized by a ridge penalty. The ridge penalty is equivalent to an assumption that the coefficients are i.i.d. normal random effects. See `smooth.construct.re.smooth.spec`. Note that random effect terms are not suitable for use in tensor product smooths.

Broadly speaking the default penalized thin plate regression splines tend to give the best MSE performance, but they are a little slower to set up than the other bases. The knot based penalized cubic regression splines (with derivative based penalties) usually come next in MSE performance, with the P-splines doing just a little worse. However the P-splines are useful in non-standard situations.

All the preceding classes (and any user defined smooths with single penalties) may be used as marginal bases for tensor product smooths specified via `te` terms, except for `"re"` terms. Tensor product smooths are smooth functions of several variables where the basis is built up from tensor products of bases for smooths of fewer (usually one) variable(s) (marginal bases). The multiple penalties for these smooths are produced automatically from the penalties of the marginal smooths. Wood (2006b) give the general recipe for this construction.

Tensor product smooths often perform better than isotropic smooths when the covariates of a smooth are not naturally on the same scale, so that their relative scaling is arbitrary. For example, if smoothing with respect to time and distance, an isotropic smoother will give very different results if the units are cm and minutes compared to if the units are metres and seconds: a tensor product smooth will give the same answer in both cases (see `te` for an example of this). Note that tensor product terms are knot based, and the thin plate splines seem to offer no advantage over cubic or P-splines as marginal bases.

Finally univariate and bivariate adaptive (`bs="ad"`) smooths are available (see `adaptive.smooth`). These are appropriate when the degree of smoothing should itself

vary with the covariates to be smoothed, and the data contain sufficient information to be able to estimate the appropriate variation. Because this flexibility is achieved by splitting the penalty into several ‘basis penalties’ these terms are not suitable as components of tensor product smooths, and are not supported by `gamm`.

### Author(s)

Simon Wood <simon.wood@r-project.org>

### References

- Eilers, P.H.C. and B.D. Marx (1996) Flexible Smoothing with B-splines and Penalties. *Statistical Science*, 11(2):89-121
- Wahba (1990) *Spline Models of Observational Data*. SIAM
- Wood, S.N. (2003) Thin plate regression splines. *J.R.Statist.Soc.B* 65(1):95-114
- Wood, S.N. (2006a) *Generalized Additive Models: an introduction with R*, CRC
- Wood, S.N. (2006b) Low rank scale invariant tensor product smooths for generalized additive mixed models. *Biometrics* 62(4):1025-1036

### See Also

[s](#), [te](#), [tprs](#), [cubic.regression.spline](#), [p.spline](#), [adaptive.smooth](#), [user.defined.smooth](#)

### Examples

```
## see examples for gam and gamm
```

---

smoothCon

*Prediction/Construction wrapper functions for GAM smooth terms*

---

### Description

Wrapper functions for construction of and prediction from smooth terms in a GAM. The purpose of the wrappers is to allow user-transparent re-parameterization of smooth terms, in order to allow identifiability constraints to be absorbed into the parameterization of each term, if required. The routine also handles ‘by’ variables and construction of identifiability constraints automatically, although this behaviour can be over-ridden.

### Usage

```
smoothCon(object, data, knots, absorb.cons=FALSE,
          scale.penalty=TRUE, n=nrow(data), dataX=NULL,
          null.space.penalty=FALSE, sparse.cons=0)
PredictMat(object, data, n=nrow(data))
```



**Arguments**

<code>object</code>	is a smooth specification object or a smooth object.
<code>data</code>	A data frame, model frame or list containing the values of the (named) covariates at which the smooth term is to be evaluated. If it's a list then <code>n</code> must be supplied.
<code>knots</code>	An optional data frame supplying any knot locations to be supplied for basis construction.
<code>absorb.cons</code>	Set to <code>TRUE</code> in order to have identifiability constraints absorbed into the basis.
<code>scale.penalty</code>	should the penalty coefficient matrix be scaled to have approximately the same 'size' as the inner product of the terms model matrix with itself? This can improve the performance of <code>gamm</code> fitting.
<code>n</code>	number of values for each covariate, or if a covariate is a matrix, the number of rows in that matrix: must be supplied explicitly if <code>data</code> is a list.
<code>dataX</code>	Sometimes the basis should be set up using data in <code>data</code> , but the model matrix should be constructed with another set of data provided in <code>dataX</code> — <code>n</code> is assumed to be the same for both. Facilitates smooth id's.
<code>null.space.penalty</code>	Should an extra penalty be added to the smooth which will penalize the components of the smooth in the penalty null space: provides a way of penalizing terms out of the model altogether.
<code>sparse.cons</code>	If 0 then default sum to zero constraints are used. If 1 then one coefficient is set to zero as constraint for sparse smooths. If 2 then sparse coefficient sum to zero constraints are used for sparse smooths. None of these options has an effect if the smooth supplies its own constraint.

**Details**

These wrapper functions exist to allow smooths specified using `smooth.construct` and `Predict.matrix` method functions to be re-parameterized so that identifiability constraints are no longer required in fitting. This is done in a user transparent manner, but is typically of no importance in use of GAMs. The routine's also handle `by` variables and will create default identifiability constraints.

If a user defined smooth constructor handles `by` variables itself, then its returned smooth object should contain an object `by.done`. If this does not exist then `smoothCon` will use the default code. Similarly if a user defined `Predict.matrix` method handles `by` variables internally then the returned matrix should have a `"by.done"` attribute.

Default centering constraints, that terms should sum to zero over the covariates, are produced unless the smooth constructor includes a matrix `C` of constraints. To have no constraints (in which case you had better have a full rank penalty!) the matrix `C` should have no rows. There is an option to use centering constraint that generate no, or limited infill, if the smoother has a sparse model matrix.

`smoothCon` returns a list of smooths because factor `by` variables result in multiple copies of a smooth, each multiplied by the dummy variable associated with one factor level. `smoothCon` modifies the smooth object labels in the presence of `by` variables, to ensure that they are unique, it also stores the level of a `by` variable factor associated with a smooth, for later use by `PredMat`.

The parameterization used by `gam` can be controlled via `gam.control`.

**Value**

From `smoothCon` a list of `smooth` objects returned by the appropriate `smooth.construct` method function. If constraints are to be absorbed then the objects will have attributes `"qrc"` and `"nCons"`. `"nCons"` is the number of constraints. `"qrc"` is usually the qr decomposition of the constraint matrix (returned by `qr`), but if it is a single positive integer it is the index of the coefficient to set to zero, and if it is a negative number then this indicates that the parameters are to sum to zero.

For `predictMat` a matrix which will map the parameters associated with the smooth to the vector of values of the smooth evaluated at the covariate values given in `object`.

**Author(s)**

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

**References**

<http://www.maths.bath.ac.uk/~sw283/>

**See Also**

[gam.control](#), [smooth.construct](#), [Predict.matrix](#)

---

sp.vcov

*Extract smoothing parameter estimator covariance matrix from (RE)ML GAM fit*

---

**Description**

Extracts the estimated covariance matrix for the log smoothing parameter estimates from a (RE)ML estimated `gam` object, provided the fit was with a method that evaluated the required Hessian.

**Usage**

```
sp.vcov(x)
```

**Arguments**

`x` a fitted model object of class `gam` as produced by `gam()`.

**Details**

Just extracts the inverse of the hessian matrix of the negative (restricted) log likelihood w.r.t the log smoothing parameters, if this has been obtained as part of fitting.

**Value**

A matrix corresponding to the estimated covariance matrix of the log smoothing parameter estimators, if this can be extracted, otherwise `NULL`. If the scale parameter has been (RE)ML estimated (i.e. if the method was `"ML"` or `"REML"` and the scale parameter was unknown) then the last row and column relate to the log scale parameter.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

Wood, S.N. (2006) On confidence intervals for generalized additive models based on penalized regression splines. *Australian and New Zealand Journal of Statistics*. 48(4): 445-464.

**See Also**

[gam](#), [gam.vcomp](#)

**Examples**

```
n <- 100
x <- runif(n); z <- runif(n)
y <- sin(x*2*pi) + rnorm(n)*.2
mod <- gam(y~s(x,bs="cc",k=10)+s(z),knots=list(x=seq(0,1,length=10)),
          method="REML")
sp.vcov(mod)
```

---

step.gam

*Alternatives to step.gam*

---

**Description**

There is no `step.gam` in package `mgcv`. The `mgcv` default for model selection is to use either prediction error criteria such as GCV, GACV, Mallows' Cp/AIC/UBRE or the likelihood based methods of REML or ML. Since the smoothness estimation part of model selection is done in this way it is logically most consistent to perform the rest of model selection in the same way. i.e. to decide which terms to include or omit by looking at changes in GCV, AIC, REML etc.

To facilitate fully automatic model selection the package implements two smooth modification techniques which can be used to allow smooths to be shrunk to zero as part of smoothness selection.

**Shrinkage smoothers** are smoothers in which a small multiple of the identity matrix is added to the smoothing penalty, so that strong enough penalization will shrink all the coefficients of the smooth to zero. Such smoothers can effectively be penalized out of the model altogether, as part of smoothing parameter estimation. 2 classes of these shrinkage smoothers are implemented: "cs" and "ts", based on cubic regression spline and thin plate regression spline smoothers (see [s](#))

**Null space penalization** An alternative is to construct an extra penalty for each smooth which penalizes the space of functions of zero wiggleness according to its existing penalties. If all the smoothing parameters for such a term tend to infinity then the term is penalized to zero, and is effectively dropped from the model. The advantage of this approach is that it can be implemented automatically for any smooth. The `select` argument to [gam](#) causes this latter approach to be used.

REML and ML smoothness selection are equivalent under this approach, and simulation evidence suggests that they tend to perform a little better than prediction error criteria, for model selection.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**See Also**

[gam.selection](#)

**Examples**

```
## an example of GCV based model selection as
## an alternative to stepwise selection, using
## shrinkage smoothers...
library(mgcv)
set.seed(0); n <- 400
dat <- gamSim(1, n=n, scale=2)
dat$x4 <- runif(n, 0, 1)
dat$x5 <- runif(n, 0, 1)
attach(dat)
## Note the increased gamma parameter below to favour
## slightly smoother models...
b<-gam(y~s(x0,bs="ts")+s(x1,bs="ts")+s(x2,bs="ts")+
      s(x3,bs="ts")+s(x4,bs="ts")+s(x5,bs="ts"), gamma=1.4)
summary(b)
plot(b, pages=1)

## Same again using REML/ML
b<-gam(y~s(x0,bs="ts")+s(x1,bs="ts")+s(x2,bs="ts")+
      s(x3,bs="ts")+s(x4,bs="ts")+s(x5,bs="ts"), method="REML")
summary(b)
plot(b, pages=1)

## And once more, but using the null space penalization
b<-gam(y~s(x0,bs="cr")+s(x1,bs="cr")+s(x2,bs="cr")+
      s(x3,bs="cr")+s(x4,bs="cr")+s(x5,bs="cr"),
      method="REML", select=TRUE)
summary(b)
plot(b, pages=1)

detach(dat); rm(dat)
```

---

summary.gam

*Summary for a GAM fit*

---

**Description**

Takes a fitted `gam` object produced by `gam()` and produces various useful summaries from it. (See [sink](#) to divert output to a file.)

**Usage**

```
## S3 method for class 'gam':
summary(object, dispersion=NULL, freq=FALSE, alpha=0, ...)

## S3 method for class 'summary.gam':
print(x, digits = max(3, getOption("digits") - 3),
      signif.stars = getOption("show.signif.stars"), ...)
```

**Arguments**

object	a fitted gam object as produced by gam().
x	a summary.gam object produced by summary.gam().
dispersion	A known dispersion parameter. NULL to use estimate or default (e.g. 1 for Poisson).
freq	By default p-values for individual terms are calculated using the frequentist estimated covariance matrix of the parameter estimators. If this is set to FALSE then the Bayesian covariance matrix of the parameters is used instead. See details.
alpha	adjustment to reference distribution per estimated smoothing parameter.
digits	controls number of digits printed in output.
signif.stars	Should significance stars be printed alongside output.
...	other arguments.

**Details**

Model degrees of freedom are taken as the trace of the influence (or hat) matrix  $\mathbf{A}$  for the model fit. Residual degrees of freedom are taken as number of data minus model degrees of freedom. Let  $\mathbf{P}_i$  be the matrix giving the parameters of the  $i$ th smooth when applied to the data (or pseudodata in the generalized case) and let  $\mathbf{X}$  be the design matrix of the model. Then  $tr(\mathbf{X}\mathbf{P}_i)$  is the edf for the  $i$ th term. Clearly this definition causes the edf's to add up properly!

`print.summary.gam` tries to print various bits of summary information useful for term selection in a pretty way.

If `freq=TRUE` then the frequentist approximation for p-values of smooth terms described in section 4.8.5 of Wood (2006) is used. The approximation is not great. If  $\mathbf{p}_i$  is the parameter vector for the  $i$ th smooth term, and this term has estimated covariance matrix  $\mathbf{V}_i$  then the statistic is  $\mathbf{p}_i' \mathbf{V}_i^{k-} \mathbf{p}_i$ , where  $\mathbf{V}_i^{k-}$  is the rank  $k$  pseudo-inverse of  $\mathbf{V}_i$ , and  $k$  is estimated rank of  $\mathbf{V}_i$ . p-values are obtained as follows. In the case of known dispersion parameter, they are obtained by comparing the chi.sq statistic to the chi-squared distribution with  $k$  degrees of freedom, where  $k$  is the estimated rank of  $\mathbf{V}_i$ . If the dispersion parameter is unknown (in which case it will have been estimated) the statistic is compared to an F distribution with  $k$  upper d.f. and lower d.f. given by the residual degrees of freedom for the model. Typically the p-values will be somewhat too low.

If `freq=FALSE` then 'Bayesian p-values' are returned for the smooth terms, based on a test statistic motivated by Nychka's (1988) analysis of the frequentist properties of Bayesian confidence intervals for smooths. These appear to have better frequentist performance (in terms of power and distribution under the null) than the alternative strictly frequentist approximation. Let  $\mathbf{f}$  denote the vector of values of a smooth term evaluated at the original covariate values and let  $\mathbf{V}_f$  denote the corresponding Bayesian covariance matrix. Let  $\mathbf{V}_f^{r-}$  denote the rank  $r$  pseudoinverse of  $\mathbf{V}_f$ , where  $r$  is the EDF for the term. The statistic used is then

$$T = \mathbf{f}^T \mathbf{V}_f^{r-} \mathbf{f}$$

(this can be calculated efficiently without forming the pseudoinverse explicitly).  $T$  is compared to a chi-squared distribution with degrees of freedom given by the EDF for the term + `alpha *` (number of estimated smoothing parameters), or  $T$  is used as a component in an F ratio statistic if the scale parameter has been estimated. The non-integer rank truncated inverse is constructed to give an approximation varying smoothly between the bounding integer rank approximations, while yielding test statistics with the correct mean and variance.

The definition of Bayesian p-value used is: the probability of observing an  $\mathbf{f}$  less probable than  $\mathbf{0}$ , under the approximation for the posterior for  $\mathbf{f}$  implied by the truncation used in the test statistic.

Note that the p-values distributional approximations start to break down below one effective degree of freedom, and p-values are not reported below 0.5 degrees of freedom.

In simulations the p-values have best behaviour under ML smoothness selection, with REML coming second.

## Value

`summary.gam` produces a list of summary information for a fitted `gam` object.

<code>p.coeff</code>	is an array of estimates of the strictly parametric model coefficients.
<code>p.t</code>	is an array of the <code>p.coeff</code> 's divided by their standard errors.
<code>p.pv</code>	is an array of p-values for the null hypothesis that the corresponding parameter is zero. Calculated with reference to the <code>t</code> distribution with the estimated residual degrees of freedom for the model fit if the dispersion parameter has been estimated, and the standard normal if not.
<code>m</code>	The number of smooth terms in the model.
<code>chi.sq</code>	An array of test statistics for assessing the significance of model smooth terms. See details.
<code>s.pv</code>	An array of approximate p-values for the null hypotheses that each smooth term is zero. Be warned, these are only approximate.
<code>se</code>	array of standard error estimates for all parameter estimates.
<code>r.sq</code>	The adjusted r-squared for the model. Defined as the proportion of variance explained, where original variance and residual variance are both estimated using unbiased estimators. This quantity can be negative if your model is worse than a one parameter constant model, and can be higher for the smaller of two nested models! Note that proportion null deviance explained is probably more appropriate for non-normal errors.
<code>dev.expl</code>	The proportion of the null deviance explained by the model.
<code>edf</code>	array of estimated degrees of freedom for the model terms.
<code>residual.df</code>	estimated residual degrees of freedom.
<code>n</code>	number of data.
<code>method</code>	The smoothing selection criterion used.
<code>sp.criterion</code>	The minimized value of the smoothness selection criterion. Note that for ML and REML methods, what is reported is the negative log marginal likelihood or negative log restricted likelihood.
<code>scale</code>	estimated (or given) scale parameter.
<code>family</code>	the family used.
<code>formula</code>	the original GAM formula.
<code>dispersion</code>	the scale parameter.

<code>pTerms.df</code>	the degrees of freedom associated with each parametric term (excluding the constant).
<code>pTerms.chi.sq</code>	a Wald statistic for testing the null hypothesis that the each parametric term is zero.
<code>pTerms.pv</code>	p-values associated with the tests that each term is zero. For penalized fits these are approximate. The reference distribution is an appropriate chi-squared when the scale parameter is known, and is based on an F when it is not.
<code>cov.unscaled</code>	The estimated covariance matrix of the parameters (or estimators if <code>freq=TRUE</code> ), divided by scale parameter.
<code>cov.scaled</code>	The estimated covariance matrix of the parameters (estimators if <code>freq=TRUE</code> ).
<code>p.table</code>	significance table for parameters
<code>s.table</code>	significance table for smooths
<code>p.Terms</code>	significance table for parametric model terms

**WARNING**

The p-values are approximate: do read the details section.

**Author(s)**

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)> with substantial improvements by Henric Nilsson.

**References**

Nychka (1988) Bayesian Confidence Intervals for Smoothing Splines. *Journal of the American Statistical Association* 83:1134-1143.

Wood S.N. (2006) *Generalized Additive Models: An Introduction with R*. Chapman and Hall/CRC Press.

**See Also**

[gam](#), [predict.gam](#), [gam.check](#), [anova.gam](#), [gam.vcomp](#), [sp.vcov](#)

**Examples**

```
library(mgcv)
set.seed(0)
dat <- gamSim(1,n=200,scale=2) ## simulate data

b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),data=dat)
plot(b,pages=1)
summary(b)

## now check the p-values by using a pure regression spline.....
b.d <- round(summary(b)$edf)+1 ## get edf per smooth
b.d <- pmax(b.d,3) # can't have basis dimension less than 3!
bc<-gam(y~s(x0,k=b.d[1],fx=TRUE)+s(x1,k=b.d[2],fx=TRUE)+
        s(x2,k=b.d[3],fx=TRUE)+s(x3,k=b.d[4],fx=TRUE),data=dat)
plot(bc,pages=1)
summary(bc)
```

```
## p-value check - increase k to make this useful!
k<-20;n <- 200;p <- rep(NA,k)
for (i in 1:k)
{ b<-gam(y~te(x,z),data=data.frame(y=rnorm(n),x=runif(n),z=runif(n)),
  method="ML")
  p[i]<-summary(b)$s.p[1]
}
plot((1:k)-0.5)/k,sort(p)
abline(0,1,col=2)
ks.test(p,"punif") ## how close to uniform are the p-values?
```

te

*Define tensor product smooths in GAM formulae***Description**

Function used in definition of tensor product smooth terms within `gam` model formulae. The function does not evaluate a smooth - it exists purely to help set up a model using tensor product based smooths. Designed to construct tensor products from any marginal smooths with a basis-penalty representation (with the restriction that each marginal smooth must have only one penalty).

**Usage**

```
te(..., k=NA,bs="cr",m=NA,d=NA,by=NA,fx=FALSE,
  mp=TRUE,np=TRUE,xt=NULL,id=NULL,sp=NULL)
```

**Arguments**

- `...` a list of variables that are the covariates that this smooth is a function of.
- `k` the dimension(s) of the bases used to represent the smooth term. If not supplied then set to  $5^d$ . If supplied as a single number then this basis dimension is used for each basis. If supplied as an array then the elements are the dimensions of the component (marginal) bases of the tensor product. See [choose.k](#) for further information.
- `bs` array (or single character string) specifying the type for each marginal basis. "cr" for cubic regression spline; "cs" for cubic regression spline with shrinkage; "cc" for periodic/cyclic cubic regression spline; "tp" for thin plate regression spline; "ts" for t.p.r.s. with extra shrinkage. See [smooth.terms](#) for details and full list. User defined bases can also be used here (see [smooth.construct](#) for an example). If only one basis code is given then this is used for all bases.
- `m` The order of the penalty (for smooth classes that use this) for each term. If a single number is given then it is used for all terms. NA autoinitializes. `m` is ignored by some bases (e.g. "cr").
- `d` array of marginal basis dimensions. For example if you want a smooth for 3 covariates made up of a tensor product of a 2 dimensional t.p.r.s. basis and a 1-dimensional basis, then set `d=c(2,1)`. Incompatibilities between built in basis types and dimension will be resolved by resetting the basis type.



<code>by</code>	a numeric or factor variable of the same dimension as each covariate. In the numeric vector case the elements multiply the smooth evaluated at the corresponding covariate values (a ‘varying coefficient model’ results). In the factor case causes a replicate of the smooth to be produced for each factor level. See <a href="#">gam.models</a> for further details. May also be a matrix if covariates are matrices: in this case implements linear functional of a smooth (see <a href="#">gam.models</a> and <a href="#">linear.functional.terms</a> for details).
<code>fx</code>	indicates whether the term is a fixed d.f. regression spline (TRUE) or a penalized regression spline (FALSE).
<code>mp</code>	TRUE to use multiple penalties for the smooth. FALSE to use only a single penalty: single penalties are not recommended - they tend to allow only rather wiggly models.
<code>np</code>	TRUE to use the ‘normal parameterization’ for a tensor product smooth. This represents any 1-d marginal smooths via parameters that are function values at ‘knots’, spread evenly through the data. The parameterization makes the penalties easily interpretable, however it can reduce numerical stability in some cases.
<code>xt</code>	Either a single object, providing any extra information to be passed to each marginal basis constructor, or a list of such objects, one for each marginal basis.
<code>id</code>	A label or integer identifying this term in order to link its smoothing parameters to others of the same type. If two or more smooth terms have the same <code>id</code> then they will have the same smoothing parameters, and, by default, the same bases (first occurrence defines basis type, but data from all terms used in basis construction).
<code>sp</code>	any supplied smoothing parameters for this term. Must be an array of the same length as the number of penalties for this smooth. Positive or zero elements are taken as fixed smoothing parameters. Negative elements signal auto-initialization. Over-rides values supplied in <code>sp</code> argument to <a href="#">gam</a> . Ignored by <a href="#">gamm</a> .

## Details

Smooths of several covariates can be constructed from tensor products of the bases used to represent smooths of one (or sometimes more) of the covariates. To do this ‘marginal’ bases are produced with associated model matrices and penalty matrices, and these are then combined in the manner described in [tensor.prod.model.matrix](#) and [tensor.prod.penalties](#), to produce a single model matrix for the smooth, but multiple penalties (one for each marginal basis). The basis dimension of the whole smooth is the product of the basis dimensions of the marginal smooths.

An option for operating with a single penalty (The Kronecker product of the marginal penalties) is provided, but it is rarely of practical use: the penalty is typically so rank deficient that even the smoothest resulting model will have rather high estimated degrees of freedom.

Tensor product smooths are especially useful for representing functions of covariates measured in different units, although they are typically not quite as nicely behaved as t.p.r.s. smooths for well scaled covariates.

Note also that GAMs constructed from lower rank tensor product smooths are nested within GAMs constructed from higher rank tensor product smooths if the same marginal bases are used in both cases (the marginal smooths themselves are just special cases of tensor product smooths.)

The ‘normal parameterization’ (`np=TRUE`) re-parameterizes the marginal smooths of a tensor product smooth so that the parameters are function values at a set of points spread evenly through the range of values of the covariate of the smooth. This means that the penalty of the tensor product associated with any particular covariate direction can be interpreted as the penalty of the appropriate

marginal smooth applied in that direction and averaged over the smooth. Currently this is only done for marginals of a single variable. This parameterization can reduce numerical stability when used with marginal smooths other than "cc", "cr" and "cs": if this causes problems, set `np=FALSE`.

Note that tensor product smooths should not be centred (have identifiability constraints imposed) if any marginals would not need centering. The constructor for tensor product smooths ensures that this happens.

The function does not evaluate the variable arguments.

## Value

A class `tensor.smooth.spec` object defining a tensor product smooth to be turned into a basis and penalties by the `smooth.construct.tensor.smooth.spec` function.

The returned object contains the following items:

<code>margin</code>	A list of <code>smooth.spec</code> objects of the type returned by <code>s</code> , defining the basis from which the tensor product smooth is constructed.
<code>term</code>	An array of text strings giving the names of the covariates that the term is a function of.
<code>by</code>	is the name of any <code>by</code> variable as text ("NA" for none).
<code>fx</code>	logical array with element for each penalty of the term (tensor product smooths have multiple penalties). TRUE if the penalty is to be ignored, FALSE, otherwise.
<code>label</code>	A suitable text label for this smooth term.
<code>dim</code>	The dimension of the smoother - i.e. the number of covariates that it is a function of.
<code>mp</code>	TRUE is multiple penalties are to be used (default).
<code>np</code>	TRUE to re-parameterize 1-D marginal smooths in terms of function values (default).
<code>id</code>	the <code>id</code> argument supplied to <code>te</code> .
<code>sp</code>	the <code>sp</code> argument supplied to <code>te</code> .

## Author(s)

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)>

## References

Wood, S.N. (2006a) Low rank scale invariant tensor product smooths for generalized additive mixed models. *Biometrics* 62(4):1025-1036

<http://www.maths.bath.ac.uk/~sw283/>

## See Also

`s`, `gam`, `gamm`, `smooth.construct.tensor.smooth.spec`

**Examples**

```

# following shows how tensor product deals nicely with
# badly scaled covariates (range of x 5% of range of z )
test1<-function(x,z,sx=0.3,sz=0.4)
{ x<-x*20
  (pi**sx*sz)*(1.2*exp(-(x-0.2)^2/sx^2-(z-0.3)^2/sz^2)+
  0.8*exp(-(x-0.7)^2/sx^2-(z-0.8)^2/sz^2))
}
n<-500
old.par<-par(mfrow=c(2,2))
x<-runif(n)/20;z<-runif(n);
xs<-seq(0,1,length=30)/20;zs<-seq(0,1,length=30)
pr<-data.frame(x=rep(xs,30),z=rep(zs,rep(30,30)))
truth<-matrix(test1(pr$x,pr$z),30,30)
f <- test1(x,z)
y <- f + rnorm(n)*0.2
b1<-gam(y~s(x,z))
persp(xs,zs,truth);title("truth")
vis.gam(b1);title("t.p.r.s")
b2<-gam(y~te(x,z))
vis.gam(b2);title("tensor product")
b3<-gam(y~te(x,z,bs=c("tp","tp")))
vis.gam(b3);title("tensor product")
par(old.par)

test2<-function(u,v,w,sv=0.3,sw=0.4)
{ ((pi**sv*sw)*(1.2*exp(-(v-0.2)^2/sv^2-(w-0.3)^2/sw^2)+
  0.8*exp(-(v-0.7)^2/sv^2-(w-0.8)^2/sw^2)))*(u-0.5)^2*20
}
n <- 500
v <- runif(n);w<-runif(n);u<-runif(n)
f <- test2(u,v,w)
y <- f + rnorm(n)*0.2
# tensor product of 2D thin plate regression spline and 1D cr spline
b <- gam(y~te(v,w,u,k=c(30,5),d=c(2,1),bs=c("tp","cr")))
op <- par(mfrow=c(2,2))
vis.gam(b,cond=list(u=0),color="heat",zlim=c(-0.2,3.5))
vis.gam(b,cond=list(u=.33),color="heat",zlim=c(-0.2,3.5))
vis.gam(b,cond=list(u=.67),color="heat",zlim=c(-0.2,3.5))
vis.gam(b,cond=list(u=1),color="heat",zlim=c(-0.2,3.5))
par(op)

```

---

tensor.prod.model.matrix

*Utility functions for constructing tensor product smooths*

---

**Description**

Produce model matrices or penalty matrices for a tensor product smooth from the model matrices or penalty matrices for the marginal bases of the smooth.

**Usage**

```
tensor.prod.model.matrix(X)
tensor.prod.penalties(S)
```

**Arguments**

X                    a list of model matrices for the marginal bases of a smooth  
 S                    a list of penalties for the marginal bases of a smooth.

**Details**

If  $X[[1]]$ ,  $X[[2]]$  ...  $X[[m]]$  are the model matrices of the marginal bases of a tensor product smooth then the  $i$ th row of the model matrix for the whole tensor product smooth is given by  $X[[1]][i, ] \%x\% X[[2]][i, ] \%x\% \dots X[[m]][i, ]$ , where  $\%x\%$  is the Kronecker product. Of course the routine operates column-wise, not row-wise!

If  $S[[1]]$ ,  $S[[2]]$  ...  $S[[m]]$  are the penalty matrices for the marginal bases, and  $I[[1]]$ ,  $I[[2]]$  ...  $I[[m]]$  are corresponding identity matrices, each of the same dimension as its corresponding penalty, then the tensor product smooth has  $m$  associate penalties of the form:

$$S[[1]] \%x\% I[[2]] \%x\% \dots I[[m]],$$

$$I[[1]] \%x\% S[[2]] \%x\% \dots I[[m]]$$

...

$$I[[1]] \%x\% I[[2]] \%x\% \dots S[[m]].$$

Of course it's important that the model matrices and penalty matrices are presented in the same order when constructing tensor product smooths.

**Value**

Either a single model matrix for a tensor product smooth, or a list of penalty terms for a tensor product smooth.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**References**

Wood, S.N. (2006) Low rank scale invariant tensor product smooths for Generalized Additive Mixed Models. *Biometrics* 62(4):1025-1036

**See Also**

[te](#), [smooth.construct.tensor.smooth.spec](#)

**Examples**

```
X <- list(matrix(1:4, 2, 2), matrix(5:10, 2, 3))
tensor.prod.model.matrix(X)
```

```
S <- list(matrix(c(2, 1, 1, 2), 2, 2), matrix(c(2, 1, 0, 1, 2, 1, 0, 1, 2), 3, 3))
tensor.prod.penalties(S)
```

Tweedie

*GAM Tweedie family***Description**

A Tweedie family, designed for use with `gam` from the `mgcv` library. Restricted to variance function powers between 1 and 2. A useful alternative to `quasi` when a full likelihood is desirable.

**Usage**

```
Tweedie(p=1, link = power(0))
```

**Arguments**

<code>p</code>	the variance of an observation is proportional to its mean to the power <code>p</code> . <code>p</code> must be greater than 1 and less than or equal to 2. 1 would be Poisson, 2 is gamma.
<code>link</code>	The link function: one of "log", "identity", "inverse", "sqrt", or a <a href="#">power</a> link.

**Details**

A Tweedie random variable with  $1 < p < 2$  is a sum of  $N$  gamma random variables where  $N$  has a Poisson distribution. The  $p=1$  case is a generalization of a Poisson distribution and is a discrete distribution supported on integer multiples of the scale parameter. For  $1 < p < 2$  the distribution is supported on the positive reals with a point mass at zero.  $p=2$  is a gamma distribution. As  $p$  gets very close to 1 the continuous distribution begins to converge on the discretely supported limit at  $p=1$ , and is therefore highly multimodal. See [ldTweedie](#) for more on this behaviour.

`Tweedie` is based partly on the [poisson](#) family, and partly on `tweedie` from the `statmod` package. It includes extra components to work with all `mgcv` GAM fitting methods as well as an `aic` function. The required log density evaluation (+ derivatives w.r.t. scale) is based on the series evaluation method of Dunn and Smyth (2005).

Without the restriction on `p` the calculation of Tweedie densities is less straightforward, and there does not currently seem to be an implementation which offers any benefit over `quasi`. If you really need to this case then the `tweedie` package is the place to start.

**Value**

An object inheriting from class `family`, with additional elements

<code>dvar</code>	the function giving the first derivative of the variance function w.r.t. <code>mu</code> .
<code>d2var</code>	the function giving the second derivative of the variance function w.r.t. <code>mu</code> .
<code>ls</code>	A function returning a 3 element array: the saturated log likelihood followed by its first 2 derivatives w.r.t. the scale parameter.

**Author(s)**

Simon N. Wood <[simon.wood@r-project.org](mailto:simon.wood@r-project.org)> modified from Venables and Ripley's `negative.binomial` family.

## References

Dunn, P.K. and G.K. Smith (2005) Series evaluation of Tweedie exponential dispersion model densities. *Statistics and Computing* 15:267-280

Tweedie, M. C. K. (1984). An index which distinguishes between some important exponential families. *Statistics: Applications and New Directions. Proceedings of the Indian Statistical Institute Golden Jubilee International Conference* (Eds. J. K. Ghosh and J. Roy), pp. 579-604. Calcutta: Indian Statistical Institute.

## See Also

[ldTweedie](#)

## Examples

```
library(mgcv)
set.seed(3)
n<-400
## Simulate data (really Poisson with log-link)
dat <- gamSim(1,n=n,dist="poisson",scale=.2)

## Fit a `nearby' Tweedie...
b <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=Tweedie(1.1,power(.1)),
        data=dat)
plot(b,pages=1)
print(b)

## Same by approximate REML...
b1 <- gam(y~s(x0)+s(x1)+s(x2)+s(x3),family=Tweedie(1.1,power(.1)),
        data=dat,method="REML")
plot(b1,pages=1)
print(b1)

rm(dat)
```

---

uniquecombs

*find the unique rows in a matrix*

---

## Description

This routine returns a matrix containing all the unique rows of the matrix supplied as its argument. That is, all the duplicate rows are stripped out. Note that the ordering of the rows on exit is not the same as on entry. It also returns an index attribute for relating the result back to the original matrix.

## Usage

```
uniquecombs(x)
```

## Arguments

`x` is an R matrix (numeric)

**Details**

Models with more parameters than unique combinations of covariates are not identifiable. This routine provides a means of evaluating the number of unique combinations of covariates in a model. The routine calls compiled C code.

**Value**

A matrix consisting of the unique rows of  $x$  (in arbitrary order).

The matrix has an "index" attribute. `index[i]` gives the row of the returned matrix that contains row  $i$  of the original matrix.

**Author(s)**

Simon N. Wood <simon.wood@r-project.org>

**See Also**

`unique` can do the same thing, including for non-numeric matrices, but more slowly and without returning the index.

**Examples**

```
X<-matrix(c(1,2,3,1,2,3,4,5,6,1,3,2,4,5,6,1,1,1),6,3,byrow=TRUE)
print(X)
Xu <- uniquecombs(X);Xu
ind <- attr(Xu,"index")
## find the value for row 3 of the original from Xu
Xu[ind[3],];X[3,]
```

---

vcov.gam

---

*Extract parameter (estimator) covariance matrix from GAM fit*


---

**Description**

Extracts the Bayesian posterior covariance matrix of the parameters or frequentist covariance matrix of the parameter estimators from a fitted `gam` object.

**Usage**

```
## S3 method for class 'gam':
vcov(object, freq = FALSE, dispersion = NULL, ...)
```

**Arguments**

<code>object</code>	fitted model object of class <code>gam</code> as produced by <code>gam()</code> .
<code>freq</code>	TRUE to return the frequentist covariance matrix of the parameter estimators, FALSE to return the Bayesian posterior covariance matrix of the parameters.
<code>dispersion</code>	a value for the dispersion parameter: not normally used.
<code>...</code>	other arguments, currently ignored.

**Details**

Basically, just extracts `object$Vc` or `object$Vp` from a `gamObject`.

**Value**

A matrix corresponding to the estimated frequentist covariance matrix of the model parameter estimators/coefficients, or the estimated posterior covariance matrix of the parameters, depending on the argument `freq`.

**Author(s)**

Henric Nilsson. Maintained by Simon N. Wood <simon.wood@r-project.org>

**References**

Wood, S.N. (2006) On confidence intervals for generalized additive models based on penalized regression splines. *Australian and New Zealand Journal of Statistics*. 48(4): 445-464.

**See Also**

[gam](#)

**Examples**

```
n <- 100
x <- runif(n)
y <- sin(x*2*pi) + rnorm(n)*.2
mod <- gam(y~s(x,bs="cc",k=10),knots=list(x=seq(0,1,length=10)))
diag(vcov(mod))
```

---

vis.gam

*Visualization of GAM objects*

---

**Description**

Produces perspective or contour plot views of `gam` model predictions, fixing all but the values in `view` to the values supplied in `cond`.

**Usage**

```
vis.gam(x,view=NULL,cond=list(),n.grid=30,too.far=0,col=NA,
        color="heat",contour.col=NULL,se=-1,type="link",
        plot.type="persp",zlim=NULL,nCol=50,...)
```

**Arguments**

`x` a `gam` object, produced by `gam()`

`view` an array containing the names of the two main effect terms to be displayed on the x and y dimensions of the plot. If omitted the first two suitable terms will be used. Note that variables coerced to factors in the model formula won't work as view variables, and `vis.gam` can not detect that this has happened when setting defaults.



<code>cond</code>	a named list of the values to use for the other predictor terms (not in <code>view</code> ). Variables omitted from this list will have the closest observed value to the median for continuous variables, or the most commonly occurring level for factors. Parametric matrix variables have all the entries in each column set to the observed column entry closest to the column median.
<code>n.grid</code>	The number of grid nodes in each direction used for calculating the plotted surface.
<code>too.far</code>	plot grid nodes that are too far from the points defined by the variables given in <code>view</code> can be excluded from the plot. <code>too.far</code> determines what is too far. The grid is scaled into the unit square along with the <code>view</code> variables and then grid nodes more than <code>too.far</code> from the predictor variables are excluded.
<code>col</code>	The colours for the facets of the plot. If this is NA then if <code>se&gt;0</code> the facets are transparent, otherwise the colour scheme specified in <code>color</code> is used. If <code>col</code> is not NA then it is used as the facet colour.
<code>color</code>	the colour scheme to use for plots when <code>se&lt;=0</code> . One of "topo", "heat", "cm", "terrain", "gray" or "bw". Schemes "gray" and "bw" also modify the colors used when <code>se&gt;0</code> .
<code>contour.col</code>	sets the colour of contours when using <code>plot.type="contour"</code> . Default scheme used if NULL.
<code>se</code>	if less than or equal to zero then only the predicted surface is plotted, but if greater than zero, then 3 surfaces are plotted, one at the predicted values minus <code>se</code> standard errors, one at the predicted values and one at the predicted values plus <code>se</code> standard errors.
<code>type</code>	"link" to plot on linear predictor scale and "response" to plot on the response scale.
<code>plot.type</code>	one of "contour" or "persp".
<code>zlim</code>	a two item array giving the lower and upper limits for the z-axis scale. NULL to choose automatically.
<code>nCol</code>	The number of colors to use in color schemes.
<code>...</code>	other options to pass on to <code>persp</code> , <code>image</code> or <code>contour</code> . In particular <code>ticktype="detailed"</code> will add proper axes labelling to the plots.

### Details

The x and y limits are determined by the ranges of the terms named in `view`. If `se<=0` then a single (height colour coded, by default) surface is produced, otherwise three (by default see-through) meshes are produced at mean and +/- `se` standard errors. Parts of the x-y plane too far from data can be excluded by setting `too.far`

All options to the underlying graphics functions can be reset by passing them as extra arguments `...`: such supplied values will always over-ride the default values used by `vis.gam`.

### Value

Simply produces a plot.

### WARNINGS

The routine can not detect that a variable has been coerced to factor within a model formula, and will therefore fail if such a variable is used as a `view` variable. When setting default `view` variables it can not detect this situation either, which can cause failures if the coerced variables are the first, otherwise suitable, variables encountered.

**Author(s)**

Simon Wood <simon.wood@r-project.org>

Based on an original idea and design by Mike Loneragan.

**See Also**

[persp](#) and [gam](#).

**Examples**

```

library(mgcv)
set.seed(0)
n<-200;sig2<-4
x0 <- runif(n, 0, 1);x1 <- runif(n, 0, 1)
x2 <- runif(n, 0, 1)
y<-x0^2+x1*x2 +runif(n,-0.3,0.3)
g<-gam(y~s(x0,x1,x2))
old.par<-par(mfrow=c(2,2))
# display the prediction surface in x0, x1 ....
vis.gam(g,ticktype="detailed",color="heat",theta=-35)
vis.gam(g,se=2,theta=-35) # with twice standard error surfaces
vis.gam(g, view=c("x1","x2"),cond=list(x0=0.75)) # different view
vis.gam(g, view=c("x1","x2"),cond=list(x0=.75),theta=210,phi=40,
        too.far=.07)
# ..... areas where there is no data are not plotted

# contour examples....
vis.gam(g, view=c("x1","x2"),plot.type="contour",color="heat")
vis.gam(g, view=c("x1","x2"),plot.type="contour",color="terrain")
vis.gam(g, view=c("x1","x2"),plot.type="contour",color="topo")
vis.gam(g, view=c("x1","x2"),plot.type="contour",color="cm")

par(old.par)

# Examples with factor and "by" variables

fac<-rep(1:4,20)
x<-runif(80)
y<-fac+2*x^2+rnorm(80)*0.1
fac<-factor(fac)
b<-gam(y~fac+s(x))

vis.gam(b,theta=-35,color="heat") # factor example

z<-rnorm(80)*0.4
y<-as.numeric(fac)+3*x^2*z+rnorm(80)*0.1
b<-gam(y~fac+s(x,by=z))

vis.gam(b,theta=-35,color="heat",cond=list(z=1)) # by variable example
vis.gam(b,view=c("z","x"),theta=35) # plot against by variable

```



## Chapter 19

# The nlme package

---

ACF

*Autocorrelation Function*

---

### Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `gls` and `lme`.

### Usage

```
ACF(object, maxLag, ...)
```

### Arguments

<code>object</code>	any object from which an autocorrelation function can be obtained. Generally an object resulting from a model fit, from which residuals can be extracted.
<code>maxLag</code>	maximum lag for which the autocorrelation should be calculated.
<code>...</code>	some methods for this generic require additional arguments.

### Value

will depend on the method function used; see the appropriate documentation.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<Bates@stat.wisc.edu>

### References

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

### See Also

[ACF.gls](#), [ACF.lme](#), [plot.ACF](#)

**Examples**

```
## see the method function documentation
```

---

ACF.gls

*Autocorrelation Function for gls Residuals*


---

**Description**

This method function calculates the empirical autocorrelation function for the residuals from a `gls` fit. If a grouping variable is specified in `form`, the autocorrelation values are calculated using pairs of residuals within the same group; otherwise all possible residual pairs are used. The autocorrelation function is useful for investigating serial correlation models for equally spaced data.

**Usage**

```
## S3 method for class 'gls':
ACF(object, maxLag, resType, form, na.action, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>gls</code> , representing a generalized least squares fitted model.
<code>maxLag</code>	an optional integer giving the maximum lag for which the autocorrelation should be calculated. Defaults to maximum lag in the residuals.
<code>resType</code>	an optional character string specifying the type of residuals to be used. If "response", the "raw" residuals (observed - fitted) are used; else, if "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".
<code>form</code>	an optional one sided formula of the form $\sim t$ , or $\sim t   g$ , specifying a time covariate <code>t</code> and, optionally, a grouping factor <code>g</code> . The time covariate must be integer valued. When a grouping factor is present in <code>form</code> , the autocorrelations are calculated using residual pairs within the same group. Defaults to $\sim 1$ , which corresponds to using the order of the observations in the data as a covariate, and no groups.
<code>na.action</code>	a function that indicates what should happen when the data contain NAs. The default action ( <code>na.fail</code> ) causes <code>ACF.gls</code> to print an error message and terminate if there are any incomplete observations.
<code>...</code>	some methods for this generic require additional arguments.

**Value**

a data frame with columns `lag` and `ACF` representing, respectively, the lag between residuals within a pair and the corresponding empirical autocorrelation. The returned value inherits from class `ACF`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**References**

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[ACF.gls](#), [plot.ACF](#)

**Examples**

```
fml <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary)
ACF(fml, form = ~ 1 | Mare)

# Pinheiro and Bates, p. 255-257
fmlDial.gls <- gls(rate ~
  (pressure+I(pressure^2)+I(pressure^3)+I(pressure^4)) *QB,
  Dialyzer)

fm2Dial.gls <- update(fmlDial.gls,
  weights = varPower(form = ~ pressure))

ACF(fm2Dial.gls, form = ~ 1 | Subject)
```

---

ACF.lme

*Autocorrelation Function for lme Residuals*

---

**Description**

This method function calculates the empirical autocorrelation function for the within-group residuals from an `lme` fit. The autocorrelation values are calculated using pairs of residuals within the innermost group level. The autocorrelation function is useful for investigating serial correlation models for equally spaced data.

**Usage**

```
## S3 method for class 'lme':
ACF(object, maxLag, resType, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>lme</code> , representing a fitted linear mixed-effects model.
<code>maxLag</code>	an optional integer giving the maximum lag for which the autocorrelation should be calculated. Defaults to maximum lag in the within-group residuals.

`resType` an optional character string specifying the type of residuals to be used. If "response", the "raw" residuals (observed - fitted) are used; else, if "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".

... some methods for this generic require additional arguments – not used.

### Value

a data frame with columns `lag` and `ACF` representing, respectively, the lag between residuals within a pair and the corresponding empirical autocorrelation. The returned value inherits from class `ACF`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

### See Also

[ACF.gls](#), [plot.ACF](#)

### Examples

```
fml <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time),
          Ovary, random = ~ sin(2*pi*Time) | Mare)
ACF(fml, maxLag = 11)

# Pinheiro and Bates, p240-241
fmlOver.lme <- lme(follicles ~ sin(2*pi*Time) +
                  cos(2*pi*Time), data=Ovary,
                  random=pdDiag(~sin(2*pi*Time)) )
(ACF.fmlOver <- ACF(fmlOver.lme, maxLag=10))
plot(ACF.fmlOver, alpha=0.01)
```

### Description

The `Alfalfa` data frame has 72 rows and 4 columns.

**Format**

This data frame contains the following columns:

**Variety** a factor with levels `Cossack`, `Ladak`, and `Ranger`

**Date** a factor with levels `None` `S1` `S20` `O7`

**Block** a factor with levels `1` `2` `3` `4` `5` `6`

**Yield** a numeric vector

**Details**

These data are described in Snedecor and Cochran (1980) as an example of a split-plot design. The treatment structure used in the experiment was a  $3 \times 4$  full factorial, with three varieties of alfalfa and four dates of third cutting in 1943. The experimental units were arranged into six blocks, each subdivided into four plots. The varieties of alfalfa (*Cossac*, *Ladak*, and *Ranger*) were assigned randomly to the blocks and the dates of third cutting (*None*, *S1*—September 1, *S20*—September 20, and *O7*—October 7) were randomly assigned to the plots. All four dates were used on each block.

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.1)

Snedecor, G. W. and Cochran, W. G. (1980), *Statistical Methods (7th ed)*, Iowa State University Press, Ames, IA

---

allCoef

*Extract Coefficients from a Set of Objects*


---

**Description**

The extractor function is applied to each object in `...`, with the result being converted to a vector. A `map` attribute is included to indicate which pieces of the returned vector correspond to the original objects in `dots`.

**Usage**

```
allCoef(..., extract)
```

**Arguments**

`...` objects to which `extract` will be applied. Generally these will be model components, such as `corStruct` and `varFunc` objects.

`extract` an optional extractor function. Defaults to `coef`.

**Value**

a vector with all elements, generally coefficients, obtained by applying `extract` to the objects in `...`

**Author(s)**

Jose' Pinheiro and Douglas Bates



**See Also**

[lmeStruct](#), [nlmeStruct](#)

**Examples**

```
cs1 <- corAR1(0.1)
vf1 <- varPower(0.5)
allCoef(cs1, vf1)
```

---

anova.gls

*Compare Likelihoods of Fitted Objects*

---

**Description**

When only one fitted model object is present, a data frame with the sums of squares, numerator degrees of freedom, F-values, and P-values for Wald tests for the terms in the model (when `Terms` and `L` are `NULL`), a combination of model terms (when `Terms` is not `NULL`), or linear combinations of the model coefficients (when `L` is not `NULL`). Otherwise, when multiple fitted objects are being compared, a data frame with the degrees of freedom, the (restricted) log-likelihood, the Akaike Information Criterion (AIC), and the Bayesian Information Criterion (BIC) of each object is returned. If `test=TRUE`, whenever two consecutive objects have different number of degrees of freedom, a likelihood ratio statistic, with the associated p-value is included in the returned data frame.

**Usage**

```
## S3 method for class 'gls':
anova(object, ..., test, type, adjustSigma, Terms, L, verbose)
```

**Arguments**

<code>object</code>	a fitted model object inheriting from class <code>gls</code> , representing a generalized least squares fit.
<code>...</code>	other optional fitted model objects inheriting from classes <code>gls</code> , <code>gnls</code> , <code>lm</code> , <code>lme</code> , <code>lmList</code> , <code>nlme</code> , <code>nlsList</code> , or <code>nls</code> .
<code>test</code>	an optional logical value controlling whether likelihood ratio tests should be used to compare the fitted models represented by <code>object</code> and the objects in <code>...</code> . Defaults to <code>TRUE</code> .
<code>type</code>	an optional character string specifying the type of sum of squares to be used in F-tests for the terms in the model. If <code>"sequential"</code> , the sequential sum of squares obtained by including the terms in the order they appear in the model is used; else, if <code>"marginal"</code> , the marginal sum of squares obtained by deleting a term from the model at a time is used. This argument is only used when a single fitted object is passed to the function. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to <code>"sequential"</code> .
<code>adjustSigma</code>	an optional logical value. If <code>TRUE</code> and the estimation method used to obtain <code>object</code> was maximum likelihood, the residual standard error is multiplied by $\sqrt{n_{obs}/(n_{obs} - n_{par})}$ , converting it to a REML-like estimate. This argument is only used when a single fitted object is passed to the function. Default is <code>TRUE</code> .

Terms	an optional integer or character vector specifying which terms in the model should be jointly tested to be zero using a Wald F-test. If given as a character vector, its elements must correspond to term names; else, if given as an integer vector, its elements must correspond to the order in which terms are included in the model. This argument is only used when a single fitted object is passed to the function. Default is <code>NULL</code> .
L	an optional numeric vector or array specifying linear combinations of the coefficients in the model that should be tested to be zero. If given as an array, its rows define the linear combinations to be tested. If names are assigned to the vector elements (array columns), they must correspond to coefficients names and will be used to map the linear combination(s) to the coefficients; else, if no names are available, the vector elements (array columns) are assumed in the same order as the coefficients appear in the model. This argument is only used when a single fitted object is passed to the function. Default is <code>NULL</code> .
verbose	an optional logical value. If <code>TRUE</code> , the calling sequences for each fitted model object are printed with the rest of the output, being omitted if <code>verbose = FALSE</code> . Defaults to <code>FALSE</code> .

**Value**

a data frame inheriting from class `anova.lme`.

**Note**

Likelihood comparisons are not meaningful for objects fit using restricted maximum likelihood and with different fixed effects.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

**See Also**

[gl](#)s, [gn](#)ls, [lme](#), [logLik.gls](#), [AIC](#), [BIC](#), [print.anova.lme](#)

**Examples**

```
# AR(1) errors within each Mare
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
          correlation = corAR1(form = ~ 1 | Mare))
anova(fm1)
# variance changes with a power of the absolute fitted values?
fm2 <- update(fm1, weights = varPower())
anova(fm1, fm2)

# Pinheiro and Bates, p. 251-252
fm1Orth.gls <- gls(distance ~ Sex * I(age - 11), Orthodont,
                  correlation = corSymm(form = ~ 1 | Subject),
```

```

        weights = varIdent(form = ~ 1 | age))
fm2Orth.gls <- update(fm1Orth.gls,
                    corr = corCompSymm(form = ~ 1 | Subject))
anova(fm1Orth.gls, fm2Orth.gls)

# Pinheiro and Bates, pp. 215-215, 255-260
#p. 215
fm1Dial.lme <-
  lme(rate ~ (pressure + I(pressure^2) + I(pressure^3) + I(pressure^4))*QB,
       Dialyzer, ~ pressure + I(pressure^2))
# p. 216
fm2Dial.lme <- update(fm1Dial.lme,
                    weights = varPower(form = ~ pressure))
# p. 255
fm1Dial.gls <- gls(rate ~ (pressure +
                        I(pressure^2) + I(pressure^3) + I(pressure^4))*QB,
                  Dialyzer)
fm2Dial.gls <- update(fm1Dial.gls,
                    weights = varPower(form = ~ pressure))
anova(fm1Dial.gls, fm2Dial.gls)
fm3Dial.gls <- update(fm2Dial.gls,
                    corr = corAR1(0.771, form = ~ 1 | Subject))
anova(fm2Dial.gls, fm3Dial.gls)
# anova.gls to compare a gls and an lme fit
anova(fm3Dial.gls, fm2Dial.lme, test = FALSE)

# Pinheiro and Bates, pp. 261-266
fm1Wheat2 <- gls(yield ~ variety - 1, Wheat2)
fm3Wheat2 <- update(fm1Wheat2,
                  corr = corRatio(c(12.5, 0.2),
                                  form = ~ latitude + longitude, nugget = TRUE))
# Test a specific contrast
anova(fm3Wheat2, L = c(-1, 0, 1))

```

---

anova.lme

---

*Compare Likelihoods of Fitted Objects*


---

## Description

When only one fitted model object is present, a data frame with the sums of squares, numerator degrees of freedom, denominator degrees of freedom, F-values, and P-values for Wald tests for the terms in the model (when `Terms` and `L` are `NULL`), a combination of model terms (when `Terms` is not `NULL`), or linear combinations of the model coefficients (when `L` is not `NULL`). Otherwise, when multiple fitted objects are being compared, a data frame with the degrees of freedom, the (restricted) log-likelihood, the Akaike Information Criterion (AIC), and the Bayesian Information Criterion (BIC) of each object is returned. If `test=TRUE`, whenever two consecutive objects have different number of degrees of freedom, a likelihood ratio statistic, with the associated p-value is included in the returned data frame.

## Usage

```

## S3 method for class 'lme':
anova(object, ..., test, type, adjustSigma, Terms, L, verbose)

```

```
## S3 method for class 'anova.lme':
print(x, verbose, ...)
```

### Arguments

object	a fitted model object inheriting from class <code>lme</code> , representing a mixed-effects model.
...	other optional fitted model objects inheriting from classes <code>gls</code> , <code>gnls</code> , <code>lm</code> , <code>lme</code> , <code>lmList</code> , <code>nlme</code> , <code>nlsList</code> , or <code>nls</code> .
test	an optional logical value controlling whether likelihood ratio tests should be used to compare the fitted models represented by <code>object</code> and the objects in ... Defaults to <code>TRUE</code> .
type	an optional character string specifying the type of sum of squares to be used in F-tests for the terms in the model. If <code>"sequential"</code> , the sequential sum of squares obtained by including the terms in the order they appear in the model is used; else, if <code>"marginal"</code> , the marginal sum of squares obtained by deleting a term from the model at a time is used. This argument is only used when a single fitted object is passed to the function. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to <code>"sequential"</code> .
adjustSigma	an optional logical value. If <code>TRUE</code> and the estimation method used to obtain <code>object</code> was maximum likelihood, the residual standard error is multiplied by $\sqrt{n_{obs}/(n_{obs} - n_{par})}$ , converting it to a REML-like estimate. This argument is only used when a single fitted object is passed to the function. Default is <code>TRUE</code> .
Terms	an optional integer or character vector specifying which terms in the model should be jointly tested to be zero using a Wald F-test. If given as a character vector, its elements must correspond to term names; else, if given as an integer vector, its elements must correspond to the order in which terms are included in the model. This argument is only used when a single fitted object is passed to the function. Default is <code>NULL</code> .
L	an optional numeric vector or array specifying linear combinations of the coefficients in the model that should be tested to be zero. If given as an array, its rows define the linear combinations to be tested. If names are assigned to the vector elements (array columns), they must correspond to coefficients names and will be used to map the linear combination(s) to the coefficients; else, if no names are available, the vector elements (array columns) are assumed in the same order as the coefficients appear in the model. This argument is only used when a single fitted object is passed to the function. Default is <code>NULL</code> .
x	an object inheriting from class <code>anova.lme</code>
verbose	an optional logical value. If <code>TRUE</code> , the calling sequences for each fitted model object are printed with the rest of the output, being omitted if <code>verbose = FALSE</code> . Defaults to <code>FALSE</code> .

### Value

a data frame inheriting from class `anova.lme`.

### Note

Likelihood comparisons are not meaningful for objects fit using restricted maximum likelihood and with different fixed effects.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[gls](#), [gnls](#), [nlme](#), [lme](#), [AIC](#), [BIC](#), [print.anova.lme](#), [logLik.lme](#),

**Examples**

```
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
anova(fm1)
fm2 <- update(fm1, random = pdDiag(~age))
anova(fm1, fm2)

# Pinheiro and Bates, pp. 251-254
fm1Orth.gls <- gls(distance ~ Sex * I(age - 11), Orthodont,
  correlation = corSymm(form = ~ 1 | Subject),
  weights = varIdent(form = ~ 1 | age))
fm2Orth.gls <- update(fm1Orth.gls,
  corr = corCompSymm(form = ~ 1 | Subject))

# anova.gls
anova(fm1Orth.gls, fm2Orth.gls)
fm3Orth.gls <- update(fm2Orth.gls, weights = NULL)
# anova.gls
anova(fm2Orth.gls, fm3Orth.gls)
fm4Orth.gls <- update(fm3Orth.gls,
  weights = varIdent(form = ~ 1 | Sex))

# anova.gls
anova(fm3Orth.gls, fm4Orth.gls)
# not in book but needed for the following command
fm3Orth.lme <-
  lme(distance~Sex*I(age-11), data = Orthodont,
    random = ~ I(age-11) | Subject,
    weights = varIdent(form = ~ 1 | Sex))
# anova.lme to compare an "lme" object with a "gls" object
anova(fm3Orth.lme, fm4Orth.gls, test = FALSE)

# Pinheiro and Bates, pp. 222-225
options(contrasts = c("contr.treatment", "contr.poly"))
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
  random = ~ Time)
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# Test a specific contrast
anova(fm2BW.lme, L = c("Time:Diet2" = 1, "Time:Diet3" = -1))

fm1Theo.lis <- nlsList(
  conc ~ SSFol(Dose, Time, lKe, lKa, lCl), data=Theoph)
fm1Theo.lis

# Pinheiro and Bates, pp. 352-365
fm1Theo.lis <- nlsList(
```

```
      conc ~ SSfol(Dose, Time, lKe, lKa, lCl), data=Theoph)
fm1Theo.nlme <- nlme(fm1Theo.lis)
fm2Theo.nlme <- update(fm1Theo.nlme,
  random=pdDiag(lKe+lKa+lCl~1) )
fm3Theo.nlme <- update(fm2Theo.nlme,
  random=pdDiag(lKa+lCl~1) )

# anova comparing 3 models
anova(fm1Theo.nlme, fm3Theo.nlme, fm2Theo.nlme)
```

---

as.matrix.corStruct

*Matrix of a corStruct Object*

---

## Description

This method function extracts the correlation matrix, or list of correlation matrices, associated with object.

## Usage

```
## S3 method for class 'corStruct':
as.matrix(x, ...)
```

## Arguments

**x** an object inheriting from class `corStruct`, representing a correlation structure.

**...** further arguments passed from other methods.

## Value

If the correlation structure includes a grouping factor, the returned value will be a list with components given by the correlation matrices for each group. Otherwise, the returned value will be a matrix representing the correlation structure associated with `object`.

## Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

## References

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

## See Also

[corClasses](#), [corMatrix](#)

**Examples**

```
cst1 <- corAR1(form = ~1|Subject)
cst1 <- Initialize(cst1, data = Orthodont)
as.matrix(cst1)
```

---

as.matrix.pdMat      *Matrix of a pdMat Object*

---

**Description**

This method function extracts the positive-definite matrix represented by `x`.

**Usage**

```
## S3 method for class 'pdMat':
as.matrix(x, ...)
```

**Arguments**

`x`                    an object inheriting from class `pdMat`, representing a positive-definite matrix.  
`...`                further arguments passed from other methods.

**Value**

a matrix corresponding to the positive-definite matrix represented by `x`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**References**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

**See Also**

[pdMat](#), [corMatrix](#)

**Examples**

```
as.matrix(pdSymm(diag(4)))
```

---

as.matrix.reStruct *Matrices of an reStruct Object*

---

### Description

This method function extracts the positive-definite matrices corresponding to the pdMat elements of object.

### Usage

```
## S3 method for class 'reStruct':  
as.matrix(x, ...)
```

### Arguments

`x` an object inheriting from class `reStruct`, representing a random effects structure and consisting of a list of `pdMat` objects.

`...` further arguments passed from other methods.

### Value

a list with components given by the positive-definite matrices corresponding to the elements of object.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

### See Also

[as.matrix.pdMat](#), [reStruct](#), [pdMat](#)

### Examples

```
rs1 <- reStruct(pdSymm(diag(3), ~age+Sex, data = Orthodont))  
as.matrix(rs1)
```



---

asOneFormula                      *Combine Formulas of a Set of Objects*

---

### Description

The names of all variables used in the formulas extracted from the objects defined in ... are converted into a single linear formula, with the variables names separated by +.

### Usage

```
asOneFormula(..., omit)
```

### Arguments

...                      objects, or lists of objects, from which a formula can be extracted.  
omit                      an optional character vector with the names of variables to be omitted from the returned formula. Defaults to c(".", "pi").

### Value

a one-sided linear formula with all variables named in the formulas extracted from the objects in ..., except the ones listed in omit.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

### See Also

[formula](#), [all.vars](#)

### Examples

```
asOneFormula(y ~ x + z | g, list(~ w, ~ t * sin(2 * pi)))
```

---

Assay                                      *Bioassay on Cell Culture Plate*

---

### Description

The Assay data frame has 60 rows and 4 columns.

### Format

This data frame contains the following columns:

**Block** an ordered factor with levels 2 < 1 identifying the block where the wells are measured.

**sample** a factor with levels a to f identifying the sample corresponding to the well.

**dilut** a factor with levels 1 to 5 indicating the dilution applied to the well

**logDens** a numeric vector of the log-optical density

## Details

These data, courtesy of Rich Wolfe and David Lansky from Searle, Inc., come from a bioassay run on a 96-well cell culture plate. The assay is performed using a split-block design. The 8 rows on the plate are labeled A–H from top to bottom and the 12 columns on the plate are labeled 1–12 from left to right. Only the central 60 wells of the plate are used for the bioassay (the intersection of rows B–G and columns 2–11). There are two blocks in the design: Block 1 contains columns 2–6 and Block 2 contains columns 7–11. Within each block, six samples are assigned randomly to rows and five (serial) dilutions are assigned randomly to columns. The response variable is the logarithm of the optical density. The cells are treated with a compound that they metabolize to produce the stain. Only live cells can make the stain, so the optical density is a measure of the number of cells that are alive and healthy.

## Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.2)

---

asTable

*Convert groupedData to a matrix*

---

## Description

Create a tabular representation of the response in a balanced groupedData object.

## Usage

```
asTable(object)
```

## Arguments

object            A balanced groupedData object

## Details

A balanced groupedData object can be represented as a matrix or table of response values corresponding to the values of a primary covariate for each level of a grouping factor. This function creates such a matrix representation of the data in object.

## Value

A matrix. The data in the matrix are the values of the response. The columns correspond to the distinct values of the primary covariate and are labelled as such. The rows correspond to the distinct levels of the grouping factor and are labelled as such.

## Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

## References

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

**See Also**

[groupedData](#), [isBalanced](#), [balancedGrouped](#)

**Examples**

```
asTable(Orthodont)

# Pinheiro and Bates, p. 109
ergoStool.mat <- asTable(ergoStool)
```

---

augPred

*Augmented Predictions*

---

**Description**

Predicted values are obtained at the specified values of `primary`. If `object` has a grouping structure (i.e. `getGroups(object)` is not `NULL`), predicted values are obtained for each group. If `level` has more than one element, predictions are obtained for each level of the `max(level)` grouping factor. If other covariates besides `primary` are used in the prediction model, their average (numeric covariates) or most frequent value (categorical covariates) are used to obtain the predicted values. The original observations are also included in the returned object.

**Usage**

```
augPred(object, primary, minimum, maximum, length.out, ...)
```

**Arguments**

<code>object</code>	a fitted model object from which predictions can be extracted, using a <code>predict</code> method.
<code>primary</code>	an optional one-sided formula specifying the primary covariate to be used to generate the augmented predictions. By default, if a covariate can be extracted from the data used to generate <code>object</code> (using <code>getCovariate</code> ), it will be used as <code>primary</code> .
<code>minimum</code>	an optional lower limit for the primary covariate. Defaults to <code>min(primary)</code> .
<code>maximum</code>	an optional upper limit for the primary covariate. Defaults to <code>max(primary)</code> .
<code>length.out</code>	an optional integer with the number of primary covariate values at which to evaluate the predictions. Defaults to 51.
<code>...</code>	some methods for the generic may require additional arguments.

**Value**

a data frame with four columns representing, respectively, the values of the primary covariate, the groups (if `object` does not have a grouping structure, all elements will be 1), the predicted or observed values, and the type of value in the third column: `original` for the observed values and `predicted` (single or no grouping factor) or `predict.groupVar` (multiple levels of grouping), with `groupVar` replaced by the actual grouping variable name (`fixed` is used for population predictions). The returned object inherits from class `augPred`.

**Note**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `gls`, `lme`, and `lmList`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

**See Also**

[plot.augPred](#), [getGroups](#), [predict](#)

**Examples**

```
fml <- lme(Orthodont, random = ~1)
augPred(fml, length.out = 2, level = c(0,1))
```

---

balancedGrouped      *Create a groupedData object from a matrix*

---

**Description**

Create a `groupedData` object from a data matrix. This function can be used only with balanced data. The opposite conversion, from a `groupedData` object to a `matrix`, is done with `asTable`.

**Usage**

```
balancedGrouped(form, data, labels=NULL, units=NULL)
```

**Arguments**

<code>form</code>	A formula of the form $y \sim x \mid g$ giving the name of the response, the primary covariate, and the grouping factor.
<code>data</code>	A matrix or data frame containing the values of the response grouped according to the levels of the grouping factor (rows) and the distinct levels of the primary covariate (columns). The <code>dimnames</code> of the matrix are used to construct the levels of the grouping factor and the primary covariate.
<code>labels</code>	an optional list of character strings giving labels for the response and the primary covariate. The label for the primary covariate is named <code>x</code> and that for the response is named <code>y</code> . Either label can be omitted.
<code>units</code>	an optional list of character strings giving the units for the response and the primary covariate. The units string for the primary covariate is named <code>x</code> and that for the response is named <code>y</code> . Either units string can be omitted.

**Value**

A balanced groupedData object.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

**See Also**

[groupedData](#), [isBalanced](#), [asTable](#)

**Examples**

```
OrthoMat <- asTable( Orthodont )
Orth2 <- balancedGrouped(distance ~ age | Subject, data = OrthoMat,
  labels = list(x = "Age",
               y = "Distance from pituitary to pterygomaxillary fissure"),
  units = list(x = "(yr)", y = "(mm)"))
Orth2[ 1:10, ]      ## check the first few entries

# Pinheiro and Bates, p. 109
ergoStool.mat <- asTable(ergoStool)
balancedGrouped(effort~Type|Subject,
  data=ergoStool.mat)
```

---

bdf

*Language scores*

---

**Description**

The bdf data frame has 2287 rows and 25 columns of language scores from grade 8 pupils in elementary schools in The Netherlands.

**Usage**

```
data(bdf)
```

**Format**

**schoolNR** a factor denoting the school.

**pupilNR** a factor denoting the pupil.

**IQ.verb** a numeric vector of verbal IQ scores

**IQ.perf** a numeric vector of IQ scores.

**sex** Sex of the student.

**Minority** a factor indicating if the student is a member of a minority group.

**repeatgr** an ordered factor indicating if one or more grades have been repeated.  
**aritPRET** a numeric vector  
**classNR** a numeric vector  
**aritPOST** a numeric vector  
**langPRET** a numeric vector  
**langPOST** a numeric vector  
**ses** a numeric vector of socioeconomic status indicators.  
**denomina** a factor indicating of the school is a public school, a Protestant private school, a Catholic private school, or a non-denominational private school.  
**schoolSES** a numeric vector  
**satiprin** a numeric vector  
**natitest** a factor with levels 0 and 1  
**meetings** a numeric vector  
**currmeet** a numeric vector  
**mixedgra** a factor indicating if the class is a mixed-grade class.  
**percmينو** a numeric vector  
**aritdiff** a numeric vector  
**homework** a numeric vector  
**classsiz** a numeric vector  
**groupsiz** a numeric vector

### Source

<http://stat.gamma.rug.nl/snijders/multilevel.htm>

### References

Snijders, Tom and Bosker, Roel (1999), *Multilevel Analysis: An Introduction to Basic and Advanced Multilevel Modeling*, Sage.

### Examples

```
summary(bdf)
```

---

BIC

*Bayesian Information Criterion*

---

### Description

This generic function calculates the Bayesian information criterion, also known as Schwarz's Bayesian criterion (SBC), for one or several fitted model objects for which a log-likelihood value can be obtained, according to the formula  $-2\log\text{-likelihood} + n_{par} \log(n_{obs})$ , where  $n_{par}$  represents the number of parameters and  $n_{obs}$  the number of observations in the fitted model.

### Usage

```
BIC(object, ...)
```

**Arguments**

`object` a fitted model object, for which there exists a `logLik` method to extract the corresponding log-likelihood, or an object inheriting from class `logLik`.

`...` optional fitted model objects.

**Value**

if just one object is provided, returns a numeric value with the corresponding BIC; if more than one object are provided, returns a `data.frame` with rows corresponding to the objects and columns representing the number of parameters in the model (`df`) and the BIC.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Schwarz, G. (1978) "Estimating the Dimension of a Model", *Annals of Statistics*, 6, 461-464.

**See Also**

[logLik](#), [AIC](#), [BIC.logLik](#)

**Examples**

```
fm1 <- lm(distance ~ age, data = Orthodont) # no random effects
BIC(fm1)

fm2 <- lme(distance ~ age, data = Orthodont) # random is ~age
BIC(fm1, fm2)
```

---

BIC.logLik

*BIC of a logLik Object*

---

**Description**

This function calculates the Bayesian information criterion, also known as Schwarz's Bayesian criterion (SBC) for an object inheriting from class `logLik`, according to the formula  $-2\log\text{-likelihood} + n_{par} \log(n_{obs})$ , where  $n_{par}$  represents the number of parameters and  $n_{obs}$  the number of observations in the fitted model. When comparing fitted objects, the smaller the BIC, the better the fit.

**Usage**

```
## S3 method for class 'logLik':
BIC(object, ...)
```

**Arguments**

`object` an object inheriting from class `logLik`, usually resulting from applying a `logLik` method to a fitted model object.

`...` some methods for this generic use optional arguments. None are used in this method.

**Value**

a numeric value with the corresponding BIC.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Schwarz, G. (1978) "Estimating the Dimension of a Model", *Annals of Statistics*, 6, 461-464.

**See Also**

[BIC](#), [logLik](#), [AIC](#).

**Examples**

```
fm1 <- lm(distance ~ age, data = Orthodont)
BIC(logLik(fm1))
```

---

BodyWeight

*Rat weight over time for different diets*

---

**Description**

The `BodyWeight` data frame has 176 rows and 4 columns.

**Format**

This data frame contains the following columns:

**weight** a numeric vector giving the body weight of the rat (grams).

**Time** a numeric vector giving the time at which the measurement is made (days).

**Rat** an ordered factor with levels 2 < 3 < 4 < 1 < 8 < 5 < 6 < 7 < 11 < 9 < 10 < 12 < 13 < 15 < 14 < 16 identifying the rat whose weight is measured.

**Diet** a factor with levels 1 to 3 indicating the diet that the rat receives.

**Details**

Hand and Crowder (1996) describe data on the body weights of rats measured over 64 days. These data also appear in Table 2.4 of Crowder and Hand (1990). The body weights of the rats (in grams) are measured on day 1 and every seven days thereafter until day 64, with an extra measurement on day 44. The experiment started several weeks before "day 1." There are three groups of rats, each on a different diet.



**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.3)

Crowder, M. and Hand, D. (1990), *Analysis of Repeated Measures*, Chapman and Hall, London.

Hand, D. and Crowder, M. (1996), *Practical Longitudinal Data Analysis*, Chapman and Hall, London.

---

Cefamandole

*Pharmacokinetics of Cefamandole*

---

**Description**

The Cefamandole data frame has 84 rows and 3 columns.

**Format**

This data frame contains the following columns:

**Subject** a factor giving the subject from which the sample was drawn.

**Time** a numeric vector giving the time at which the sample was drawn (minutes post-injection).

**conc** a numeric vector giving the observed plasma concentration of cefamandole (mcg/ml).

**Details**

Davidian and Giltinan (1995, 1.1, p. 2) describe data obtained during a pilot study to investigate the pharmacokinetics of the drug cefamandole. Plasma concentrations of the drug were measured on six healthy volunteers at 14 time points following an intravenous dose of 15 mg/kg body weight of cefamandole.

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.4)

Davidian, M. and Giltinan, D. M. (1995), *Nonlinear Models for Repeated Measurement Data*, Chapman and Hall, London.

**Examples**

```
plot(Cefamandole)
fml <- nlsList(SSbiexp, data = Cefamandole)
summary(fml)
```

---

Coef *Assign Values to Coefficients*

---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include all `pdMat`, `corStruct`, and `varFunc` classes, `reStruct`, and `modelStruct`.

**Usage**

```
coef(object, ...) <- value
```

**Arguments**

<code>object</code>	any object representing a fitted model, or, by default, any object with a <code>coef</code> component.
<code>...</code>	some methods for this generic function may require additional arguments.
<code>value</code>	a value to be assigned to the coefficients associated with <code>object</code> .

**Value**

will depend on the method function; see the appropriate documentation.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[coef](#)

**Examples**

```
## see the method function documentation
```

---

`coef.corStruct` *Coefficients of a corStruct Object*

---

**Description**

This method function extracts the coefficients associated with the correlation structure represented by `object`.

**Usage**

```
## S3 method for class 'corStruct':
coef(object, unconstrained, ...)
## S3 method for class 'corStruct':
coef(object, ...) <- value
```

**Arguments**

<code>object</code>	an object inheriting from class <code>corStruct</code> , representing a correlation structure.
<code>unconstrained</code>	a logical value. If <code>TRUE</code> the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If <code>FALSE</code> the coefficients are returned in "natural", possibly constrained, form. Defaults to <code>TRUE</code> .
<code>value</code>	a vector with the replacement values for the coefficients associated with <code>object</code> . It must be a vector with the same length of <code>coef{object}</code> and must be given in unconstrained form.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a vector with the coefficients corresponding to `object`.

**SIDE EFFECTS**

On the left side of an assignment, sets the values of the coefficients of `object` to `value`. `Object` must be initialized (using `Initialize`) before new values can be assigned to its coefficients.

**Author(s)**

Jose Pinheiro and Douglas Bates

**References**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

**See Also**

`corAR1`, `corARMA`, `corCAR1`, `corCompSymm`, `corExp`, `corGaus`, `corLin`, `corRatio`, `corSpatial`, `corSpher`, `corSymm`, `Initialize`

**Examples**

```
cst1 <- corARMA(p = 1, q = 1)
coef(cst1)
```

---

coef.gnls

*Extract gnls Coefficients*

---

**Description**

The estimated coefficients for the nonlinear model represented by `object` are extracted.

**Usage**

```
## S3 method for class 'gnls':
coef(object, ...)
```

**Arguments**

- `object` an object inheriting from class `gnls`, representing a generalized nonlinear least squares fitted model.
- `...` some methods for this generic require additional arguments. None are used in this method.

**Value**

a vector with the estimated coefficients for the nonlinear model represented by `object`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[gnls](#)

**Examples**

```
fm1 <- gnls(weight ~ SSlogis(Time, Asym, xmid, scal), Soybean,
            weights = varPower())
coef(fm1)
```

---

coef.lme

*Extract lme Coefficients*

---

**Description**

The estimated coefficients at level  $i$  are obtained by adding together the fixed effects estimates and the corresponding random effects estimates at grouping levels less or equal to  $i$ . The resulting estimates are returned as a data frame, with rows corresponding to groups and columns to coefficients. Optionally, the returned data frame may be augmented with covariates summarized over groups.

**Usage**

```
## S3 method for class 'lme':
coef(object, augFrame, level, data, which, FUN,
      omitGroupingFactor, subset, ...)
```

**Arguments**

- `object` an object inheriting from class `lme`, representing a fitted linear mixed-effects model.
- `augFrame` an optional logical value. If `TRUE`, the returned data frame is augmented with variables defined in `data`; else, if `FALSE`, only the coefficients are returned. Defaults to `FALSE`.
- `level` an optional positive integer giving the level of grouping to be used in extracting the coefficients from an object with multiple nested grouping levels. Defaults to the highest or innermost level of grouping.

data	an optional data frame with the variables to be used for augmenting the returned data frame when <code>augFrame = TRUE</code> . Defaults to the data frame used to fit object.
which	an optional positive integer or character vector specifying which columns of data should be used in the augmentation of the returned data frame. Defaults to all columns in data.
FUN	an optional summary function or a list of summary functions to be applied to group-varying variables, when collapsing data by groups. Group-invariant variables are always summarized by the unique value that they assume within that group. If FUN is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If FUN is a list of functions, the names in the list should designate classes of variables in the frame such as <code>ordered</code> , <code>factor</code> , or <code>numeric</code> . The indicated function will be applied to any group-varying variables of that class. The default functions to be used are <code>mean</code> for numeric factors, and <code>Mode</code> for both <code>factor</code> and <code>ordered</code> . The <code>Mode</code> function, defined internally in <code>gsummary</code> , returns the modal or most popular value of the variable. It is different from the <code>mode</code> function that returns the S-language mode of the variable.
omitGroupingFactor	an optional logical value. When <code>TRUE</code> the grouping factor itself will be omitted from the group-wise summary of data but the levels of the grouping factor will continue to be used as the row names for the returned data frame. Defaults to <code>FALSE</code> .
subset	an optional expression specifying a subset
...	some methods for this generic require additional arguments. None are used in this method.

### Value

a data frame inheriting from class `coef.lme` with the estimated coefficients at level `level` and, optionally, other covariates summarized over groups. The returned object also inherits from classes `ranef.lme` and `data.frame`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York, esp. pp. 455-457.

### See Also

[lme](#), [ranef.lme](#), [plot.ranef.lme](#), [gsummary](#)

### Examples

```
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
coef(fm1)
coef(fm1, augFrame = TRUE)
```

---

 coef.lmList                      *Extract lmList Coefficients*


---

### Description

The coefficients of each `lm` object in the `object` list are extracted and organized into a data frame, with rows corresponding to the `lm` components and columns corresponding to the coefficients. Optionally, the returned data frame may be augmented with covariates summarized over the groups associated with the `lm` components.

### Usage

```
## S3 method for class 'lmList':
coef(object, augFrame, data, which, FUN,
      omitGroupingFactor, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>lmList</code> , representing a list of <code>lm</code> objects with a common model.
<code>augFrame</code>	an optional logical value. If <code>TRUE</code> , the returned data frame is augmented with variables defined in the data frame used to produce <code>object</code> ; else, if <code>FALSE</code> , only the coefficients are returned. Defaults to <code>FALSE</code> .
<code>data</code>	an optional data frame with the variables to be used for augmenting the returned data frame when <code>augFrame = TRUE</code> . Defaults to the data frame used to fit <code>object</code> .
<code>which</code>	an optional positive integer or character vector specifying which columns of the data frame used to produce <code>object</code> should be used in the augmentation of the returned data frame. Defaults to all variables in the data.
<code>FUN</code>	an optional summary function or a list of summary functions to be applied to group-varying variables, when collapsing the data by groups. Group-invariant variables are always summarized by the unique value that they assume within that group. If <code>FUN</code> is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If <code>FUN</code> is a list of functions, the names in the list should designate classes of variables in the frame such as <code>ordered</code> , <code>factor</code> , or <code>numeric</code> . The indicated function will be applied to any group-varying variables of that class. The default functions to be used are <code>mean</code> for numeric factors, and <code>Mode</code> for both <code>factor</code> and <code>ordered</code> . The <code>Mode</code> function, defined internally in <code>gsummary</code> , returns the modal or most popular value of the variable. It is different from the <code>mode</code> function that returns the S-language mode of the variable.
<code>omitGroupingFactor</code>	an optional logical value. When <code>TRUE</code> the grouping factor itself will be omitted from the group-wise summary of <code>data</code> but the levels of the grouping factor will continue to be used as the row names for the returned data frame. Defaults to <code>FALSE</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a data frame inheriting from class `coef.lmList` with the estimated coefficients for each `lm` component of `object` and, optionally, other covariates summarized over the groups corresponding to the `lm` components. The returned object also inherits from classes `ranef.lmList` and `data.frame`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York, esp. pp. 457-458.

**See Also**

[lmList](#), [fixed.effects.lmList](#), [ranef.lmList](#), [plot.ranef.lmList](#), [gsummary](#)

**Examples**

```
fml <- lmList(distance ~ age|Subject, data = Orthodont)
coef(fml)
coef(fml, augFrame = TRUE)
```

---

`coef.modelStruct`     *Extract modelStruct Object Coefficients*

---

**Description**

This method function extracts the coefficients associated with each component of the `modelStruct` list.

**Usage**

```
## S3 method for class 'modelStruct':
coef(object, unconstrained, ...)
## S3 method for class 'modelStruct':
coef(object, ...) <- value
```

**Arguments**

`object`            an object inheriting from class `modelStruct`, representing a list of model components, such as `corStruct` and `varFunc` objects.

`unconstrained`    a logical value. If `TRUE` the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If `FALSE` the coefficients are returned in "natural", possibly constrained, form. Defaults to `TRUE`.

value a vector with the replacement values for the coefficients associated with object. It must be a vector with the same length of `coef{object}` and must be given in unconstrained form.

... some methods for this generic require additional arguments. None are used in this method.

### Value

a vector with all coefficients corresponding to the components of object.

### SIDE EFFECTS

On the left side of an assignment, sets the values of the coefficients of object to value. Object must be initialized (using `Initialize`) before new values can be assigned to its coefficients.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[Initialize](#)

### Examples

```
lms1 <- lmeStruct(reStruct = reStruct(pdDiag(diag(2), ~age)),
  corStruct = corAR1(0.3))
coef(lms1)
```

---

coef.pdMat

*pdMat Object Coefficients*

---

### Description

This method function extracts the coefficients associated with the positive-definite matrix represented by object.

### Usage

```
## S3 method for class 'pdMat':
coef(object, unconstrained, ...)
## S3 method for class 'pdMat':
coef(object, ...) <- value
```



**Arguments**

`object` an object inheriting from class `pdMat`, representing a positive-definite matrix.

`unconstrained` a logical value. If `TRUE` the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If `FALSE` the upper triangular elements of the positive-definite matrix represented by `object` are returned. Defaults to `TRUE`.

`value` a vector with the replacement values for the coefficients associated with `object`. It must be a vector with the same length of `coef{object}` and must be given in unconstrained form.

`...` some methods for this generic require additional arguments. None are used in this method.

**Value**

a vector with the coefficients corresponding to `object`.

**SIDE EFFECTS**

On the left side of an assignment, sets the values of the coefficients of `object` to `value`.

**Author(s)**

Jose Pinheiro and Douglas Bates

**References**

Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", *Statistics and Computing*, 6, 289-296.

**See Also**

[pdMat](#)

**Examples**

```
coef(pdSymm(diag(3)))
```

---

`coef.reStruct`      *reStruct Object Coefficients*

---

**Description**

This method function extracts the coefficients associated with the positive-definite matrix represented by `object`.

**Usage**

```
## S3 method for class 'reStruct':
coef(object, unconstrained, ...)
## S3 method for class 'reStruct':
coef(object, ...) <- value
```

**Arguments**

<code>object</code>	an object inheriting from class <code>reStruct</code> , representing a random effects structure and consisting of a list of <code>pdMat</code> objects.
<code>unconstrained</code>	a logical value. If <code>TRUE</code> the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If <code>FALSE</code> the coefficients are returned in "natural", possibly constrained, form. Defaults to <code>TRUE</code> .
<code>value</code>	a vector with the replacement values for the coefficients associated with <code>object</code> . It must be a vector with the same length of <code>coef(object)</code> and must be given in unconstrained form.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a vector with the coefficients corresponding to `object`.

**SIDE EFFECTS**

On the left side of an assignment, sets the values of the coefficients of `object` to `value`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[coef.pdMat](#), [reStruct](#), [pdMat](#)

**Examples**

```
rs1 <- reStruct(list(A = pdSymm(diag(1:3), form = ~Score),
  B = pdDiag(2 * diag(4), form = ~Educ)))
coef(rs1)
```

---

coef.varFunc

*varFunc Object Coefficients*

---

**Description**

This method function extracts the coefficients associated with the variance function structure represented by `object`.

**Usage**

```
## S3 method for class 'varFunc':
coef(object, unconstrained, allCoef, ...)
## S3 method for class 'varIdent':
coef(object, ...) <- value
```

**Arguments**

<code>object</code>	an object inheriting from class <code>varFunc</code> representing a variance function structure.
<code>unconstrained</code>	a logical value. If <code>TRUE</code> the coefficients are returned in unconstrained form (the same used in the optimization algorithm). If <code>FALSE</code> the coefficients are returned in "natural", generally constrained form. Defaults to <code>TRUE</code> .
<code>allCoef</code>	a logical value. If <code>FALSE</code> only the coefficients which may vary during the optimization are returned. If <code>TRUE</code> all coefficients are returned. Defaults to <code>FALSE</code> .
<code>value</code>	a vector with the replacement values for the coefficients associated with <code>object</code> . It must have the same length of <code>coef{object}</code> and must be given in unconstrained form. <code>Object</code> must be initialized before new values can be assigned to its coefficients.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a vector with the coefficients corresponding to `object`.

**SIDE EFFECTS**

On the left side of an assignment, sets the values of the coefficients of `object` to `value`.

**Author(s)**

Jose Pinheiro and Douglas Bates

**See Also**

[varFunc](#)

**Examples**

```
vf1 <- varPower(1)
coef(vf1)

coef(vf1) <- 2
```

---

collapse

*Collapse According to Groups*

---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Currently, only a `groupedData` method is available.

**Usage**

```
collapse(object, ...)
```

**Arguments**

`object` an object to be collapsed, usually a data frame.  
`...` some methods for the generic may require additional arguments.

**Value**

will depend on the method function used; see the appropriate documentation.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
 <bates@stat.wisc.edu>

**See Also**

[collapse.groupedData](#)

**Examples**

```
## see the method function documentation
```

---

```
collapse.groupedData
```

*Collapse a groupedData Object*

---

**Description**

If `object` has a single grouping factor, it is returned unchanged. Else, it is summarized by the values of the `displayLevel` grouping factor (or the combination of its values and the values of the covariate indicated in `preserve`, if any is present). The collapsed data is used to produce a new `groupedData` object, with grouping factor given by the `displayLevel` factor.

**Usage**

```
## S3 method for class 'groupedData':
collapse(object, collapseLevel, displayLevel,
         outer, inner, preserve, FUN, subset, ...)
```

**Arguments**

`object` an object inheriting from class `groupedData`, generally with multiple grouping factors.

`collapseLevel` an optional positive integer or character string indicating the grouping level to use when collapsing the data. Level values increase from outermost to innermost grouping. Default is the highest or innermost level of grouping.

`displayLevel` an optional positive integer or character string indicating the grouping level to use as the grouping factor for the collapsed data. Default is `collapseLevel`.

outer	an optional logical value or one-sided formula, indicating covariates that are outer to the <code>displayLevel</code> grouping factor. If equal to <code>TRUE</code> , the <code>displayLevel</code> element <code>attr(object, "outer")</code> is used to indicate the outer covariates. An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. Defaults to <code>NULL</code> , meaning that no outer covariates are to be used.
inner	an optional logical value or one-sided formula, indicating a covariate that is inner to the <code>displayLevel</code> grouping factor. If equal to <code>TRUE</code> , <code>attr(object, "outer")</code> is used to indicate the inner covariate. An inner covariate can change within the sets of rows defined by the grouping factor. Defaults to <code>NULL</code> , meaning that no inner covariate is present.
preserve	an optional one-sided formula indicating a covariate whose levels should be preserved when collapsing the data according to the <code>collapseLevel</code> grouping factor. The collapsing factor is obtained by pasting together the levels of the <code>collapseLevel</code> grouping factor and the values of the covariate to be preserved. Default is <code>NULL</code> , meaning that no covariates need to be preserved.
FUN	an optional summary function or a list of summary functions to be used for collapsing the data. The function or functions are applied only to variables in <code>object</code> that vary within the groups defined by <code>collapseLevel</code> . Invariant variables are always summarized by group using the unique value that they assume within that group. If <code>FUN</code> is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If <code>FUN</code> is a list of functions, the names in the list should designate classes of variables in the data such as <code>ordered</code> , <code>factor</code> , or <code>numeric</code> . The indicated function will be applied to any non-invariant variables of that class. The default functions to be used are <code>mean</code> for numeric factors, and <code>Mode</code> for both <code>factor</code> and <code>ordered</code> . The <code>Mode</code> function, defined internally in <code>gsummary</code> , returns the modal or most popular value of the variable. It is different from the <code>mode</code> function that returns the S-language mode of the variable.
subset	an optional named list. Names can be either positive integers representing grouping levels, or names of grouping factors. Each element in the list is a vector indicating the levels of the corresponding grouping factor to be preserved in the collapsed data. Default is <code>NULL</code> , meaning that all levels are used.
...	some methods for this generic require additional arguments. None are used in this method.

**Value**

a `groupedData` object with a single grouping factor given by the `displayLevel` grouping factor, resulting from collapsing `object` over the levels of the `collapseLevel` grouping factor.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[groupedData](#), [plot.nmGroupedData](#)

## Examples

```
# collapsing by Dog
collapse(Pixel, collapse = 1) # same as collapse(Pixel, collapse = "Dog")
```

---

compareFits	<i>Compare Fitted Objects</i>
-------------	-------------------------------

---

## Description

The columns in `object1` and `object2` are put together in matrices which allow direct comparison of the individual elements for each object. Missing columns in either object are replaced by NAs.

## Usage

```
compareFits(object1, object2, which)
```

## Arguments

`object1, object2`  
data frames, or matrices, with the same row names, but possibly different column names. These will usually correspond to coefficients from fitted objects with a grouping structure (e.g. `lme` and `lmList` objects).

`which`  
an optional integer or character vector indicating which columns in `object1` and `object2` are to be used in the returned object. Defaults to all columns.

## Value

a three-dimensional array, with the third dimension given by the number of unique column names in either `object1` or `object2`. To each column name there corresponds a matrix with as many rows as the rows in `object1` and two columns, corresponding to `object1` and `object2`. The returned object inherits from class `compareFits`.

## Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

## See Also

[plot.compareFits](#), [pairs.compareFits](#), [comparePred](#), [coef](#), [random.effects](#)

## Examples

```
fm1 <- lmList(Orthodont)
fm2 <- lme(fm1)
compareFits(coef(fm1), coef(fm2))
```

---

comparePred	<i>Compare Predictions</i>
-------------	----------------------------

---

**Description**

Predicted values are obtained at the specified values of `primary` for each object. If either `object1` or `object2` have a grouping structure (i.e. `getGroups(object)` is not `NULL`), predicted values are obtained for each group. When both objects determine groups, the group levels must be the same. If other covariates besides `primary` are used in the prediction model, their group-wise averages (numeric covariates) or most frequent values (categorical covariates) are used to obtain the predicted values. The original observations are also included in the returned object.

**Usage**

```
comparePred(object1, object2, primary, minimum, maximum,
            length.out, level, ...)
```

**Arguments**

<code>object1, object2</code>	fitted model objects, from which predictions can be extracted using the <code>predict</code> method.
<code>primary</code>	an optional one-sided formula specifying the primary covariate to be used to generate the augmented predictions. By default, if a covariate can be extracted from the data used to generate the objects (using <code>getCovariate</code> ), it will be used as <code>primary</code> .
<code>minimum</code>	an optional lower limit for the primary covariate. Defaults to <code>min(primary)</code> , after <code>primary</code> is evaluated in the data used in fitting <code>object1</code> .
<code>maximum</code>	an optional upper limit for the primary covariate. Defaults to <code>max(primary)</code> , after <code>primary</code> is evaluated in the data used in fitting <code>object1</code> .
<code>length.out</code>	an optional integer with the number of primary covariate values at which to evaluate the predictions. Defaults to 51.
<code>level</code>	an optional integer specifying the desired prediction level. Levels increase from outermost to innermost grouping, with level 0 representing the population (fixed effects) predictions. Only one level can be specified. Defaults to the innermost level.
<code>...</code>	some methods for the generic may require additional arguments.

**Value**

a data frame with four columns representing, respectively, the values of the primary covariate, the groups (if `object` does not have a grouping structure, all elements will be 1), the predicted or observed values, and the type of value in the third column: the objects' names are used to classify the predicted values and `original` is used for the observed values. The returned object inherits from classes `comparePred` and `augPred`.

**Note**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `gls`, `lme`, and `lmList`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[augPred](#), [getGroups](#)

**Examples**

```
fm1 <- lme(distance ~ age * Sex, data = Orthodont, random = ~ age)
fm2 <- update(fm1, distance ~ age)
comparePred(fm1, fm2, length.out = 2)
```

---

corAR1

*AR(1) Correlation Structure*

---

**Description**

This function is a constructor for the `corAR1` class, representing an autocorrelation structure of order 1. Objects created using this constructor must later be initialized using the appropriate `Initialize` method.

**Usage**

```
corAR1(value, form, fixed)
```

**Arguments**

<code>value</code>	the value of the lag 1 autocorrelation, which must be between -1 and 1. Defaults to 0 (no autocorrelation).
<code>form</code>	a one sided formula of the form $\sim t$ , or $\sim t \mid g$ , specifying a time covariate $t$ and, optionally, a grouping factor $g$ . A covariate for this correlation structure must be integer valued. When a grouping factor is present in <code>form</code> , the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to $\sim 1$ , which corresponds to using the order of the observations in the data as a covariate, and no groups.
<code>fixed</code>	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to <code>FALSE</code> , in which case the coefficients are allowed to vary.

**Value**

an object of class `corAR1`, representing an autocorrelation structure of order 1.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>



## References

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 235, 397.

## See Also

[ACF.lme](#), [corARMA](#), [corClasses](#), [Dim.corSpatial](#), [Initialize.corStruct](#), [summary.corStruct](#)

## Examples

```
## covariate is observation order and grouping factor is Mare
csl1 <- corAR1(0.2, form = ~ 1 | Mare)

# Pinheiro and Bates, p. 236
cslAR1 <- corAR1(0.8, form = ~ 1 | Subject)
cslAR1. <- Initialize(cslAR1, data = Orthodont)
corMatrix(cslAR1.)

# Pinheiro and Bates, p. 240
fm1Ovar.lme <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time),
                  data = Ovary, random = pdDiag(~sin(2*pi*Time)))
fm2Ovar.lme <- update(fm1Ovar.lme, correlation = corAR1())

# Pinheiro and Bates, pp. 255-258: use in gls
fm1Dial.gls <-
  gls(rate ~ (pressure + I(pressure^2) + I(pressure^3) + I(pressure^4))*QB,
       Dialyzer)
fm2Dial.gls <- update(fm1Dial.gls,
                     weights = varPower(form = ~ pressure))
fm3Dial.gls <- update(fm2Dial.gls,
                     corr = corAR1(0.771, form = ~ 1 | Subject))

# Pinheiro and Bates use in nlme:
# from p. 240 needed on p. 396
fm1Ovar.lme <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time),
                  data = Ovary, random = pdDiag(~sin(2*pi*Time)))
fm5Ovar.lme <- update(fm1Ovar.lme,
                     corr = corARMA(p = 1, q = 1))

# p. 396
fm1Ovar.nlme <- nlme(follicles~
                    A+B*sin(2*pi*w*Time)+C*cos(2*pi*w*Time),
                    data=Ovary, fixed=A+B+C+w~1,
                    random=pdDiag(A+B+w~1),
                    start=c(fixef(fm5Ovar.lme), 1) )

# p. 397
fm2Ovar.nlme <- update(fm1Ovar.nlme,
                     corr=corAR1(0.311) )
```

corARMA

*ARMA(p,q) Correlation Structure***Description**

This function is a constructor for the `corARMA` class, representing an autocorrelation-moving average correlation structure of order  $(p, q)$ . Objects created using this constructor must later be initialized using the appropriate `Initialize` method.

**Usage**

```
corARMA(value, form, p, q, fixed)
```

**Arguments**

<code>value</code>	a vector with the values of the autoregressive and moving average parameters, which must have length $p + q$ and all elements between -1 and 1. Defaults to a vector of zeros, corresponding to uncorrelated observations.
<code>form</code>	a one sided formula of the form $\sim t$ , or $\sim t   g$ , specifying a time covariate $t$ and, optionally, a grouping factor $g$ . A covariate for this correlation structure must be integer valued. When a grouping factor is present in <code>form</code> , the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to $\sim 1$ , which corresponds to using the order of the observations in the data as a covariate, and no groups.
<code>p, q</code>	non-negative integers specifying respectively the autoregressive order and the moving average order of the ARMA structure. Both default to 0.
<code>fixed</code>	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to <code>FALSE</code> , in which case the coefficients are allowed to vary.

**Value**

an object of class `corARMA`, representing an autocorrelation-moving average correlation structure.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 236, 397.

**See Also**

[corAR1](#), [corClasses Initialize.corStruct](#), [summary.corStruct](#)

**Examples**

```
## ARMA(1,2) structure, with observation order as a covariate and
## Mare as grouping factor
cs1 <- corARMA(c(0.2, 0.3, -0.1), form = ~ 1 | Mare, p = 1, q = 2)

# Pinheiro and Bates, p. 237
cs1ARMA <- corARMA(0.4, form = ~ 1 | Subject, q = 1)
cs1ARMA <- Initialize(cs1ARMA, data = Orthodont)
corMatrix(cs1ARMA)

cs2ARMA <- corARMA(c(0.8, 0.4), form = ~ 1 | Subject, p=1, q=1)
cs2ARMA <- Initialize(cs2ARMA, data = Orthodont)
corMatrix(cs2ARMA)

# Pinheiro and Bates use in nlme:
# from p. 240 needed on p. 396
fm1Ovar.lme <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time),
                  data = Ovary, random = pdDiag(~sin(2*pi*Time)))
fm5Ovar.lme <- update(fm1Ovar.lme,
                     corr = corARMA(p = 1, q = 1))

# p. 396
fm1Ovar.nlme <- nlme(follicles~
                    A+B*sin(2*pi*w*Time)+C*cos(2*pi*w*Time),
                    data=Ovary, fixed=A+B+C+w~1,
                    random=pdDiag(A+B+w~1),
                    start=c(fixef(fm5Ovar.lme), 1) )
# p. 397
fm3Ovar.nlme <- update(fm1Ovar.nlme,
                      corr=corARMA(p=0, q=2) )
```

corCAR1

*Continuous AR(1) Correlation Structure***Description**

This function is a constructor for the `corCAR1` class, representing an autocorrelation structure of order 1, with a continuous time covariate. Objects created using this constructor must be later initialized using the appropriate `Initialize` method.

**Usage**

```
corCAR1(value, form, fixed)
```

**Arguments**

value	the correlation between two observations one unit of time apart. Must be between 0 and 1. Defaults to 0.2.
form	a one sided formula of the form $\sim t$ , or $\sim t   g$ , specifying a time covariate $t$ and, optionally, a grouping factor $g$ . Covariates for this correlation structure need not be integer valued. When a grouping factor is present in <code>form</code> , the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to $\sim 1$ , which corresponds to using the order of the observations in the data as a covariate, and no groups.

`fixed` an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to `FALSE`, in which case the coefficients are allowed to vary.

### Value

an object of class `corCAR1`, representing an autocorrelation structure of order 1, with a continuous time covariate.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Jones, R.H. (1993) "Longitudinal Data with Serial Correlation: A State-space Approach", Chapman and Hall.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 236, 243.

### See Also

[corClasses](#), [Initialize.corStruct](#), [summary.corStruct](#)

### Examples

```
## covariate is Time and grouping factor is Mare
cs1 <- corCAR1(0.2, form = ~ Time | Mare)

# Pinheiro and Bates, pp. 240, 243
fm1Ovar.lme <- lme(follicles ~
  sin(2*pi*Time) + cos(2*pi*Time),
  data = Ovary, random = pdDiag(~sin(2*pi*Time)))
fm4Ovar.lme <- update(fm1Ovar.lme,
  correlation = corCAR1(form = ~Time))
```

---

corClasses

*Correlation Structure Classes*

---

### Description

Standard classes of correlation structures (`corStruct`) available in the `nlme` library.

**Value**

Available standard classes:

<code>corAR1</code>	autoregressive process of order 1.
<code>corARMA</code>	autoregressive moving average process, with arbitrary orders for the autoregressive and moving average components.
<code>corCAR1</code>	continuous autoregressive process (AR(1) process for a continuous time covariate).
<code>corCompSymm</code>	compound symmetry structure corresponding to a constant correlation.
<code>corExp</code>	exponential spatial correlation.
<code>corGaus</code>	Gaussian spatial correlation.
<code>corLin</code>	linear spatial correlation.
<code>corRatio</code>	Rational quadratics spatial correlation.
<code>corSpher</code>	spherical spatial correlation.
<code>corSymm</code>	general correlation matrix, with no additional structure.

**Note**

Users may define their own `corStruct` classes by specifying a constructor function and, at a minimum, methods for the functions `corMatrix` and `coef`. For examples of these functions, see the methods for classes `corSymm` and `corAR1`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[corAR1](#), [corARMA](#), [corCAR1](#), [corCompSymm](#), [corExp](#), [corGaus](#), [corLin](#), [corRatio](#), [corSpher](#), [corSymm](#), [summary.corStruct](#)

---

`corCompSymm`

*Compound Symmetry Correlation Structure*

---

**Description**

This function is a constructor for the `corCompSymm` class, representing a compound symmetry structure corresponding to uniform correlation. Objects created using this constructor must later be initialized using the appropriate `Initialize` method.

**Usage**

```
corCompSymm(value, form, fixed)
```

**Arguments**

value	the correlation between any two correlated observations. Defaults to 0.
form	a one sided formula of the form $\sim t$ , or $\sim t \mid g$ , specifying a time covariate $t$ and, optionally, a grouping factor $g$ . When a grouping factor is present in <code>form</code> , the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to $\sim 1$ , which corresponds to using the order of the observations in the data as a covariate, and no groups.
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to <code>FALSE</code> , in which case the coefficients are allowed to vary.

**Value**

an object of class `corCompSymm`, representing a compound symmetry correlation structure.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

- Milliken, G. A. and Johnson, D. E. (1992) "Analysis of Messy Data, Volume I: Designed Experiments", Van Nostrand Reinhold.
- Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 233-234.

**See Also**

[corClasses](#), [Initialize.corStruct](#), [summary.corStruct](#)

**Examples**

```
## covariate is observation order and grouping factor is Subject
cs1 <- corCompSymm(0.5, form = ~ 1 | Subject)

# Pinheiro and Bates, pp. 222-225
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
               random = ~ Time)

# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())

# p. 225
cs1CompSymm <- corCompSymm(value = 0.3, form = ~ 1 | Subject)
cs2CompSymm <- corCompSymm(value = 0.3, form = ~ age | Subject)
cs1CompSymm <- Initialize(cs1CompSymm, data = Orthodont)
corMatrix(cs1CompSymm)
```

corExp

*Exponential Correlation Structure***Description**

This function is a constructor for the `corExp` class, representing an exponential spatial correlation structure. Letting  $d$  denote the range and  $n$  denote the nugget effect, the correlation between two observations a distance  $r$  apart is  $\exp(-r/d)$  when no nugget effect is present and  $(1 - n) \exp(-r/d)$  when a nugget effect is assumed. Objects created using this constructor must later be initialized using the appropriate `Initialize` method.

**Usage**

```
corExp(value, form, nugget, metric, fixed)
```

**Arguments**

value	an optional vector with the parameter values in constrained form. If <code>nugget</code> is <code>FALSE</code> , <code>value</code> can have only one element, corresponding to the "range" of the exponential correlation structure, which must be greater than zero. If <code>nugget</code> is <code>TRUE</code> , meaning that a nugget effect is present, <code>value</code> can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to <code>numeric(0)</code> , which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when <code>object</code> is initialized.
form	a one sided formula of the form $\sim S_1 + \dots + S_p$ , or $\sim S_1 + \dots + S_p \mid g$ , specifying spatial covariates $S_1$ through $S_p$ and, optionally, a grouping factor $g$ . When a grouping factor is present in <code>form</code> , the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to $\sim 1$ , which corresponds to using the order of the observations in the data as a covariate, and no groups.
nugget	an optional logical value indicating whether a nugget effect is present. Defaults to <code>FALSE</code> .
metric	an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to <code>FALSE</code> , in which case the coefficients are allowed to vary.

**Value**

an object of class `corExp`, also inheriting from class `corSpatial`, representing an exponential spatial correlation structure.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**References**

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons. Venables, W.N. and Ripley, B.D. (1997) "Modern Applied Statistics with S-plus", 2nd Edition, Springer-Verlag.

Littel, Milliken, Stroup, and Wolfinger (1996) "SAS Systems for Mixed Models", SAS Institute.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. p. 238.

**See Also**

[corClasses](#), [Initialize.corStruct](#), [summary.corStruct](#), [dist](#)

**Examples**

```

spl <- corExp(form = ~ x + y + z)

# Pinheiro and Bates, p. 238
spatDat <- data.frame(x = (0:4)/4, y = (0:4)/4)

cs1Exp <- corExp(1, form = ~ x + y)
cs1Exp <- Initialize(cs1Exp, spatDat)
corMatrix(cs1Exp)

cs2Exp <- corExp(1, form = ~ x + y, metric = "man")
cs2Exp <- Initialize(cs2Exp, spatDat)
corMatrix(cs2Exp)

cs3Exp <- corExp(c(1, 0.2), form = ~ x + y,
                 nugget = TRUE)
cs3Exp <- Initialize(cs3Exp, spatDat)
corMatrix(cs3Exp)

# example lme(..., corExp ...)
# Pinheiro and Bates, pp. 222-247
# p. 222
options(contrasts = c("contr.treatment", "contr.poly"))
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
                random = ~ Time)

# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# p. 246
fm3BW.lme <- update(fm2BW.lme,
                   correlation = corExp(form = ~ Time))

# p. 247
fm4BW.lme <-
  update(fm3BW.lme, correlation = corExp(form = ~ Time,
                                         nugget = TRUE))
anova(fm3BW.lme, fm4BW.lme)

```



---

 corFactor

*Factor of a Correlation Matrix*


---

### Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include all `corStruct` classes.

### Usage

```
corFactor(object, ...)
```

### Arguments

`object` an object from which a correlation matrix can be extracted.  
`...` some methods for this generic function require additional arguments.

### Value

will depend on the method function used; see the appropriate documentation.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
 <bates@stat.wisc.edu>

### See Also

[corFactor.corStruct](#), [recalc.corStruct](#)

### Examples

```
## see the method function documentation
```

---

 corFactor.corStruct

*Factor of a corStruct Object Matrix*


---

### Description

This method function extracts a transpose inverse square-root factor, or a series of transpose inverse square-root factors, of the correlation matrix, or list of correlation matrices, represented by `object`. Letting  $\Sigma$  denote a correlation matrix, a square-root factor of  $\Sigma$  is any square matrix  $L$  such that  $\Sigma = L'L$ . This method extracts  $L^{-t}$ .

### Usage

```
## S3 method for class 'corStruct':
corFactor(object, ...)
```

**Arguments**

`object` an object inheriting from class `corStruct` representing a correlation structure, which must have been initialized (using `Initialize`).

`...` some methods for this generic require additional arguments. None are used in this method.

**Value**

If the correlation structure does not include a grouping factor, the returned value will be a vector with a transpose inverse square-root factor of the correlation matrix associated with `object` stacked column-wise. If the correlation structure includes a grouping factor, the returned value will be a vector with transpose inverse square-root factors of the correlation matrices for each group, stacked by group and stacked column-wise within each group.

**Note**

This method function is used intensively in optimization algorithms and its value is returned as a vector for efficiency reasons. The `corMatrix` method function can be used to obtain transpose inverse square-root factors in matrix form.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[corFactor](#), [corMatrix.corStruct](#), [recalc.corStruct](#), [Initialize.corStruct](#)

**Examples**

```
cs1 <- corAR1(form = ~1 | Subject)
cs1 <- Initialize(cs1, data = Orthodont)
corFactor(cs1)
```

---

corGaus

*Gaussian Correlation Structure*

---

**Description**

This function is a constructor for the `corGaus` class, representing a Gaussian spatial correlation structure. Letting  $d$  denote the range and  $n$  denote the nugget effect, the correlation between two observations a distance  $r$  apart is  $\exp(-(r/d)^2)$  when no nugget effect is present and  $(1-n)\exp(-(r/d)^2)$  when a nugget effect is assumed. Objects created using this constructor must later be initialized using the appropriate `Initialize` method.

**Usage**

```
corGaus(value, form, nugget, metric, fixed)
```

**Arguments**

value	an optional vector with the parameter values in constrained form. If <code>nugget</code> is <code>FALSE</code> , <code>value</code> can have only one element, corresponding to the "range" of the Gaussian correlation structure, which must be greater than zero. If <code>nugget</code> is <code>TRUE</code> , meaning that a nugget effect is present, <code>value</code> can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to <code>numeric(0)</code> , which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when <code>object</code> is initialized.
form	a one sided formula of the form <code>~ S1+...+Sp</code> , or <code>~ S1+...+Sp   g</code> , specifying spatial covariates <code>S1</code> through <code>Sp</code> and, optionally, a grouping factor <code>g</code> . When a grouping factor is present in <code>form</code> , the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to <code>~ 1</code> , which corresponds to using the order of the observations in the data as a covariate, and no groups.
nugget	an optional logical value indicating whether a nugget effect is present. Defaults to <code>FALSE</code> .
metric	an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to <code>FALSE</code> , in which case the coefficients are allowed to vary.

**Value**

an object of class `corGaus`, also inheriting from class `corSpatial`, representing a Gaussian spatial correlation structure.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

- Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.
- Venables, W.N. and Ripley, B.D. (1997) "Modern Applied Statistics with S-plus", 2nd Edition, Springer-Verlag.
- Littel, Milliken, Stroup, and Wolfinger (1996) "SAS Systems for Mixed Models", SAS Institute.
- Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[Initialize.corStruct](#), [summary.corStruct](#), [dist](#)

**Examples**

```

spl <- corGaus(form = ~ x + y + z)

# example lme(..., corGaus ...)
# Pinheiro and Bates, pp. 222-249
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
  random = ~ Time)

# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# p 246
fm3BW.lme <- update(fm2BW.lme,
  correlation = corExp(form = ~ Time))

# p. 249
fm8BW.lme <- update(fm3BW.lme, correlation = corGaus(form = ~ Time))

```

corLin

*Linear Correlation Structure***Description**

This function is a constructor for the `corLin` class, representing a linear spatial correlation structure. Letting  $d$  denote the range and  $n$  denote the nugget effect, the correlation between two observations a distance  $r < d$  apart is  $1 - (r/d)$  when no nugget effect is present and  $(1 - n)(1 - (r/d))$  when a nugget effect is assumed. If  $r \geq d$  the correlation is zero. Objects created using this constructor must later be initialized using the appropriate `Initialize` method.

**Usage**

```
corLin(value, form, nugget, metric, fixed)
```

**Arguments**

value	an optional vector with the parameter values in constrained form. If <code>nugget</code> is <code>FALSE</code> , <code>value</code> can have only one element, corresponding to the "range" of the linear correlation structure, which must be greater than zero. If <code>nugget</code> is <code>TRUE</code> , meaning that a nugget effect is present, <code>value</code> can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to <code>numeric(0)</code> , which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when <code>object</code> is initialized.
form	a one sided formula of the form $\sim S_1 + \dots + S_p$ , or $\sim S_1 + \dots + S_p \mid g$ , specifying spatial covariates $S_1$ through $S_p$ and, optionally, a grouping factor $g$ . When a grouping factor is present in <code>form</code> , the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to $\sim 1$ , which corresponds to using the order of the observations in the data as a covariate, and no groups.
nugget	an optional logical value indicating whether a nugget effect is present. Defaults to <code>FALSE</code> .

<code>metric</code>	an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".
<code>fixed</code>	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to FALSE, in which case the coefficients are allowed to vary.

### Value

an object of class `corLin`, also inheriting from class `corSpatial`, representing a linear spatial correlation structure.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

- Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.
- Venables, W.N. and Ripley, B.D. (1997) "Modern Applied Statistics with S-plus", 2nd Edition, Springer-Verlag.
- Littel, Milliken, Stroup, and Wolfinger (1996) "SAS Systems for Mixed Models", SAS Institute.
- Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

### See Also

[Initialize.corStruct](#), [summary.corStruct](#), [dist](#)

### Examples

```
spl <- corLin(form = ~ x + y)

# example lme(..., corLin ...)
# Pinheiro and Bates, pp. 222-249
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
               random = ~ Time)
# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# p 246
fm3BW.lme <- update(fm2BW.lme,
                  correlation = corExp(form = ~ Time))
# p. 249
fm7BW.lme <- update(fm3BW.lme, correlation = corLin(form = ~ Time))
```

---

corMatrix                      *Extract Correlation Matrix*

---

### Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include all `corStruct` classes.

### Usage

```
corMatrix(object, ...)
```

### Arguments

`object`                      an object for which a correlation matrix can be extracted.  
`...`                              some methods for this generic function require additional arguments.

### Value

will depend on the method function used; see the appropriate documentation.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
 <bates@stat.wisc.edu>

### See Also

[corMatrix.corStruct](#), [corMatrix.pdMat](#)

### Examples

```
## see the method function documentation
```

---

`corMatrix.corStruct`  
*Matrix of a corStruct Object*

---

### Description

This method function extracts the correlation matrix (or its transpose inverse square-root factor), or list of correlation matrices (or their transpose inverse square-root factors) corresponding to `covariate` and `object`. Letting  $\Sigma$  denote a correlation matrix, a square-root factor of  $\Sigma$  is any square matrix  $L$  such that  $\Sigma = L'L$ . When `corr = FALSE`, this method extracts  $L^{-t}$ .

### Usage

```
## S3 method for class 'corStruct':  
corMatrix(object, covariate, corr, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>corStruct</code> representing a correlation structure.
<code>covariate</code>	an optional covariate vector (matrix), or list of covariate vectors (matrices), at which values the correlation matrix, or list of correlation matrices, are to be evaluated. Defaults to <code>getCovariate(object)</code> .
<code>corr</code>	a logical value. If <code>TRUE</code> the function returns the correlation matrix, or list of correlation matrices, represented by <code>object</code> . If <code>FALSE</code> the function returns a transpose inverse square-root of the correlation matrix, or a list of transpose inverse square-root factors of the correlation matrices.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

If `covariate` is a vector (matrix), the returned value will be an array with the corresponding correlation matrix (or its transpose inverse square-root factor). If the `covariate` is a list of vectors (matrices), the returned value will be a list with the correlation matrices (or their transpose inverse square-root factors) corresponding to each component of `covariate`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[corFactor.corStruct](#), [Initialize.corStruct](#)

**Examples**

```

csl <- corAR1(0.3)
corMatrix(csl, covariate = 1:4)
corMatrix(csl, covariate = 1:4, corr = FALSE)

# Pinheiro and Bates, p. 225
cslCompSymm <- corCompSymm(value = 0.3, form = ~ 1 | Subject)
cslCompSymm <- Initialize(cslCompSymm, data = Orthodont)
corMatrix(cslCompSymm)

# Pinheiro and Bates, p. 226
cslSymm <- corSymm(value = c(0.2, 0.1, -0.1, 0, 0.2, 0),
                  form = ~ 1 | Subject)
cslSymm <- Initialize(cslSymm, data = Orthodont)
corMatrix(cslSymm)

# Pinheiro and Bates, p. 236
cslAR1 <- corAR1(0.8, form = ~ 1 | Subject)
cslAR1 <- Initialize(cslAR1, data = Orthodont)
corMatrix(cslAR1)

```

```
# Pinheiro and Bates, p. 237
cslARMA <- corARMA(0.4, form = ~ 1 | Subject, q = 1)
cslARMA <- Initialize(cslARMA, data = Orthodont)
corMatrix(cslARMA)

# Pinheiro and Bates, p. 238
spatDat <- data.frame(x = (0:4)/4, y = (0:4)/4)
cslExp <- corExp(1, form = ~ x + y)
cslExp <- Initialize(cslExp, spatDat)
corMatrix(cslExp)
```

---

corMatrix.pdMat      *Extract Correlation Matrix from a pdMat Object*

---

### Description

The correlation matrix corresponding to the positive-definite matrix represented by `object` is obtained.

### Usage

```
## S3 method for class 'pdMat':
corMatrix(object, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>pdMat</code> , representing a positive definite matrix.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

the correlation matrix corresponding to the positive-definite matrix represented by `object`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[as.matrix.pdMat](#), [pdMatrix](#)

### Examples

```
pd1 <- pdSymm(diag(1:4))
corMatrix(pd1)
```



---

`corMatrix.reStruct` *Extract Correlation Matrix from Components of an reStruct Object*

---

### Description

This method function extracts the correlation matrices corresponding to the `pdMat` elements of `object`.

### Usage

```
## S3 method for class 'reStruct':
corMatrix(object, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>reStruct</code> , representing a random effects structure and consisting of a list of <code>pdMat</code> objects.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

a list with components given by the correlation matrices corresponding to the elements of `object`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[as.matrix.reStruct](#), [corMatrix](#), [reStruct](#), [pdMat](#)

### Examples

```
rs1 <- reStruct(pdSymm(diag(3), ~age+Sex, data = Orthodont))
corMatrix(rs1)
```

---

`corNatural`

*General correlation in natural parameterization*

---

### Description

This function is a constructor for the `corNatural` class, representing a general correlation structure in the “natural” parameterization, which is described under [pdNatural](#). Objects created using this constructor must later be initialized using the appropriate `Initialize` method.

### Usage

```
corNatural(value, form, fixed)
```

**Arguments**

value	an optional vector with the parameter values. Default is <code>numeric(0)</code> , which results in a vector of zeros of appropriate dimension being assigned to the parameters when <code>object</code> is initialized (corresponding to an identity correlation structure).
form	a one sided formula of the form <code>~ t</code> , or <code>~ t   g</code> , specifying a time covariate <code>t</code> and, optionally, a grouping factor <code>g</code> . A covariate for this correlation structure must be integer valued. When a grouping factor is present in <code>form</code> , the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to <code>~ 1</code> , which corresponds to using the order of the observations in the data as a covariate, and no groups.
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to <code>FALSE</code> , in which case the coefficients are allowed to vary.

**Value**

an object of class `corNatural` representing a general correlation structure.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[Initialize.corNatural](#), [pdNatural](#), [summary.corNatural](#)

**Examples**

```
## covariate is observation order and grouping factor is Subject
csl <- corNatural(form = ~ 1 | Subject)
```

---

corRatio

*Rational Quadratic Correlation Structure*

---

**Description**

This function is a constructor for the `corRatio` class, representing a rational quadratic spatial correlation structure. Letting  $d$  denote the range and  $n$  denote the nugget effect, the correlation between two observations a distance  $r$  apart is  $1/(1 + (r/d)^2)$  when no nugget effect is present and  $(1 - n)/(1 + (r/d)^2)$  when a nugget effect is assumed. Objects created using this constructor need to be later initialized using the appropriate `Initialize` method.

**Usage**

```
corRatio(value, form, nugget, metric, fixed)
```

**Arguments**

value	an optional vector with the parameter values in constrained form. If <code>nugget</code> is <code>FALSE</code> , <code>value</code> can have only one element, corresponding to the "range" of the rational quadratic correlation structure, which must be greater than zero. If <code>nugget</code> is <code>TRUE</code> , meaning that a nugget effect is present, <code>value</code> can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to <code>numeric(0)</code> , which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when <code>object</code> is initialized.
form	a one sided formula of the form <code>~ S1+...+Sp</code> , or <code>~ S1+...+Sp   g</code> , specifying spatial covariates <code>S1</code> through <code>Sp</code> and, optionally, a grouping factor <code>g</code> . When a grouping factor is present in <code>form</code> , the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to <code>~ 1</code> , which corresponds to using the order of the observations in the data as a covariate, and no groups.
nugget	an optional logical value indicating whether a nugget effect is present. Defaults to <code>FALSE</code> .
metric	an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to <code>FALSE</code> , in which case the coefficients are allowed to vary.

**Value**

an object of class `corRatio`, also inheriting from class `corSpatial`, representing a rational quadratic spatial correlation structure.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

- Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.
- Venables, W.N. and Ripley, B.D. (1997) "Modern Applied Statistics with S-plus", 2nd Edition, Springer-Verlag.
- Littel, Milliken, Stroup, and Wolfinger (1996) "SAS Systems for Mixed Models", SAS Institute.
- Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[Initialize.corStruct](#), [summary.corStruct](#), [dist](#)

**Examples**

```

spl <- corRatio(form = ~ x + y + z)

# example lme(..., corRatio ...)
# Pinheiro and Bates, pp. 222-249
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
               random = ~ Time)

# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# p 246
fm3BW.lme <- update(fm2BW.lme,
                  correlation = corExp(form = ~ Time))

# p. 249
fm5BW.lme <- update(fm3BW.lme, correlation =
                  corRatio(form = ~ Time))

# example gls(..., corRatio ...)
# Pinheiro and Bates, pp. 261, 263
fm1Wheat2 <- gls(yield ~ variety - 1, Wheat2)
# p. 263
fm3Wheat2 <- update(fm1Wheat2, corr =
                  corRatio(c(12.5, 0.2),
                          form = ~ latitude + longitude,
                          nugget = TRUE))

```

corSpatial

*Spatial Correlation Structure***Description**

This function is a constructor for the `corSpatial` class, representing a spatial correlation structure. This class is "virtual", having four "real" classes, corresponding to specific spatial correlation structures, associated with it: `corExp`, `corGaus`, `corLin`, `corRatio`, and `corSpher`. The returned object will inherit from one of these "real" classes, determined by the `type` argument, and from the "virtual" `corSpatial` class. Objects created using this constructor must later be initialized using the appropriate `Initialize` method.

**Usage**

```
corSpatial(value, form, nugget, type, metric, fixed)
```

**Arguments**

`value` an optional vector with the parameter values in constrained form. If `nugget` is `FALSE`, `value` can have only one element, corresponding to the "range" of the spatial correlation structure, which must be greater than zero. If `nugget` is `TRUE`, meaning that a nugget effect is present, `value` can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to `numeric(0)`, which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when `object` is initialized.

form	a one sided formula of the form $\sim S_1 + \dots + S_p$ , or $\sim S_1 + \dots + S_p \mid g$ , specifying spatial covariates $S_1$ through $S_p$ and, optionally, a grouping factor $g$ . When a grouping factor is present in <code>form</code> , the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to $\sim 1$ , which corresponds to using the order of the observations in the data as a covariate, and no groups.
nugget	an optional logical value indicating whether a nugget effect is present. Defaults to <code>FALSE</code> .
type	an optional character string specifying the desired type of correlation structure. Available types include "spherical", "exponential", "gaussian", "linear", and "rational". See the documentation on the functions <code>corSpher</code> , <code>corExp</code> , <code>corGaus</code> , <code>corLin</code> , and <code>corRatio</code> for a description of these correlation structures. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "spherical".
metric	an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to <code>FALSE</code> , in which case the coefficients are allowed to vary.

### Value

an object of class determined by the `type` argument and also inheriting from class `corSpatial`, representing a spatial correlation structure.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

- Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.  
 Venables, W.N. and Ripley, B.D. (1997) "Modern Applied Statistics with S-plus", 2nd Edition, Springer-Verlag.  
 Littell, Milliken, Stroup, and Wolfinger (1996) "SAS Systems for Mixed Models", SAS Institute.

### See Also

`corExp`, `corGaus`, `corLin`, `corRatio`, `corSpher`, `Initialize.corStruct`, `summary.corStruct`, `dist`

### Examples

```
sp1 <- corSpatial(form = ~ x + y + z, type = "g", metric = "man")
```

corSpher

*Spherical Correlation Structure***Description**

This function is a constructor for the `corSpher` class, representing a spherical spatial correlation structure. Letting  $d$  denote the range and  $n$  denote the nugget effect, the correlation between two observations a distance  $r < d$  apart is  $1 - 1.5(r/d) + 0.5(r/d)^3$  when no nugget effect is present and  $(1 - n)(1 - 1.5(r/d) + 0.5(r/d)^3)$  when a nugget effect is assumed. If  $r \geq d$  the correlation is zero. Objects created using this constructor must later be initialized using the appropriate `Initialize` method.

**Usage**

```
corSpher(value, form, nugget, metric, fixed)
```

**Arguments**

value	an optional vector with the parameter values in constrained form. If <code>nugget</code> is <code>FALSE</code> , <code>value</code> can have only one element, corresponding to the "range" of the spherical correlation structure, which must be greater than zero. If <code>nugget</code> is <code>TRUE</code> , meaning that a nugget effect is present, <code>value</code> can contain one or two elements, the first being the "range" and the second the "nugget effect" (one minus the correlation between two observations taken arbitrarily close together); the first must be greater than zero and the second must be between zero and one. Defaults to <code>numeric(0)</code> , which results in a range of 90% of the minimum distance and a nugget effect of 0.1 being assigned to the parameters when <code>object</code> is initialized.
form	a one sided formula of the form $\sim S_1 + \dots + S_p$ , or $\sim S_1 + \dots + S_p \mid g$ , specifying spatial covariates $S_1$ through $S_p$ and, optionally, a grouping factor $g$ . When a grouping factor is present in <code>form</code> , the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to $\sim 1$ , which corresponds to using the order of the observations in the data as a covariate, and no groups.
nugget	an optional logical value indicating whether a nugget effect is present. Defaults to <code>FALSE</code> .
metric	an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to <code>FALSE</code> , in which case the coefficients are allowed to vary.

**Value**

an object of class `corSpher`, also inheriting from class `corSpatial`, representing a spherical spatial correlation structure.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**References**

- Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.  
 Venables, W.N. and Ripley, B.D. (1997) "Modern Applied Statistics with S-plus", 2nd Edition, Springer-Verlag.  
 Littell, Milliken, Stroup, and Wolfinger (1996) "SAS Systems for Mixed Models", SAS Institute.  
 Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[Initialize.corStruct](#), [summary.corStruct](#), [dist](#)

**Examples**

```
spl <- corSpher(form = ~ x + y)

# example lme(..., corSpher ...)
# Pinheiro and Bates, pp. 222-249
fm1BW.lme <- lme(weight ~ Time * Diet, BodyWeight,
               random = ~ Time)

# p. 223
fm2BW.lme <- update(fm1BW.lme, weights = varPower())
# p 246
fm3BW.lme <- update(fm2BW.lme,
                  correlation = corExp(form = ~ Time))

# p. 249
fm6BW.lme <- update(fm3BW.lme,
                  correlation = corSpher(form = ~ Time))

# example gls(..., corSpher ...)
# Pinheiro and Bates, pp. 261, 263
fm1Wheat2 <- gls(yield ~ variety - 1, Wheat2)
# p. 262
fm2Wheat2 <- update(fm1Wheat2, corr =
                  corSpher(c(28, 0.2),
                          form = ~ latitude + longitude, nugget = TRUE))
```

---

corSymm

*General Correlation Structure*

---

**Description**

This function is a constructor for the `corSymm` class, representing a general correlation structure. The internal representation of this structure, in terms of unconstrained parameters, uses the spherical parametrization defined in Pinheiro and Bates (1996). Objects created using this constructor must later be initialized using the appropriate `Initialize` method.

**Usage**

```
corSymm(value, form, fixed)
```

**Arguments**

value	an optional vector with the parameter values. Default is <code>numeric(0)</code> , which results in a vector of zeros of appropriate dimension being assigned to the parameters when <code>object</code> is initialized (corresponding to an identity correlation structure).
form	a one sided formula of the form <code>~ t</code> , or <code>~ t   g</code> , specifying a time covariate <code>t</code> and, optionally, a grouping factor <code>g</code> . A covariate for this correlation structure must be integer valued. When a grouping factor is present in <code>form</code> , the correlation structure is assumed to apply only to observations within the same grouping level; observations with different grouping levels are assumed to be uncorrelated. Defaults to <code>~ 1</code> , which corresponds to using the order of the observations in the data as a covariate, and no groups.
fixed	an optional logical value indicating whether the coefficients should be allowed to vary in the optimization, or kept fixed at their initial value. Defaults to <code>FALSE</code> , in which case the coefficients are allowed to vary.

**Value**

an object of class `corSymm` representing a general correlation structure.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", *Statistics and Computing*, 6, 289-296.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[Initialize.corSymm](#), [summary.corSymm](#)

**Examples**

```
## covariate is observation order and grouping factor is Subject
csl <- corSymm(form = ~ 1 | Subject)

# Pinheiro and Bates, p. 225
cslCompSymm <- corCompSymm(value = 0.3, form = ~ 1 | Subject)
cslCompSymm <- Initialize(cslCompSymm, data = Orthodont)
corMatrix(cslCompSymm)

# Pinheiro and Bates, p. 226
cslSymm <- corSymm(value =
  c(0.2, 0.1, -0.1, 0, 0.2, 0),
  form = ~ 1 | Subject)
```



```

cs1Symm <- Initialize(cs1Symm, data = Orthodont)
corMatrix(cs1Symm)

# example gls(..., corSpher ...)
# Pinheiro and Bates, pp. 261, 263
fm1Wheat2 <- gls(yield ~ variety - 1, Wheat2)
# p. 262
fm2Wheat2 <- update(fm1Wheat2, corr =
  corSpher(c(28, 0.2),
    form = ~ latitude + longitude, nugget = TRUE))

# example gls(..., corSymm ...)
# Pinheiro and Bates, p. 251
fm1Orth.gls <- gls(distance ~ Sex * I(age - 11), Orthodont,
  correlation = corSymm(form = ~ 1 | Subject),
  weights = varIdent(form = ~ 1 | age))

```

---

Covariate

*Assign Covariate Values*


---

### Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include all `varFunc` classes.

### Usage

```
covariate(object) <- value
```

### Arguments

<code>object</code>	any object with a covariate component.
<code>value</code>	a value to be assigned to the covariate associated with <code>object</code> .

### Value

will depend on the method function; see the appropriate documentation.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

### See Also

[getCovariate](#)

### Examples

```
## see the method function documentation
```

---

Covariate.varFunc *Assign varFunc Covariate*

---

### Description

The covariate(s) used in the calculation of the weights of the variance function represented by object is (are) replaced by value. If object has been initialized, value must have the same dimensions as getCovariate(object).

### Usage

```
## S3 replacement method for class 'varFunc':  
covariate(object) <- value
```

### Arguments

object            an object inheriting from class varFunc, representing a variance function structure.  
value            a value to be assigned to the covariate associated with object.

### Value

a varFunc object similar to object, but with its covariate attribute replaced by value.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[getCovariate.varFunc](#)

### Examples

```
vf1 <- varPower(1.1, form = ~age)  
covariate(vf1) <- Orthodont[["age"]]
```

---

Dialyzer

*High-Flux Hemodialyzer*

---

### Description

The Dialyzer data frame has 140 rows and 5 columns.

**Format**

This data frame contains the following columns:

**Subject** an ordered factor with levels 10 < 8 < 2 < 6 < 3 < 5 < 9 < 7 < 1 < 4 < 17 < 20 < 11 < 12 < 16 < 13 < 14 < 18 < 15 < 19 giving the unique identifier for each subject

**QB** a factor with levels 200 and 300 giving the bovine blood flow rate (dL/min).

**pressure** a numeric vector giving the transmembrane pressure (dmHg).

**rate** the hemodialyzer ultrafiltration rate (mL/hr).

**index** index of observation within subject—1 through 7.

**Details**

Vonesh and Carter (1992) describe data measured on high-flux hemodialyzers to assess their *in vivo* ultrafiltration characteristics. The ultrafiltration rates (in mL/hr) of 20 high-flux dialyzers were measured at seven different transmembrane pressures (in dmHg). The *in vitro* evaluation of the dialyzers used bovine blood at flow rates of either 200~dl/min or 300~dl/min. The data, are also analyzed in Littell, Milliken, Stroup, and Wolfinger (1996).

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.6)

Vonesh, E. F. and Carter, R. L. (1992), Mixed-effects nonlinear regression for unbalanced repeated measures, *Biometrics*, **48**, 1-18.

Littell, R. C., Milliken, G. A., Stroup, W. W. and Wolfinger, R. D. (1996), *SAS System for Mixed Models*, SAS Institute, Cary, NC.

---

 Dim

---

*Extract Dimensions from an Object*


---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `corSpatial`, `corStruct`, `pdCompSymm`, `pdDiag`, `pdIdent`, `pdMat`, and `pdSymm`.

**Usage**

```
Dim(object, ...)
```

**Arguments**

`object` any object for which dimensions can be extracted.  
`...` some methods for this generic function require additional arguments.

**Value**

will depend on the method function used; see the appropriate documentation.

**Note**

If `dim` allowed more than one argument, there would be no need for this generic function.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[Dim.pdMat](#), [Dim.corStruct](#)

**Examples**

```
## see the method function documentation
```

---

`Dim.corSpatial`      *Dimensions of a corSpatial Object*

---

**Description**

if `groups` is missing, it returns the `Dim` attribute of `object`; otherwise, calculates the dimensions associated with the grouping factor.

**Usage**

```
## S3 method for class 'corSpatial':
Dim(object, groups, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>corSpatial</code> , representing a spatial correlation structure.
<code>groups</code>	an optional factor defining the grouping of the observations; observations within a group are correlated and observations in different groups are uncorrelated.
<code>...</code>	further arguments to be passed to or from methods.

**Value**

a list with components:

<code>N</code>	length of <code>groups</code>
<code>M</code>	number of groups
<code>spClass</code>	an integer representing the spatial correlation class; 0 = user defined class, 1 = <code>corSpher</code> , 2 = <code>corExp</code> , 3 = <code>corGaus</code> , 4 = <code>corLin</code>
<code>sumLenSq</code>	sum of the squares of the number of observations per group
<code>len</code>	an integer vector with the number of observations per group
<code>start</code>	an integer vector with the starting position for the distance vectors in each group, beginning from zero

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[Dim](#), [Dim.corStruct](#)

**Examples**

```
Dim(corGaus(), getGroups(Orthodont))

cslARMA <- corARMA(0.4, form = ~ 1 | Subject, q = 1)
cslARMA <- Initialize(cslARMA, data = Orthodont)
Dim(cslARMA)
```

---

Dim.corStruct

*Dimensions of a corStruct Object*

---

**Description**

if `groups` is missing, it returns the `Dim` attribute of `object`; otherwise, calculates the dimensions associated with the grouping factor.

**Usage**

```
## S3 method for class 'corStruct':
Dim(object, groups, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>corStruct</code> , representing a correlation structure.
<code>groups</code>	an optional factor defining the grouping of the observations; observations within a group are correlated and observations in different groups are uncorrelated.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a list with components:

<code>N</code>	length of <code>groups</code>
<code>M</code>	number of groups
<code>maxLen</code>	maximum number of observations in a group
<code>sumLenSq</code>	sum of the squares of the number of observations per group
<code>len</code>	an integer vector with the number of observations per group
<code>start</code>	an integer vector with the starting position for the observations in each group, beginning from zero

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[Dim](#), [Dim.corSpatial](#)

**Examples**

```
Dim(corAR1(), getGroups(Orthodont))
```

---

Dim.pdMat

*Dimensions of a pdMat Object*

---

**Description**

This method function returns the dimensions of the matrix represented by `object`.

**Usage**

```
## S3 method for class 'pdMat':  
Dim(object, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>pdMat</code> , representing a positive-definite matrix.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

an integer vector with the number of rows and columns of the matrix represented by `object`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[Dim](#)

**Examples**

```
Dim(pdSymm(diag(3)))
```

---

 Earthquake

*Earthquake Intensity*


---

### Description

The Earthquake data frame has 182 rows and 5 columns.

### Format

This data frame contains the following columns:

**Quake** an ordered factor with levels 20 < 16 < 14 < 10 < 3 < 8 < 23 < 22 < 6 < 13 < 7 < 21 < 18 < 15 < 4 < 12 < 19 < 5 < 9 < 1 < 2 < 17 < 11 indicating the earthquake on which the measurements were made.

**Richter** a numeric vector giving the intensity of the earthquake on the Richter scale.

**distance** the distance from the seismological measuring station to the epicenter of the earthquake (km).

**soil** a factor with levels 0 and 1 giving the soil condition at the measuring station, either soil or rock.

**accel** maximum horizontal acceleration observed (g).

### Details

Measurements recorded at available seismometer locations for 23 large earthquakes in western North America between 1940 and 1980. They were originally given in Joyner and Boore (1981); are mentioned in Brillinger (1987); and are analyzed in Davidian and Giltinan (1995).

### Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.8)

Davidian, M. and Giltinan, D. M. (1995), *Nonlinear Models for Repeated Measurement Data*, Chapman and Hall, London.

Joyner and Boor (1981), Peak horizontal acceleration and velocity from strong-motion records including records from the 1979 Imperial Valley, California, earthquake, *Bulletin of the Seismological Society of America*, **71**, 2011-2038.

Brillinger, D. (1987), Comment on a paper by C. R. Rao, *Statistical Science*, **2**, 448-450.

---

 ergoStool

*Ergometrics experiment with stool types*


---

### Description

The ergoStool data frame has 36 rows and 3 columns.

**Format**

This data frame contains the following columns:

**effort** a numeric vector giving the effort (Borg scale) required to arise from a stool.

**Type** a factor with levels T1, T2, T3, and T4 giving the stool type.

**Subject** an ordered factor giving a unique identifier for the subject in the experiment.

**Details**

Devore (2000) cites data from an article in *Ergometrics* (1993, pp. 519-535) on “The Effects of a Pneumatic Stool and a One-Legged Stool on Lower Limb Joint Load and Muscular Activity.”

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.9)

Devore, J. L. (2000), *Probability and Statistics for Engineering and the Sciences (5th ed)*, Duxbury, Boston, MA.

**Examples**

```
fml <-
  lme(effort ~ Type, data = ergoStool, random = ~ 1 | Subject)
anova( fml )
```

---

Fatigue

*Cracks caused by metal fatigue*

---

**Description**

The `Fatigue` data frame has 262 rows and 3 columns.

**Format**

This data frame contains the following columns:

**Path** an ordered factor with levels 1 < 2 < 3 < 4 < 5 < 6 < 7 < 8 < 9 < 10 < 11 < 12 < 13 < 14 < 15 < 16 < 17 < 18 < 19 < 20 < 21 giving the test path (or test unit) number. The order is in terms of increasing failure time or decreasing terminal crack length.

**cycles** number of test cycles at which the measurement is made (millions of cycles).

**relLength** relative crack length (dimensionless).

**Details**

These data are given in Lu and Meeker (1993) where they state “We obtained the data in Table 1 visually from figure 4.5.2 on page 242 of Bogdanoff and Kozin (1985).” The data represent the growth of cracks in metal for 21 test units. An initial notch of length 0.90 inches was made on each unit which then was subjected to several thousand test cycles. After every 10,000 test cycles the crack length was measured. Testing was stopped if the crack length exceeded 1.60 inches, defined as a failure, or at 120,000 cycles.



**Source**

Lu, C. Joseph , and Meeker, William Q. (1993), Using degradation measures to estimate a time-to-failure distribution, *Technometrics*, **35**, 161-174

fdHess

*Finite difference Hessian***Description**

Evaluate an approximate Hessian and gradient of a scalar function using finite differences.

**Usage**

```
fdHess(pars, fun, ..., .relStep=(.Machine$double.eps)^(1/3), minAbsPar=0)
```

**Arguments**

pars	the numeric values of the parameters at which to evaluate the function <code>fun</code> and its derivatives.
fun	a function depending on the parameters <code>pars</code> that returns a numeric scalar.
...	Optional additional arguments to <code>fun</code>
.relStep	The relative step size to use in the finite differences. It defaults to the cube root of <code>.Machine\$double.eps</code>
minAbsPar	The minimum magnitude of a parameter value that is considered non-zero. It defaults to zero meaning that any non-zero value will be considered different from zero.

**Details**

This function uses a second-order response surface design known as a Koschal design to determine the parameter values at which the function is evaluated.

**Value**

A list with components

mean	the value of function <code>fun</code> evaluated at the parameter values <code>pars</code>
gradient	an approximate gradient
Hessian	a matrix whose upper triangle contains an approximate Hessian.

**Author(s)**

Jose Pinheiro	<jcp@research.bell-labs.com>	Douglas Bates	<bates@stat.wisc.edu>
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**Examples**

```
fdHess(c(12.3, 2.34), function(x) x[1]*(1-exp(-0.4*x[2])))
```

---

fitted.glsStruct     *Calculate glsStruct Fitted Values*

---

### Description

The fitted values for the linear model represented by `object` are extracted.

### Usage

```
## S3 method for class 'glsStruct':  
fitted(object, glsFit, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>glsStruct</code> , representing a list of linear model components, such as <code>corStruct</code> and <code>varFunc</code> objects.
<code>glsFit</code>	an optional list with components <code>logLik</code> (log-likelihood), <code>beta</code> (coefficients), <code>sigma</code> (standard deviation for error term), <code>varBeta</code> (coefficients' covariance matrix), <code>fitted</code> (fitted values), and <code>residuals</code> (residuals). Defaults to <code>attr(object, "glsFit")</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

a vector with the fitted values for the linear model represented by `object`.

### Note

This method function is generally only used inside `gls` and `fitted.gls`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

### See Also

[gls](#), [residuals.glsStruct](#)

---

fitted.gnlsStruct    *Calculate gnlsStruct Fitted Values*

---

### Description

The fitted values for the nonlinear model represented by `object` are extracted.

### Usage

```
## S3 method for class 'gnlsStruct':
fitted(object, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>gnlsStruct</code> , representing a list of model components, such as <code>corStruct</code> and <code>varFunc</code> objects, and attributes specifying the underlying nonlinear model and the response variable.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

a vector with the fitted values for the nonlinear model represented by `object`.

### Note

This method function is generally only used inside `gnls` and `fitted.gnls`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[gnls](#), [residuals.gnlsStruct](#)

---

fitted.lme    *Extract lme Fitted Values*

---

### Description

The fitted values at level  $i$  are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels less or equal to  $i$ . The resulting values estimate the best linear unbiased predictions (BLUPs) at level  $i$ .

### Usage

```
## S3 method for class 'lme':
fitted(object, level, asList, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>lme</code> , representing a fitted linear mixed-effects model.
<code>level</code>	an optional integer vector giving the level(s) of grouping to be used in extracting the fitted values from <code>object</code> . Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.
<code>asList</code>	an optional logical value. If <code>TRUE</code> and a single value is given in <code>level</code> , the returned object is a list with the fitted values split by groups; else the returned value is either a vector or a data frame, according to the length of <code>level</code> . Defaults to <code>FALSE</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

If a single level of grouping is specified in `level`, the returned value is either a list with the fitted values split by groups (`asList = TRUE`) or a vector with the fitted values (`asList = FALSE`); else, when multiple grouping levels are specified in `level`, the returned object is a data frame with columns given by the fitted values at different levels and the grouping factors. For a vector or data frame result the `napredict` method is applied.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Bates, D.M. and Pinheiro, J.C. (1998) "Computational methods for multilevel models" available in PostScript or PDF formats at <http://nlme.stat.wisc.edu/pub/NLME/>

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 235, 397.

**See Also**

[lme](#), [residuals.lme](#)

**Examples**

```
fml <- lme(distance ~ age + Sex, data = Orthodont, random = ~ 1)
fitted(fml, level = 0:1)
```

---

fitted.lmeStruct    *Calculate lmeStruct Fitted Values*

---

### Description

The fitted values at level  $i$  are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels less or equal to  $i$ . The resulting values estimate the best linear unbiased predictions (BLUPs) at level  $i$ .

### Usage

```
## S3 method for class 'lmeStruct':
fitted(object, level, conLin, lmeFit, ...)
```

### Arguments

object	an object inheriting from class <code>lmeStruct</code> , representing a list of linear mixed-effects model components, such as <code>reStruct</code> , <code>corStruct</code> , and <code>varFunc</code> objects.
level	an optional integer vector giving the level(s) of grouping to be used in extracting the fitted values from <code>object</code> . Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.
conLin	an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying lme model. Defaults to <code>attr(object, "conLin")</code> .
lmeFit	an optional list with components <code>beta</code> and <code>b</code> containing respectively the fixed effects estimates and the random effects estimates to be used to calculate the fitted values. Defaults to <code>attr(object, "lmeFit")</code> .
...	some methods for this generic accept other optional arguments.

### Value

if a single level of grouping is specified in `level`, the returned value is a vector with the fitted values at the desired level; else, when multiple grouping levels are specified in `level`, the returned object is a matrix with columns given by the fitted values at different levels.

### Note

This method function is generally only used inside `lme` and `fitted.lme`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[lme](#), [fitted.lme](#), [residuals.lmeStruct](#)

---

fitted.lmList      *Extract lmList Fitted Values*

---

### Description

The fitted values are extracted from each `lm` component of `object` and arranged into a list with as many components as `object`, or combined into a single vector.

### Usage

```
## S3 method for class 'lmList':  
fitted(object, subset, asList, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>lmList</code> , representing a list of <code>lm</code> objects with a common model.
<code>subset</code>	an optional character or integer vector naming the <code>lm</code> components of <code>object</code> from which the fitted values are to be extracted. Default is <code>NULL</code> , in which case all components are used.
<code>asList</code>	an optional logical value. If <code>TRUE</code> , the returned object is a list with the fitted values split by groups; else the returned value is a vector. Defaults to <code>FALSE</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

a list with components given by the fitted values of each `lm` component of `object`, or a vector with the fitted values for all `lm` components of `object`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[lmList](#), [residuals.lmList](#)

### Examples

```
fml <- lmList(distance ~ age | Subject, Orthodont)  
fitted(fml)
```

---

fitted.nlmeStruct *Calculate nlmeStruct Fitted Values*

---

### Description

The fitted values at level  $i$  are obtained by adding together the contributions from the estimated fixed effects and the estimated random effects at levels less or equal to  $i$  and evaluating the model function at the resulting estimated parameters. The resulting values estimate the predictions at level  $i$ .

### Usage

```
## S3 method for class 'nlmeStruct':
fitted(object, level, conLin, ...)
```

### Arguments

object	an object inheriting from class <code>nlmeStruct</code> , representing a list of mixed-effects model components, such as <code>reStruct</code> , <code>corStruct</code> , and <code>varFunc</code> objects, plus attributes specifying the underlying nonlinear model and the response variable.
level	an optional integer vector giving the level(s) of grouping to be used in extracting the fitted values from <code>object</code> . Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.
conLin	an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying nlme model. Defaults to <code>attr(object, "conLin")</code> .
...	additional arguments that could be given to this method. None are used.

### Value

if a single level of grouping is specified in `level`, the returned value is a vector with the fitted values at the desired level; else, when multiple grouping levels are specified in `level`, the returned object is a matrix with columns given by the fitted values at different levels.

### Note

This method function is generally only used inside `nlme` and `fitted.nlme`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Bates, D.M. and Pinheiro, J.C. (1998) "Computational methods for multilevel models" available in PostScript or PDF formats at <http://nlme.stat.wisc.edu/pub/NLME/>

**See Also**

[nlme](#), [residuals.nlmeStruct](#)

---

fixed.effects      *Extract Fixed Effects*

---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `lmList` and `lme`.

**Usage**

```
fixed.effects(object, ...)  
fixef(object, ...)
```

**Arguments**

`object`      any fitted model object from which fixed effects estimates can be extracted.  
`...`      some methods for this generic function require additional arguments.

**Value**

will depend on the method function used; see the appropriate documentation.

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[fixef.lmList](#)

**Examples**

```
## see the method function documentation
```



---

`fixef.lmList`      *Extract lmList Fixed Effects*

---

### Description

The average of the coefficients corresponding to the `lm` components of `object` is calculated.

### Usage

```
## S3 method for class 'lmList':  
fixef(object, ...)
```

### Arguments

`object`      an object inheriting from class `lmList`, representing a list of `lm` objects with a common model.

`...`      some methods for this generic require additional arguments. None are used in this method.

### Value

a vector with the average of the individual `lm` coefficients in `object`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[lmList](#), [random.effects.lmList](#)

### Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)  
fixed.effects(fm1)
```

---

`formula.pdBlocked`      *Extract pdBlocked Formula*

---

### Description

The `formula` attributes of the `pdMat` elements of `x` are extracted and returned as a list, in case `asList=TRUE`, or converted to a single one-sided formula when `asList=FALSE`. If the `pdMat` elements do not have a `formula` attribute, a `NULL` value is returned.

### Usage

```
## S3 method for class 'pdBlocked':  
formula(x, asList, ...)
```

**Arguments**

<code>x</code>	an object inheriting from class <code>pdBlocked</code> , representing a positive definite block diagonal matrix.
<code>asList</code>	an optional logical value. If <code>TRUE</code> , a list with the formulas for the individual block diagonal elements of <code>x</code> is returned; else, if <code>FALSE</code> , a one-sided formula combining all individual formulas is returned. Defaults to <code>FALSE</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a list of one-sided formulas, or a single one-sided formula, or `NULL`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[pdBlocked](#), [pdMat](#)

**Examples**

```
pd1 <- pdBlocked(list(~ age, ~ Sex - 1))
formula(pd1)
formula(pd1, asList = TRUE)
```

---

formula.pdMat	<i>Extract pdMat Formula</i>
---------------	------------------------------

---

**Description**

This method function extracts the formula associated with a `pdMat` object, in which the column and row names are specified.

**Usage**

```
## S3 method for class 'pdMat':
formula(x, asList, ...)
```

**Arguments**

<code>x</code>	an object inheriting from class <code>pdMat</code> , representing a positive definite matrix.
<code>asList</code>	logical. Should the <code>asList</code> argument be applied to each of the components? Never used.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

if `x` has a `formula` attribute, its value is returned, else `NULL` is returned.

**Note**

Because factors may be present in `formula(x)`, the `pdMat` object needs to have access to a data frame where the variables named in the formula can be evaluated, before it can resolve its row and column names from the formula.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[pdMat](#)

**Examples**

```
pd1 <- pdSymm(~Sex*age)
formula(pd1)
```

---

`formula.reStruct`     *Extract reStruct Object Formula*

---

**Description**

This method function extracts a formula from each of the components of `x`, returning a list of formulas.

**Usage**

```
## S3 method for class 'reStruct':
formula(x, asList, ...)
```

**Arguments**

<code>x</code>	an object inheriting from class <code>reStruct</code> , representing a random effects structure and consisting of a list of <code>pdMat</code> objects.
<code>asList</code>	logical. Should the <code>asList</code> argument be applied to each of the components?
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a list with the formulas of each component of `x`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[formula](#)

**Examples**

```
rs1 <- reStruct(list(A = pdDiag(diag(2), ~age), B = ~1))
formula(rs1)
```

---

gapply

*Apply a Function by Groups*


---

**Description**

Applies the function to the distinct sets of rows of the data frame defined by groups.

**Usage**

```
gapply(object, which, FUN, form, level, groups, ...)
```

**Arguments**

object	an object to which the function will be applied - usually a <code>groupedData</code> object or a <code>data.frame</code> . Must inherit from class <code>data.frame</code> .
which	an optional character or positive integer vector specifying which columns of <code>object</code> should be used with <code>FUN</code> . Defaults to all columns in <code>object</code> .
FUN	function to apply to the distinct sets of rows of the data frame <code>object</code> defined by the values of <code>groups</code> .
form	an optional one-sided formula that defines the groups. When this formula is given the right-hand side is evaluated in <code>object</code> , converted to a factor if necessary, and the unique levels are used to define the groups. Defaults to <code>formula(object)</code> .
level	an optional positive integer giving the level of grouping to be used in an object with multiple nested grouping levels. Defaults to the highest or innermost level of grouping.
groups	an optional factor that will be used to split the rows into groups. Defaults to <code>getGroups(object, form, level)</code> .
...	optional additional arguments to the summary function <code>FUN</code> . Often it is helpful to specify <code>na.rm = TRUE</code> .

**Value**

Returns a data frame with as many rows as there are levels in the `groups` argument.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

## References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. sec. 3.4.

## See Also

[gsummary](#)

## Examples

```
## Find number of non-missing "conc" observations for each Subject
gapply( Phenobarb, FUN = function(x) sum(!is.na(x$conc)) )

# Pinheiro and Bates, p. 127
table( gapply(Quinidine, "conc", function(x) sum(!is.na(x))) )
changeRecords <- gapply( Quinidine, FUN = function(frm)
  any(is.na(frm[["conc"]]) & is.na(frm[["dose"]])) ) )
```

---

Gasoline

*Refinery yield of gasoline*

---

## Description

The Gasoline data frame has 32 rows and 6 columns.

## Format

This data frame contains the following columns:

**yield** a numeric vector giving the percentage of crude oil converted to gasoline after distillation and fractionation

**endpoint** a numeric vector giving the temperature (degrees F) at which all the gasoline is vaporized

**Sample** an ordered factor giving the inferred crude oil sample number

**API** a numeric vector giving the crude oil gravity (degrees API)

**vapor** a numeric vector giving the vapor pressure of the crude oil (lbf/in<sup>2</sup>)

**ASTM** a numeric vector giving the crude oil 10% point ASTM—the temperature at which 10% of the crude oil has become vapor.

## Details

Prater (1955) provides data on crude oil properties and gasoline yields. Atkinson (1985) uses these data to illustrate the use of diagnostics in multiple regression analysis. Three of the covariates—API, vapor, and ASTM—measure characteristics of the crude oil used to produce the gasoline. The other covariate — endpoint—is a characteristic of the refining process. Daniel and Wood (1980) notice that the covariates characterizing the crude oil occur in only ten distinct groups and conclude that the data represent responses measured on ten different crude oil samples.

**Source**

Prater, N. H. (1955), Estimate gasoline yields from crudes, *Petroleum Refiner*, **35** (5).  
Atkinson, A. C. (1985), *Plots, Transformations, and Regression*, Oxford Press, New York.  
Daniel, C. and Wood, F. S. (1980), *Fitting Equations to Data*, Wiley, New York  
Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS (3rd ed)*, Springer, New York.

---

getCovariate	<i>Extract Covariate from an Object</i>
--------------	---

---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `corStruct`, `corSpatial`, `data.frame`, and `varFunc`.

**Usage**

```
getCovariate(object, form, data)
```

**Arguments**

<code>object</code>	any object with a <code>covariate</code> component
<code>form</code>	an optional one-sided formula specifying the covariate(s) to be extracted. Defaults to <code>formula(object)</code> .
<code>data</code>	a data frame in which to evaluate the variables defined in <code>form</code> .

**Value**

will depend on the method function used; see the appropriate documentation.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. p. 100.

**See Also**

[getCovariate.corStruct](#), [getCovariate.data.frame](#),  
[getCovariate.varFunc](#), [getCovariateFormula](#)

**Examples**

```
## see the method function documentation
```

---

`getCovariate.corStruct`*Extract corStruct Object Covariate*

---

## Description

This method function extracts the covariate(s) associated with `object`.

## Usage

```
## S3 method for class 'corStruct':  
getCovariate(object, form, data)
```

## Arguments

<code>object</code>	an object inheriting from class <code>corStruct</code> representing a correlation structure.
<code>form</code>	this argument is included to make the method function compatible with the generic. It will be assigned the value of <code>formula(object)</code> and should not be modified.
<code>data</code>	an optional data frame in which to evaluate the variables defined in <code>form</code> , in case <code>object</code> is not initialized and the covariate needs to be evaluated.

## Value

when the correlation structure does not include a grouping factor, the returned value will be a vector or a matrix with the covariate(s) associated with `object`. If a grouping factor is present, the returned value will be a list of vectors or matrices with the covariate(s) corresponding to each grouping level.

## Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

## References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

## See Also

[getCovariate](#)

## Examples

```
cs1 <- corAR1(form = ~ 1 | Subject)  
getCovariate(cs1, data = Orthodont)
```

---

```
getCovariate.data.frame
```

*Extract Data Frame Covariate*

---

### Description

The right hand side of `form`, stripped of any conditioning expression (i.e. an expression following a `|` operator), is evaluated in `object`.

### Usage

```
## S3 method for class 'data.frame':  
getCovariate(object, form, data)
```

### Arguments

<code>object</code>	an object inheriting from class <code>data.frame</code> .
<code>form</code>	an optional formula specifying the covariate to be evaluated in <code>object</code> . Defaults to <code>formula(object)</code> .
<code>data</code>	some methods for this generic require a separate data frame. Not used in this method.

### Value

the value of the right hand side of `form`, stripped of any conditional expression, evaluated in `object`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[getCovariateFormula](#)

### Examples

```
getCovariate(Orthodont)
```



---

`getCovariate.varFunc`*Extract varFunc Covariate*

---

### Description

This method function extracts the covariate(s) associated with the variance function represented by `object`, if any is present.

### Usage

```
## S3 method for class 'varFunc':  
getCovariate(object, form, data)
```

### Arguments

<code>object</code>	an object inheriting from class <code>varFunc</code> , representing a variance function structure.
<code>form</code>	an optional formula specifying the covariate to be evaluated in <code>object</code> . Defaults to <code>formula(object)</code> .
<code>data</code>	some methods for this generic require a <code>data</code> object. Not used in this method.

### Value

if `object` has a `covariate` attribute, its value is returned; else `NULL` is returned.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

### See Also

[covariate<-.varFunc](#)

### Examples

```
vf1 <- varPower(1.1, form = ~age)  
covariate(vf1) <- Orthodont[["age"]]  
getCovariate(vf1)
```

---

```
getCovariateFormula
```

*Extract Covariates Formula*

---

**Description**

The right hand side of `formula(object)`, without any conditioning expressions (i.e. any expressions after a `|` operator) is returned as a one-sided formula.

**Usage**

```
getCovariateFormula(object)
```

**Arguments**

`object` any object from which a formula can be extracted.

**Value**

a one-sided formula describing the covariates associated with `formula(object)`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[getCovariate](#)

**Examples**

```
getCovariateFormula(y ~ x | g)
getCovariateFormula(y ~ x)
```

---

```
getData
```

*Extract Data from an Object*

---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `gls`, `lme`, and `lmList`.

**Usage**

```
getData(object)
```

**Arguments**

`object` an object from which a data.frame can be extracted, generally a fitted model object.

**Value**

will depend on the method function used; see the appropriate documentation.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[getData.gls](#), [getData.lme](#), [getData.lmList](#)

**Examples**

```
## see the method function documentation
```

---

getData.gls	<i>Extract gls Object Data</i>
-------------	--------------------------------

---

**Description**

If present in the calling sequence used to produce `object`, the data frame used to fit the model is obtained.

**Usage**

```
## S3 method for class 'gls':  
getData(object)
```

**Arguments**

`object` an object inheriting from class `gls`, representing a generalized least squares fitted linear model.

**Value**

if a `data` argument is present in the calling sequence that produced `object`, the corresponding data frame (with `na.action` and `subset` applied to it, if also present in the call that produced `object`) is returned; else, `NULL` is returned.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[gls](#), [getData](#)

**Examples**

```
fml <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), data = Ovary,  
          correlation = corAR1(form = ~ 1 | Mare))  
getData(fml)
```

---

getData.lme                    *Extract lme Object Data*

---

**Description**

If present in the calling sequence used to produce `object`, the data frame used to fit the model is obtained.

**Usage**

```
## S3 method for class 'lme':  
getData(object)
```

**Arguments**

`object`                    an object inheriting from class `lme`, representing a linear mixed-effects fitted model.

**Value**

if a data argument is present in the calling sequence that produced `object`, the corresponding data frame (with `na.action` and `subset` applied to it, if also present in the call that produced `object`) is returned; else, `NULL` is returned.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[lme](#), [getData](#)

**Examples**

```
fm1 <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), data = Ovary,  
          random = ~ sin(2*pi*Time))  
getData(fm1)
```

---

getData.lmList                *Extract lmList Object Data*

---

**Description**

If present in the calling sequence used to produce `object`, the data frame used to fit the model is obtained.

**Usage**

```
## S3 method for class 'lmList':  
getData(object)
```

**Arguments**

`object` an object inheriting from class `lmList`, representing a list of `lm` objects with a common model.

**Value**

if a `data` argument is present in the calling sequence that produced `object`, the corresponding data frame (with `na.action` and `subset` applied to it, if also present in the call that produced `object`) is returned; else, `NULL` is returned.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[lmList](#), [getData](#)

**Examples**

```
fml <- lmList(distance ~ age | Subject, Orthodont)
getData(fml)
```

---

getGroups

*Extract Grouping Factors from an Object*

---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `corStruct`, `data.frame`, `gls`, `lme`, `lmList`, and `varFunc`.

**Usage**

```
getGroups(object, form, level, data, sep)
```

**Arguments**

`object` any object

`form` an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the `|` operator). Defaults to `formula(object)`.

`level` a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. This argument is optional for most methods of this generic function and defaults to all levels of nesting.

`data` a data frame in which to interpret the variables named in `form`. Optional for most methods.

`sep` character, the separator to use between group levels when multiple levels are collapsed. The default is `' / '`.

**Value**

will depend on the method function used; see the appropriate documentation.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 100, 461.

**See Also**

`getGroupsFormula`, `getGroups.data.frame`, `getGroups.gls`,  
`getGroups.lmList`, `getGroups.lme`

**Examples**

```
## see the method function documentation
```

---

```
getGroups.corStruct
      Extract corStruct Groups
```

---

**Description**

This method function extracts the grouping factor associated with `object`, if any is present.

**Usage**

```
## S3 method for class 'corStruct':
getGroups(object, form, level, data, sep)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>corStruct</code> representing a correlation structure.
<code>form</code>	this argument is included to make the method function compatible with the generic. It will be assigned the value of <code>formula(object)</code> and should not be modified.
<code>level</code>	this argument is included to make the method function compatible with the generic and is not used.
<code>data</code>	an optional data frame in which to evaluate the variables defined in <code>form</code> , in case <code>object</code> is not initialized and the grouping factor needs to be evaluated.
<code>sep</code>	character, the separator to use between group levels when multiple levels are collapsed. The default is <code>'/'</code> .

**Value**

if a grouping factor is present in the correlation structure represented by `object`, the function returns the corresponding factor vector; else the function returns `NULL`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[getGroups](#)

**Examples**

```
cs1 <- corAR1(form = ~ 1 | Subject)
getGroups(cs1, data = Orthodont)
```

---

```
getGroups.data.frame
```

*Extract Groups from a Data Frame*

---

**Description**

Each variable named in the expression after the `|` operator on the right hand side of `form` is evaluated in `object`. If more than one variable is indicated in `level` they are combined into a data frame; else the selected variable is returned as a vector. When multiple grouping levels are defined in `form` and `level > 1`, the levels of the returned factor are obtained by pasting together the levels of the grouping factors of level greater or equal to `level`, to ensure their uniqueness.

**Usage**

```
## S3 method for class 'data.frame':
getGroups(object, form, level, data, sep)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>data.frame</code> .
<code>form</code>	an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the <code> </code> operator). Defaults to <code>formula(object)</code> .
<code>level</code>	a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. Defaults to all levels of nesting.
<code>data</code>	unused
<code>sep</code>	character, the separator to use between group levels when multiple levels are collapsed. The default is <code>'/'</code> .

**Value**

either a data frame with columns given by the grouping factors indicated in `level`, from outer to inner, or, when a single level is requested, a factor representing the selected grouping factor.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 100, 461.

**See Also**

[getGroupsFormula](#)

**Examples**

```
getGroups(Pixel)
getGroups(Pixel, level = 2)
```

---

getGroups.gls      *Extract gls Object Groups*

---

**Description**

If present, the grouping factor associated to the correlation structure for the linear model represented by `object` is extracted.

**Usage**

```
## S3 method for class 'gls':
getGroups(object, form, level, data, sep)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>gls</code> , representing a generalized least squares fitted linear model.
<code>form</code>	an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the <code> </code> operator). Defaults to <code>formula(object)</code> . Not used.
<code>level</code>	a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. This argument is optional for most methods of this generic function and defaults to all levels of nesting. Not used.
<code>data</code>	a data frame in which to interpret the variables named in <code>form</code> . Optional for most methods. Not used.
<code>sep</code>	character, the separator to use between group levels when multiple levels are collapsed. The default is <code>'/'</code> . Not used.

**Value**

if the linear model represented by `object` incorporates a correlation structure and the corresponding `corStruct` object has a grouping factor, a vector with the group values is returned; else, `NULL` is returned.



**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[gls](#), [corClasses](#)

**Examples**

```
fml <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
          correlation = corAR1(form = ~ 1 | Mare))
getGroups(fml)
```

---

getGroups.lme      *Extract lme Object Groups*

---

**Description**

The grouping factors corresponding to the linear mixed-effects model represented by `object` are extracted. If more than one level is indicated in `level`, the corresponding grouping factors are combined into a data frame; else the selected grouping factor is returned as a vector.

**Usage**

```
## S3 method for class 'lme':
getGroups(object, form, level, data, sep)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>lme</code> , representing a fitted linear mixed-effects model.
<code>form</code>	this argument is included to make the method function compatible with the generic and is ignored in this method.
<code>level</code>	an optional integer vector giving the level(s) of grouping to be extracted from <code>object</code> . Defaults to the highest or innermost level of grouping.
<code>data</code>	unused
<code>sep</code>	character, the separator to use between group levels when multiple levels are collapsed. The default is <code>'/'</code> .

**Value**

either a data frame with columns given by the grouping factors indicated in `level`, or, when a single level is requested, a factor representing the selected grouping factor.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**[lme](#)**Examples**

```
fml <- lme(pixel ~ day + day^2, Pixel,
  random = list(Dog = ~day, Side = ~1))
getGroups(fml, level = 1:2)
```

---

getGroups.lmList     *Extract lmList Object Groups*

---

**Description**

The grouping factor determining the partitioning of the observations used to produce the `lm` components of `object` is extracted.

**Usage**

```
## S3 method for class 'lmList':
getGroups(object, form, level, data, sep)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>lmList</code> , representing a list of <code>lm</code> objects with a common model.
<code>form</code>	an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the <code> </code> operator). Defaults to <code>formula(object)</code> . Not used.
<code>level</code>	a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. This argument is optional for most methods of this generic function and defaults to all levels of nesting. Not used.
<code>data</code>	a data frame in which to interpret the variables named in <code>form</code> . Optional for most methods. Not used.
<code>sep</code>	character, the separator to use between group levels when multiple levels are collapsed. The default is <code>'/'</code> . Not used.

**Value**

a vector with the grouping factor corresponding to the `lm` components of `object`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**[lmList](#)

## Examples

```
fml <- lmList(distance ~ age | Subject, Orthodont)
getGroups(fml)
```

---

getGroups.varFunc *Extract varFunc Groups*

---

## Description

This method function extracts the grouping factor associated with the variance function represented by `object`, if any is present.

## Usage

```
## S3 method for class 'varFunc':
getGroups(object, form, level, data, sep)
```

## Arguments

<code>object</code>	an object inheriting from class <code>varFunc</code> , representing a variance function structure.
<code>form</code>	an optional formula with a conditioning expression on its right hand side (i.e. an expression involving the <code> </code> operator). Defaults to <code>formula(object)</code> . Not used.
<code>level</code>	a positive integer vector with the level(s) of grouping to be used when multiple nested levels of grouping are present. This argument is optional for most methods of this generic function and defaults to all levels of nesting. Not used.
<code>data</code>	a data frame in which to interpret the variables named in <code>form</code> . Optional for most methods. Not used.
<code>sep</code>	character, the separator to use between group levels when multiple levels are collapsed. The default is <code>'/'</code> . Not used.

## Value

if `object` has a `groups` attribute, its value is returned; else `NULL` is returned.

## Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

## Examples

```
vf1 <- varPower(form = ~ age | Sex)
vf1 <- Initialize(vf1, Orthodont)
getGroups(vf1)
```

---

getGroupsFormula     *Extract Grouping Formula*

---

### Description

The conditioning expression associated with `formula(object)` (i.e. the expression after the `|` operator) is returned either as a named list of one-sided formulas, or a single one-sided formula, depending on the value of `asList`. The components of the returned list are ordered from outermost to innermost level and are named after the grouping factor expression.

### Usage

```
getGroupsFormula(object, asList, sep)
```

### Arguments

<code>object</code>	any object from which a formula can be extracted.
<code>asList</code>	an optional logical value. If <code>TRUE</code> the returned value will be a list of formulas; else, if <code>FALSE</code> the returned value will be a one-sided formula. Defaults to <code>FALSE</code> .
<code>sep</code>	character, the separator to use between group levels when multiple levels are collapsed. The default is <code>'/'</code> .

### Value

a one-sided formula, or a list of one-sided formulas, with the grouping structure associated with `formula(object)`. If no conditioning expression is present in `formula(object)` a `NULL` value is returned.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

### See Also

[getGroupsFormula.gls](#), [getGroupsFormula.lmList](#), [getGroupsFormula.lme](#),  
[getGroupsFormula.reStruct](#), [getGroups](#)

### Examples

```
getGroupsFormula(y ~ x | g1/g2)
```

---

getResponse                    *Extract Response Variable from an Object*

---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `data.frame`, `gls`, `lme`, and `lmList`.

**Usage**

```
getResponse(object, form)
```

**Arguments**

`object`                    any object  
`form`                      an optional two-sided formula. Defaults to `formula(object)`.

**Value**

will depend on the method function used; see the appropriate documentation.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[getResponseFormula](#)

**Examples**

```
getResponse(Orthodont)
```

---

getResponseFormula    *Extract Formula Specifying Response Variable*

---

**Description**

The left hand side of `formula{object}` is returned as a one-sided formula.

**Usage**

```
getResponseFormula(object)
```

**Arguments**

`object`                    any object from which a formula can be extracted.

**Value**

a one-sided formula with the response variable associated with `formula{object}`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[getResponse](#)

**Examples**

```
getResponseFormula(y ~ x | g)
```

---

getVarCov	<i>Extract variance-covariance matrix</i>
-----------	---

---

**Description**

Extract the variance-covariance matrix from a fitted model, such as a mixed-effects model.

**Usage**

```
getVarCov(obj, ...)
## S3 method for class 'lme':
getVarCov(obj, individuals,
          type = c("random.effects", "conditional", "marginal"), ...)
## S3 method for class 'gls':
getVarCov(obj, individual = 1, ...)
```

**Arguments**

obj	A fitted model. Methods are available for models fit by <a href="#">lme</a> and by <a href="#">gls</a>
individuals	For models fit by <a href="#">lme</a> a vector of levels of the grouping factor can be specified for the conditional or marginal variance-covariance matrices.
individual	For models fit by <a href="#">gls</a> the only type of variance-covariance matrix provided is the marginal variance-covariance of the responses by group. The optional argument <code>individual</code> specifies the group of responses.
type	For models fit by <a href="#">lme</a> the <code>type</code> argument specifies the type of variance-covariance matrix, either <code>"random.effects"</code> for the random-effects variance-covariance (the default), or <code>"conditional"</code> for the conditional variance-covariance of the responses or <code>"marginal"</code> for the the marginal variance-covariance of the responses.
...	Optional arguments for some methods, as described above

**Value**

A variance-covariance matrix or a list of variance-covariance matrices.

**Author(s)**

Mary Lindstrom <lindstro@biostat.wisc.edu>

**See Also**

[lme](#), [gls](#)

**Examples**

```
fm1 <- lme(distance ~ age, data = Orthodont, subset = Sex == "Female")
getVarCov(fm1)
getVarCov(fm1, individual = "F01", type = "marginal")
getVarCov(fm1, type = "conditional")
fm2 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
           correlation = corAR1(form = ~ 1 | Mare))
getVarCov(fm2)
```

---

gls

*Fit Linear Model Using Generalized Least Squares*


---

**Description**

This function fits a linear model using generalized least squares. The errors are allowed to be correlated and/or have unequal variances.

**Usage**

```
gls(model, data, correlation, weights, subset, method, na.action,
     control, verbose)
## S3 method for class 'gls':
update(object, model., ..., evaluate = TRUE)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>gls</code> , representing a generalized least squares fitted linear model.
<code>model</code>	a two-sided linear formula object describing the model, with the response on the left of a <code>~</code> operator and the terms, separated by <code>+</code> operators, on the right.
<code>model.</code>	Changes to the model – see <code>update.formula</code> for details.
<code>data</code>	an optional data frame containing the variables named in <code>model</code> , <code>correlation</code> , <code>weights</code> , and <code>subset</code> . By default the variables are taken from the environment from which <code>gls</code> is called.
<code>correlation</code>	an optional <code>corStruct</code> object describing the within-group correlation structure. See the documentation of <code>corClasses</code> for a description of the available <code>corStruct</code> classes. If a grouping variable is to be used, it must be specified in the <code>form</code> argument to the <code>corStruct</code> constructor. Defaults to <code>NULL</code> , corresponding to uncorrelated errors.

<code>weights</code>	an optional <code>varFunc</code> object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to <code>varFixed</code> , corresponding to fixed variance weights. See the documentation on <code>varClasses</code> for a description of the available <code>varFunc</code> classes. Defaults to <code>NULL</code> , corresponding to homoscedastic errors.
<code>subset</code>	an optional expression indicating which subset of the rows of <code>data</code> should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
<code>method</code>	a character string. If <code>"REML"</code> the model is fit by maximizing the restricted log-likelihood. If <code>"ML"</code> the log-likelihood is maximized. Defaults to <code>"REML"</code> .
<code>na.action</code>	a function that indicates what should happen when the data contain <code>NA</code> s. The default action ( <code>na.fail</code> ) causes <code>gls</code> to print an error message and terminate if there are any incomplete observations.
<code>control</code>	a list of control values for the estimation algorithm to replace the default values returned by the function <code>glsControl</code> . Defaults to an empty list.
<code>verbose</code>	an optional logical value. If <code>TRUE</code> information on the evolution of the iterative algorithm is printed. Default is <code>FALSE</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.
<code>evaluate</code>	If <code>TRUE</code> evaluate the new call else return the call.

### Value

an object of class `gls` representing the linear model fit. Generic functions such as `print`, `plot`, and `summary` have methods to show the results of the fit. See `glsObject` for the components of the fit. The functions `resid`, `coef`, and `fitted` can be used to extract some of its components.

### Author(s)

Jose Pinheiro <jcp@research.bell-labs.com>, Douglas Bates  
<bates@stat.wisc.edu>

### References

The different correlation structures available for the `correlation` argument are described in Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994), Littell, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996), and Venables, W.N. and Ripley, B.D. (1997). The use of variance functions for linear and nonlinear models is presented in detail in Carroll, R.J. and Ruppert, D. (1988) and Davidian, M. and Giltinan, D.M. (1995).

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Carroll, R.J. and Ruppert, D. (1988) "Transformation and Weighting in Regression", Chapman and Hall.

Davidian, M. and Giltinan, D.M. (1995) "Nonlinear Mixed Effects Models for Repeated Measurement Data", Chapman and Hall.

Littell, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996) "SAS Systems for Mixed Models", SAS Institute.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 100, 461.



Venables, W.N. and Ripley, B.D. (1997) "Modern Applied Statistics with S-PLUS", 2nd Edition, Springer-Verlag.

### See Also

[corClasses](#), [glsControl](#), [glsObject](#), [glsStruct](#), [plot.gls](#), [predict.gls](#), [qqnorm.gls](#), [residuals.gls](#), [summary.gls](#), [varClasses](#), [varFunc](#)

### Examples

```
# AR(1) errors within each Mare
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
          correlation = corAR1(form = ~ 1 | Mare))
# variance increases as a power of the absolute fitted values
fm2 <- update(fm1, weights = varPower())
```

---

glsControl

*Control Values for gls Fit*

---

### Description

The values supplied in the function call replace the defaults and a list with all possible arguments is returned. The returned list is used as the `control` argument to the `gls` function.

### Usage

```
glsControl(maxIter, msMaxIter, tolerance, msTol, msScale, msVerbose,
           singular.ok, qrTol, returnObject, apVar, .relStep,
           nlmStepMax, opt=c("nlminb", "optim"), optimMethod,
           minAbsParApVar, natural)
```

### Arguments

<code>maxIter</code>	maximum number of iterations for the <code>gls</code> optimization algorithm. Default is 50.
<code>msMaxIter</code>	maximum number of iterations for the optimization step inside the <code>gls</code> optimization. Default is 50.
<code>tolerance</code>	tolerance for the convergence criterion in the <code>gls</code> algorithm. Default is 1e-6.
<code>msTol</code>	tolerance for the convergence criterion in <code>ms</code> , passed as the <code>rel.tolerance</code> argument to the function (see documentation on <code>ms</code> ). Default is 1e-7.
<code>msScale</code>	scale function passed as the <code>scale</code> argument to the <code>ms</code> function (see documentation on that function). Default is <code>lmeScale</code> .
<code>msVerbose</code>	a logical value passed as the <code>trace</code> argument to <code>ms</code> (see documentation on that function). Default is <code>FALSE</code> .
<code>singular.ok</code>	a logical value indicating whether non-estimable coefficients (resulting from linear dependencies among the columns of the regression matrix) should be allowed. Default is <code>FALSE</code> .
<code>qrTol</code>	a tolerance for detecting linear dependencies among the columns of the regression matrix in its QR decomposition. Default is <code>.Machine\$single.eps</code> .

returnObject	a logical value indicating whether the fitted object should be returned when the maximum number of iterations is reached without convergence of the algorithm. Default is FALSE.
apVar	a logical value indicating whether the approximate covariance matrix of the variance-covariance parameters should be calculated. Default is TRUE.
.relStep	relative step for numerical derivatives calculations. Default is $.Machine\$double.eps^{(1/3)}$ .
nlmStepMax	stepmax value to be passed to nlm. See <a href="#">nlm</a> for details. Default is 100.0
opt	the optimizer to be used, either <a href="#">nlminb</a> (the default since (R 2.2.0) or <a href="#">optim</a> (the previous default).
optimMethod	character - the optimization method to be used with the <a href="#">optim</a> optimizer. The default is "BFGS". An alternative is "L-BFGS-B".
minAbsParApVar	numeric value - minimum absolute parameter value in the approximate variance calculation. The default is 0.05.
natural	logical. Should the natural parameterization be used for the approximate variance calculations? Default is TRUE.

**Value**

a list with components for each of the possible arguments.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[gls](#), [lmeScale](#)

**Examples**

```
# decrease the maximum number iterations in the optimization call and
# request that information on the evolution of the ms iterations be printed
glsControl(msMaxIter = 20, msVerbose = TRUE)
```

---

glsObject

*Fitted gls Object*


---

**Description**

An object returned by the `gls` function, inheriting from class `gls` and representing a generalized least squares fitted linear model. Objects of this class have methods for the generic functions `anova`, `coef`, `fitted`, `formula`, `getGroups`, `getResponse`, `intervals`, `logLik`, `plot`, `predict`, `print`, `residuals`, `summary`, and `update`.

**Value**

The following components must be included in a legitimate `gls` object.

<code>apVar</code>	an approximate covariance matrix for the variance-covariance coefficients. If <code>apVar = FALSE</code> in the list of control values used in the call to <code>gls</code> , this component is equal to <code>NULL</code> .
<code>call</code>	a list containing an image of the <code>gls</code> call that produced the object.
<code>coefficients</code>	a vector with the estimated linear model coefficients.
<code>contrasts</code>	a list with the contrasts used to represent factors in the model formula. This information is important for making predictions from a new data frame in which not all levels of the original factors are observed. If no factors are used in the model, this component will be an empty list.
<code>dims</code>	a list with basic dimensions used in the model fit, including the components <code>N</code> - the number of observations in the data and <code>p</code> - the number of coefficients in the linear model.
<code>fitted</code>	a vector with the fitted values..
<code>glsStruct</code>	an object inheriting from class <code>glsStruct</code> , representing a list of linear model components, such as <code>corStruct</code> and <code>varFunc</code> objects.
<code>groups</code>	a vector with the correlation structure grouping factor, if any is present.
<code>logLik</code>	the log-likelihood at convergence.
<code>method</code>	the estimation method: either "ML" for maximum likelihood, or "REML" for restricted maximum likelihood.
<code>numIter</code>	the number of iterations used in the iterative algorithm.
<code>residuals</code>	a vector with the residuals.
<code>sigma</code>	the estimated residual standard error.
<code>varBeta</code>	an approximate covariance matrix of the coefficients estimates.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

`gls`, `glsStruct`

---

`glsStruct`

*Generalized Least Squares Structure*

---

**Description**

A generalized least squares structure is a list of model components representing different sets of parameters in the linear model. A `glsStruct` may contain `corStruct` and `varFunc` objects. `NULL` arguments are not included in the `glsStruct` list.

**Usage**

```
glsStruct(corStruct, varStruct)
```

**Arguments**

- `corStruct` an optional `corStruct` object, representing a correlation structure. Default is `NULL`.
- `varStruct` an optional `varFunc` object, representing a variance function structure. Default is `NULL`.

**Value**

a list of model variance-covariance components determining the parameters to be estimated for the associated linear model.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[corClasses](#), [gls](#), [residuals.glsStruct](#), [varFunc](#)

**Examples**

```
gls1 <- glsStruct(corAR1(), varPower())
```

---

Glucose

*Glucose levels over time*

---

**Description**

The `Glucose` data frame has 378 rows and 4 columns.

**Format**

This data frame contains the following columns:

**Subject** an ordered factor with levels 6 < 2 < 3 < 5 < 1 < 4

**Time** a numeric vector

**conc** a numeric vector of glucose levels

**Meal** an ordered factor with levels 2am < 6am < 10am < 2pm < 6pm < 10pm

**Source**

Hand, D. and Crowder, M. (1996), *Practical Longitudinal Data Analysis*, Chapman and Hall, London.

---

`Glucose2`*Glucose Levels Following Alcohol Ingestion*

---

**Description**

The `Glucose2` data frame has 196 rows and 4 columns.

**Format**

This data frame contains the following columns:

**Subject** a factor with levels 1 to 7 identifying the subject whose glucose level is measured.

**Date** a factor with levels 1 2 indicating the occasion in which the experiment was conducted.

**Time** a numeric vector giving the time since alcohol ingestion (in min/10).

**glucose** a numeric vector giving the blood glucose level (in mg/dl).

**Details**

Hand and Crowder (Table A.14, pp. 180-181, 1996) describe data on the blood glucose levels measured at 14 time points over 5 hours for 7 volunteers who took alcohol at time 0. The same experiment was repeated on a second date with the same subjects but with a dietary additive used for all subjects.

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.10)

Hand, D. and Crowder, M. (1996), *Practical Longitudinal Data Analysis*, Chapman and Hall, London.

---

`gnls`*Fit Nonlinear Model Using Generalized Least Squares*

---

**Description**

This function fits a nonlinear model using generalized least squares. The errors are allowed to be correlated and/or have unequal variances.

**Usage**

```
gnls(model, data, params, start, correlation, weights, subset,  
      na.action, naPattern, control, verbose)
```

**Arguments**

<code>model</code>	a two-sided formula object describing the model, with the response on the left of a <code>~</code> operator and a nonlinear expression involving parameters and covariates on the right. If <code>data</code> is given, all names used in the formula should be defined as parameters or variables in the data frame.
<code>data</code>	an optional data frame containing the variables named in <code>model</code> , <code>correlation</code> , <code>weights</code> , <code>subset</code> , and <code>naPattern</code> . By default the variables are taken from the environment from which <code>gnls</code> is called.
<code>params</code>	an optional two-sided linear formula of the form $p_1 + \dots + p_n \sim x_1 + \dots + x_m$ , or list of two-sided formulas of the form $p_1 \sim x_1 + \dots + x_m$ , with possibly different models for each parameter. The $p_1, \dots, p_n$ represent parameters included on the right hand side of <code>model</code> and $x_1 + \dots + x_m$ define a linear model for the parameters (when the left hand side of the formula contains several parameters, they are all assumed to follow the same linear model described by the right hand side expression). A <code>1</code> on the right hand side of the formula(s) indicates a single fixed effects for the corresponding parameter(s). By default, the parameters are obtained from the names of <code>start</code> .
<code>start</code>	an optional named list, or numeric vector, with the initial values for the parameters in <code>model</code> . It can be omitted when a <code>selfStarting</code> function is used in <code>model</code> , in which case the starting estimates will be obtained from a single call to the <code>nls</code> function.
<code>correlation</code>	an optional <code>corStruct</code> object describing the within-group correlation structure. See the documentation of <code>corClasses</code> for a description of the available <code>corStruct</code> classes. If a grouping variable is to be used, it must be specified in the <code>form</code> argument to the <code>corStruct</code> constructor. Defaults to <code>NULL</code> , corresponding to uncorrelated errors.
<code>weights</code>	an optional <code>varFunc</code> object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to <code>varFixed</code> , corresponding to fixed variance weights. See the documentation on <code>varClasses</code> for a description of the available <code>varFunc</code> classes. Defaults to <code>NULL</code> , corresponding to homoscedastic errors.
<code>subset</code>	an optional expression indicating which subset of the rows of <code>data</code> should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
<code>na.action</code>	a function that indicates what should happen when the data contain NAs. The default action ( <code>na.fail</code> ) causes <code>gnls</code> to print an error message and terminate if there are any incomplete observations.
<code>naPattern</code>	an expression or formula object, specifying which returned values are to be regarded as missing.
<code>control</code>	a list of control values for the estimation algorithm to replace the default values returned by the function <code>gnlsControl</code> . Defaults to an empty list.
<code>verbose</code>	an optional logical value. If <code>TRUE</code> information on the evolution of the iterative algorithm is printed. Default is <code>FALSE</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

an object of class `gnls`, also inheriting from class `gls`, representing the nonlinear model fit. Generic functions such as `print`, `plot` and `summary` have methods to show the results of the fit. See `gnlsObject` for the components of the fit. The functions `resid`, `coef`, and `fitted` can be used to extract some of its components.

**Author(s)**

Jose Pinheiro <jose.pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

The different correlation structures available for the `correlation` argument are described in Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994), Littell, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996), and Venables, W.N. and Ripley, B.D. (1997). The use of variance functions for linear and nonlinear models is presented in detail in Carrol, R.J. and Rupert, D. (1988) and Davidian, M. and Giltinan, D.M. (1995).

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Carrol, R.J. and Rupert, D. (1988) "Transformation and Weighting in Regression", Chapman and Hall.

Davidian, M. and Giltinan, D.M. (1995) "Nonlinear Mixed Effects Models for Repeated Measurement Data", Chapman and Hall.

Littell, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996) "SAS Systems for Mixed Models", SAS Institute.

Venables, W.N. and Ripley, B.D. (1997) "Modern Applied Statistics with S-plus", 2nd Edition, Springer-Verlag.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

`corClasses`, `gnlsControl`, `gnlsObject`, `gnlsStruct`, `predict.gnls`, `varClasses`, `varFunc`

**Examples**

```
# variance increases with a power of the absolute fitted values
fm1 <- gnls(weight ~ SSlogis(Time, Asym, xmid, scal), Soybean,
           weights = varPower())
summary(fm1)
```

---

`gnlsControl`

*Control Values for gnls Fit*

---

**Description**

The values supplied in the function call replace the defaults and a list with all possible arguments is returned. The returned list is used as the `control` argument to the `gnls` function.

**Usage**

```
gnlsControl(maxIter, nlsMaxIter, msMaxIter, minScale, tolerance,
            nlsTol, msTol, msScale, returnObject, msVerbose,
            apVar, .relStep, nlmStepMax,
            opt = c("nlminb", "optim"), optimMethod,
            minAbsParApVar)
```

**Arguments**

maxIter	maximum number of iterations for the <code>gnls</code> optimization algorithm. Default is 50.
nlsMaxIter	maximum number of iterations for the <code>nls</code> optimization step inside the <code>gnls</code> optimization. Default is 7.
msMaxIter	maximum number of iterations for the <code>ms</code> optimization step inside the <code>gnls</code> optimization. Default is 50.
minScale	minimum factor by which to shrink the default step size in an attempt to decrease the sum of squares in the <code>nls</code> step. Default 0.001.
tolerance	tolerance for the convergence criterion in the <code>gnls</code> algorithm. Default is 1e-6.
nlsTol	tolerance for the convergence criterion in <code>nls</code> step. Default is 1e-3.
msTol	tolerance for the convergence criterion in <code>ms</code> , passed as the <code>rel.tolerance</code> argument to the function (see documentation on <code>ms</code> ). Default is 1e-7.
msScale	scale function passed as the <code>scale</code> argument to the <code>ms</code> function (see documentation on that function). Default is <code>lmeScale</code> .
returnObject	a logical value indicating whether the fitted object should be returned when the maximum number of iterations is reached without convergence of the algorithm. Default is <code>FALSE</code> .
msVerbose	a logical value passed as the <code>trace</code> argument to <code>ms</code> (see documentation on that function). Default is <code>FALSE</code> .
apVar	a logical value indicating whether the approximate covariance matrix of the variance-covariance parameters should be calculated. Default is <code>TRUE</code> .
.relStep	relative step for numerical derivatives calculations. Default is <code>.Machine\$double.eps^(1/3)</code> .
opt	the optimizer to be used, either <code>nlminb</code> (the default since (R 2.2.0) or <code>optim</code> (the previous default).
optimMethod	character - the optimization method to be used with the <code>optim</code> optimizer. The default is <code>"BFGS"</code> . An alternative is <code>"L-BFGS-B"</code> .
nlmStepMax	stepmax value to be passed to <code>nlm</code> . See <code>nlm</code> for details. Default is 100.0
minAbsParApVar	numeric value - minimum absolute parameter value in the approximate variance calculation. The default is 0.05.

**Value**

a list with components for each of the possible arguments.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>



**See Also**

[gnls](#), [lmeScale](#)

**Examples**

```
# decrease the maximum number iterations in the ms call and
# request that information on the evolution of the ms iterations be printed
gnlsControl(msMaxIter = 20, msVerbose = TRUE)
```

---

gnlsObject

*Fitted gnls Object*

---

**Description**

An object returned by the `gnls` function, inheriting from class `gnls` and also from class `gls`, and representing a generalized nonlinear least squares fitted model. Objects of this class have methods for the generic functions `anova`, `coef`, `fitted`, `formula`, `getGroups`, `getResponse`, `intervals`, `logLik`, `plot`, `predict`, `print`, `residuals`, `summary`, and `update`.

**Value**

The following components must be included in a legitimate `gnls` object.

<code>apVar</code>	an approximate covariance matrix for the variance-covariance coefficients. If <code>apVar = FALSE</code> in the list of control values used in the call to <code>gnls</code> , this component is equal to <code>NULL</code> .
<code>call</code>	a list containing an image of the <code>gnls</code> call that produced the object.
<code>coefficients</code>	a vector with the estimated nonlinear model coefficients.
<code>contrasts</code>	a list with the contrasts used to represent factors in the model formula. This information is important for making predictions from a new data frame in which not all levels of the original factors are observed. If no factors are used in the model, this component will be an empty list.
<code>dims</code>	a list with basic dimensions used in the model fit, including the components <code>N</code> - the number of observations used in the fit and <code>p</code> - the number of coefficients in the nonlinear model.
<code>fitted</code>	a vector with the fitted values.
<code>modelStruct</code>	an object inheriting from class <code>gnlsStruct</code> , representing a list of model components, such as <code>corStruct</code> and <code>varFunc</code> objects.
<code>groups</code>	a vector with the correlation structure grouping factor, if any is present.
<code>logLik</code>	the log-likelihood at convergence.
<code>numIter</code>	the number of iterations used in the iterative algorithm.
<code>plist</code>	
<code>pmap</code>	
<code>residuals</code>	a vector with the residuals.
<code>sigma</code>	the estimated residual standard error.
<code>varBeta</code>	an approximate covariance matrix of the coefficients estimates.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[gnls](#), [gnlsStruct](#)

---

gnlsStruct

*Generalized Nonlinear Least Squares Structure*

---

**Description**

A generalized nonlinear least squares structure is a list of model components representing different sets of parameters in the nonlinear model. A `gnlsStruct` may contain `corStruct` and `varFunc` objects. NULL arguments are not included in the `gnlsStruct` list.

**Usage**

```
gnlsStruct(corStruct, varStruct)
```

**Arguments**

`corStruct` an optional `corStruct` object, representing a correlation structure. Default is NULL.

`varStruct` an optional `varFunc` object, representing a variance function structure. Default is NULL.

**Value**

a list of model variance-covariance components determining the parameters to be estimated for the associated nonlinear model.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[gnls](#), [corClasses](#), [residuals.gnlsStruct](#) [varFunc](#)

**Examples**

```
gnls1 <- gnlsStruct(corAR1(), varPower())
```

groupedData

*Construct a groupedData Object***Description**

An object of the `groupedData` class is constructed from the `formula` and `data` by attaching the `formula` as an attribute of the data, along with any of `outer`, `inner`, `labels`, and `units` that are given. If `order.groups` is `TRUE` the grouping factor is converted to an ordered factor with the ordering determined by `FUN`. Depending on the number of grouping levels and the type of primary covariate, the returned object will be of one of three classes: `nfnGroupedData` - numeric covariate, single level of nesting; `nffGroupedData` - factor covariate, single level of nesting; and `nmGroupedData` - multiple levels of nesting. Several modeling and plotting functions can use the formula stored with a `groupedData` object to construct default plots and models.

**Usage**

```
groupedData(formula, data, order.groups, FUN, outer, inner,
            labels, units)
## S3 method for class 'groupedData':
update(object, formula, data, order.groups, FUN,
       outer, inner, labels, units, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>groupedData</code> .
<code>formula</code>	a formula of the form <code>resp ~ cov   group</code> where <code>resp</code> is the response, <code>cov</code> is the primary covariate, and <code>group</code> is the grouping factor. The expression <code>1</code> can be used for the primary covariate when there is no other suitable candidate. Multiple nested grouping factors can be listed separated by the <code>/</code> symbol as in <code>fact1/fact2</code> . In an expression like this the <code>fact2</code> factor is nested within the <code>fact1</code> factor.
<code>data</code>	a data frame in which the expressions in <code>formula</code> can be evaluated. The resulting <code>groupedData</code> object will consist of the same data values in the same order but with additional attributes.
<code>order.groups</code>	an optional logical value, or list of logical values, indicating if the grouping factors should be converted to ordered factors according to the function <code>FUN</code> applied to the response from each group. If multiple levels of grouping are present, this argument can be either a single logical value (which will be repeated for all grouping levels) or a list of logical values. If no names are assigned to the list elements, they are assumed in the same order as the group levels (outermost to innermost grouping). Ordering within a level of grouping is done within the levels of the grouping factors which are outer to it. Changing the grouping factor to an ordered factor does not affect the ordering of the rows in the data frame but it does affect the order of the panels in a trellis display of the data or models fitted to the data. Defaults to <code>TRUE</code> .
<code>FUN</code>	an optional summary function that will be applied to the values of the response for each level of the grouping factor, when <code>order.groups = TRUE</code> , to determine the ordering. Defaults to the <code>max</code> function.

<code>outer</code>	an optional one-sided formula, or list of one-sided formulas, indicating covariates that are outer to the grouping factor(s). If multiple levels of grouping are present, this argument can be either a single one-sided formula, or a list of one-sided formulas. If no names are assigned to the list elements, they are assumed in the same order as the group levels (outermost to innermost grouping). An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. When plotting a groupedData object, the argument <code>outer = TRUE</code> causes the panels to be determined by the <code>outer</code> formula. The points within the panels are associated by level of the grouping factor. Defaults to <code>NULL</code> , meaning that no outer covariates are present.
<code>inner</code>	an optional one-sided formula, or list of one-sided formulas, indicating covariates that are inner to the grouping factor(s). If multiple levels of grouping are present, this argument can be either a single one-sided formula, or a list of one-sided formulas. If no names are assigned to the list elements, they are assumed in the same order as the group levels (outermost to innermost grouping). An inner covariate can change within the sets of rows defined by the grouping factor. An inner formula can be used to associate points in a plot of a groupedData object. Defaults to <code>NULL</code> , meaning that no inner covariates are present.
<code>labels</code>	an optional list of character strings giving labels for the response and the primary covariate. The label for the primary covariate is named <code>x</code> and that for the response is named <code>y</code> . Either label can be omitted.
<code>units</code>	an optional list of character strings giving the units for the response and the primary covariate. The units string for the primary covariate is named <code>x</code> and that for the response is named <code>y</code> . Either units string can be omitted.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

an object of one of the classes `nfnGroupedData`, `nffGroupedData`, or `nmGroupedData`, and also inheriting from classes `groupedData` and `data.frame`.

**Author(s)**

Douglas Bates and Jose Pinheiro

**References**

Bates, D.M. and Pinheiro, J.C. (1997), "Software Design for Longitudinal Data", in "Modelling Longitudinal and Spatially Correlated Data: Methods, Applications and Future Directions", T.G. Gregoire (ed.), Springer-Verlag, New York.

Pinheiro, J.C. and Bates, D.M. (1997) "Future Directions in Mixed-Effects Software: Design of NLME 3.0" available at <http://nlme.stat.wisc.edu/>

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[formula](#), [gapply](#), [gsummary](#), [lme](#), [plot.nffGroupedData](#), [plot.nfnGroupedData](#), [plot.nmGroupedData](#), [reStruct](#)

**Examples**

```
Orth.new <- # create a new copy of the groupedData object
  groupedData( distance ~ age | Subject,
    data = as.data.frame( Orthodont ),
    FUN = mean,
    outer = ~ Sex,
    labels = list( x = "Age",
      y = "Distance from pituitary to pterygomaxillary fissure" ),
    units = list( x = "(yr)", y = "(mm)" )

## Not run:
plot( Orth.new )          # trellis plot by Subject

## End(Not run)
formula( Orth.new )      # extractor for the formula
gsummary( Orth.new )     # apply summary by Subject
fml <- lme( Orth.new )   # fixed and groups formulae extracted from object
Orthodont2 <- update(Orthodont, FUN = mean)
```

gsummary

*Summarize by Groups***Description**

Provide a summary of the variables in a data frame by groups of rows. This is most useful with a `groupedData` object to examine the variables by group.

**Usage**

```
gsummary(object, FUN, omitGroupingFactor, form, level,
  groups, invariantsOnly, ...)
```

**Arguments**

`object` an object to be summarized - usually a `groupedData` object or a `data.frame`.

`FUN` an optional summary function or a list of summary functions to be applied to each variable in the frame. The function or functions are applied only to variables in `object` that vary within the groups defined by `groups`. Invariant variables are always summarized by group using the unique value that they assume within that group. If `FUN` is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If `FUN` is a list of functions, the names in the list should designate classes of variables in the frame such as `ordered`, `factor`, or `numeric`. The indicated function will be applied to any non-invariant variables of that class. The default functions to be used are `mean` for numeric factors, and `Mode` for both `factor` and `ordered`. The `Mode` function, defined internally in `gsummary`, returns the modal or most popular value of the variable. It is different from the `mode` function that returns the S-language mode of the variable.

`omitGroupingFactor` an optional logical value. When `TRUE` the grouping factor itself will be omitted from the group-wise summary but the levels of the grouping factor will continue to be used as the row names for the data frame that is produced by the summary. Defaults to `FALSE`.

form	an optional one-sided formula that defines the groups. When this formula is given, the right-hand side is evaluated in <code>object</code> , converted to a factor if necessary, and the unique levels are used to define the groups. Defaults to <code>formula(object)</code> .
level	an optional positive integer giving the level of grouping to be used in an object with multiple nested grouping levels. Defaults to the highest or innermost level of grouping.
groups	an optional factor that will be used to split the rows into groups. Defaults to <code>getGroups(object, form, level)</code> .
invariantsOnly	an optional logical value. When <code>TRUE</code> only those covariates that are invariant within each group will be summarized. The summary value for the group is always the unique value taken on by that covariate within the group. The columns in the summary are of the same class as the corresponding columns in <code>object</code> . By definition, the grouping factor itself must be an invariant. When combined with <code>omitGroupingFactor = TRUE</code> , this option can be used to discover if there are invariant covariates in the data frame. Defaults to <code>FALSE</code> .
...	optional additional arguments to the summary functions that are invoked on the variables by group. Often it is helpful to specify <code>na.rm = TRUE</code> .

### Value

A `data.frame` with one row for each level of the grouping factor. The number of columns is at most the number of columns in `object`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

### See Also

[summary](#), [groupedData](#), [getGroups](#)

### Examples

```
gsummary(Orthodont) # default summary by Subject
## gsummary with invariantsOnly = TRUE and omitGroupingFactor = TRUE
## determines whether there are covariates like Sex that are invariant
## within the repeated observations on the same Subject.
gsummary(Orthodont, inv = TRUE, omit = TRUE)
```

---

 Gun

*Methods for firing naval guns*


---

### Description

The Gun data frame has 36 rows and 4 columns.

### Format

This data frame contains the following columns:

**rounds** a numeric vector

**Method** a factor with levels M1 M2

**Team** an ordered factor with levels T1S < T3S < T2S < T1A < T2A < T3A < T1H < T3H < T2H

**Physique** an ordered factor with levels Slight < Average < Heavy

### Details

Hicks (p.180, 1993) reports data from an experiment on methods for firing naval guns. Gunners of three different physiques (slight, average, and heavy) tested two firing methods. Both methods were tested twice by each of nine teams of three gunners with identical physique. The response was the number of rounds fired per minute.

### Source

Hicks, C. R. (1993), *Fundamental Concepts in the Design of Experiments (4th ed)*, Harcourt Brace, New York.

---

 IGF

*Radioimmunoassay of IGF-I Protein*


---

### Description

The IGF data frame has 237 rows and 3 columns.

### Format

This data frame contains the following columns:

**Lot** an ordered factor giving the radioactive tracer lot.

**age** a numeric vector giving the age (in days) of the radioactive tracer.

**conc** a numeric vector giving the estimated concentration of IGF-I protein (ng/ml)

### Details

Davidian and Giltinan (1995) describe data obtained during quality control radioimmunoassays for ten different lots of radioactive tracer used to calibrate the Insulin-like Growth Factor (IGF-I) protein concentration measurements.

**Source**

Davidian, M. and Giltinan, D. M. (1995), *Nonlinear Models for Repeated Measurement Data*, Chapman and Hall, London.

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.11)

---

`Initialize`*Initialize Object*

---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `corStruct`, `lmeStruct`, `reStruct`, and `varFunc`.

**Usage**

```
Initialize(object, data, ...)
```

**Arguments**

<code>object</code>	any object requiring initialization, e.g. "plug-in" structures such as <code>corStruct</code> and <code>varFunc</code> objects.
<code>data</code>	a data frame to be used in the initialization procedure.
<code>...</code>	some methods for this generic function require additional arguments.

**Value**

an initialized object with the same class as `object`. Changes introduced by the initialization procedure will depend on the method function used; see the appropriate documentation.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[Initialize.corStruct](#), [Initialize.lmeStruct](#), [Initialize.glsStruct](#), [Initialize.varFunc](#), [isInitialized](#)

**Examples**

```
## see the method function documentation
```



`Initialize.corStruct`*Initialize corStruct Object*

---

### Description

This method initializes `object` by evaluating its associated covariate(s) and grouping factor, if any is present, in `data`, calculating various dimensions and constants used by optimization algorithms involving `corStruct` objects (see the appropriate `Dim` method documentation), and assigning initial values for the coefficients in `object`, if none were present.

### Usage

```
## S3 method for class 'corStruct':  
Initialize(object, data, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>corStruct</code> representing a correlation structure.
<code>data</code>	a data frame in which to evaluate the variables defined in <code>formula(object)</code> .
<code>...</code>	this argument is included to make this method compatible with the generic.

### Value

an initialized object with the same class as `object` representing a correlation structure.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

### References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

### See Also

[Dim.corStruct](#)

### Examples

```
cs1 <- corAR1(form = ~ 1 | Subject)  
cs1 <- Initialize(cs1, data = Orthodont)
```

---

`Initialize.glsStruct`*Initialize a glsStruct Object*

---

**Description**

The individual linear model components of the `glsStruct` list are initialized.

**Usage**

```
## S3 method for class 'glsStruct':  
Initialize(object, data, control, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>glsStruct</code> , representing a list of linear model components, such as <code>corStruct</code> and <code>varFunc</code> objects.
<code>data</code>	a data frame in which to evaluate the variables defined in <code>formula(object)</code> .
<code>control</code>	an optional list with control parameters for the initialization and optimization algorithms used in <code>gls</code> . Defaults to <code>list(singular.ok = FALSE, qrTol = .Machine\$single.eps)</code> , implying that linear dependencies are not allowed in the model and that the tolerance for detecting linear dependencies among the columns of the regression matrix is <code>.Machine\$single.eps</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a `glsStruct` object similar to `object`, but with initialized model components.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[gls](#), [Initialize.corStruct](#), [Initialize.varFunc](#), [Initialize](#)

---

`Initialize.lmeStruct`*Initialize an lmeStruct Object*

---

**Description**

The individual linear mixed-effects model components of the `lmeStruct` list are initialized.

**Usage**

```
## S3 method for class 'lmeStruct':
Initialize(object, data, groups, conLin, control, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>lmeStruct</code> , representing a list of linear mixed-effects model components, such as <code>reStruct</code> , <code>corStruct</code> , and <code>varFunc</code> objects.
<code>data</code>	a data frame in which to evaluate the variables defined in <code>formula(object)</code> .
<code>groups</code>	a data frame with the grouping factors corresponding to the lme model associated with <code>object</code> as columns, sorted from innermost to outermost grouping level.
<code>conLin</code>	an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying lme model. Defaults to <code>attr(object, "conLin")</code> .
<code>control</code>	an optional list with control parameters for the initialization and optimization algorithms used in lme. Defaults to <code>list(niterEM=20, gradHess=TRUE)</code> , implying that 20 EM iterations are to be used in the derivation of initial estimates for the coefficients of the <code>reStruct</code> component of <code>object</code> and, if possible, numerical gradient vectors and Hessian matrices for the log-likelihood function are to be used in the optimization algorithm.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

an `lmeStruct` object similar to `object`, but with initialized model components.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[lme](#), [Initialize.reStruct](#), [Initialize.corStruct](#), [Initialize.varFunc](#), [Initialize](#)

---

Initialize.reStruct

*Initialize reStruct Object*

---

**Description**

Initial estimates for the parameters in the `pdMat` objects forming `object`, which have not yet been initialized, are obtained using the methodology described in Bates and Pinheiro (1998). These estimates may be refined using a series of EM iterations, as described in Bates and Pinheiro (1998). The number of EM iterations to be used is defined in `control`.

**Usage**

```
## S3 method for class 'reStruct':
Initialize(object, data, conLin, control, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>reStruct</code> , representing a random effects structure and consisting of a list of <code>pdMat</code> objects.
<code>data</code>	a data frame in which to evaluate the variables defined in <code>formula(object)</code> .
<code>conLin</code>	a condensed linear model object, consisting of a list with components <code>"Xy"</code> , corresponding to a regression matrix ( $X$ ) combined with a response vector ( $y$ ), and <code>"logLik"</code> , corresponding to the log-likelihood of the underlying model.
<code>control</code>	an optional list with a single component <code>niterEM</code> controlling the number of iterations for the EM algorithm used to refine initial parameter estimates. It is given as a list for compatibility with other <code>Initialize</code> methods. Defaults to <code>list(niterEM = 20)</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

an `reStruct` object similar to `object`, but with all `pdMat` components initialized.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[reStruct](#), [pdMat](#), [Initialize](#)

---

Initialize.varFunc *Initialize varFunc Object*

---

**Description**

This method initializes `object` by evaluating its associated covariate(s) and grouping factor, if any is present, in `data`; determining if the covariate(s) need to be updated when the values of the coefficients associated with `object` change; initializing the log-likelihood and the weights associated with `object`; and assigning initial values for the coefficients in `object`, if none were present. The covariate(s) will only be initialized if no update is needed when `coef(object)` changes.

**Usage**

```
## S3 method for class 'varFunc':
Initialize(object, data, ...)
```

**Arguments**

`object` an object inheriting from class `varFunc`, representing a variance function structure.

`data` a data frame in which to evaluate the variables named in `formula(object)`.

`...` this argument is included to make this method compatible with the generic.

**Value**

an initialized object with the same class as `object` representing a variance function structure.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[Initialize](#)

**Examples**

```
vf1 <- varPower( form = ~ age | Sex )
vf1 <- Initialize( vf1, Orthodont )
```

---

intervals

*Confidence Intervals on Coefficients*

---

**Description**

Confidence intervals on the parameters associated with the model represented by `object` are obtained. This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `gls`, `lme`, and `lmList`.

**Usage**

```
intervals(object, level, ...)
```

**Arguments**

`object` a fitted model object from which parameter estimates can be extracted.

`level` an optional numeric value for the interval confidence level. Defaults to 0.95.

`...` some methods for the generic may require additional arguments.

**Value**

will depend on the method function used; see the appropriate documentation.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[intervals.lme](#), [intervals.lmList](#), [intervals.gls](#)

**Examples**

```
## see the method documentation
```

---

```
intervals.gls
```

*Confidence Intervals on gls Parameters*

---

**Description**

Approximate confidence intervals for the parameters in the linear model represented by `object` are obtained, using a normal approximation to the distribution of the (restricted) maximum likelihood estimators (the estimators are assumed to have a normal distribution centered at the true parameter values and with covariance matrix equal to the negative inverse Hessian matrix of the (restricted) log-likelihood evaluated at the estimated parameters). Confidence intervals are obtained in an unconstrained scale first, using the normal approximation, and, if necessary, transformed to the constrained scale.

**Usage**

```
## S3 method for class 'gls':
intervals(object, level, which, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>gls</code> , representing a generalized least squares fitted linear model.
<code>level</code>	an optional numeric value for the interval confidence level. Defaults to 0.95.
<code>which</code>	an optional character string specifying the subset of parameters for which to construct the confidence intervals. Possible values are "all" for all parameters, "var-cov" for the variance-covariance parameters only, and "coef" for the linear model coefficients only. Defaults to "all".
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a list with components given by data frames with rows corresponding to parameters and columns `lower`, `est`, and `upper` representing respectively lower confidence limits, the estimated values, and upper confidence limits for the parameters. Possible components are:

<code>coef</code>	linear model coefficients, only present when <code>which</code> is not equal to "var-cov".
<code>corStruct</code>	correlation parameters, only present when <code>which</code> is not equal to "coef" and a correlation structure is used in <code>object</code> .

varFunc        variance function parameters, only present when which is not equal to "coef" and a variance function structure is used in object.

sigma         residual standard error.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[gls](#), [intervals](#), [print.intervals.gls](#)

**Examples**

```
fml <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
          correlation = corAR1(form = ~ 1 | Mare))
intervals(fml)
```

---

intervals.lme

*Confidence Intervals on lme Parameters*


---

**Description**

Approximate confidence intervals for the parameters in the linear mixed-effects model represented by `object` are obtained, using a normal approximation to the distribution of the (restricted) maximum likelihood estimators (the estimators are assumed to have a normal distribution centered at the true parameter values and with covariance matrix equal to the negative inverse Hessian matrix of the (restricted) log-likelihood evaluated at the estimated parameters). Confidence intervals are obtained in an unconstrained scale first, using the normal approximation, and, if necessary, transformed to the constrained scale. The `pdNatural` parametrization is used for general positive-definite matrices.

**Usage**

```
## S3 method for class 'lme':
intervals(object, level, which, ...)
```

**Arguments**

`object`        an object inheriting from class `lme`, representing a fitted linear mixed-effects model.

`level`         an optional numeric value with the confidence level for the intervals. Defaults to 0.95.

`which`         an optional character string specifying the subset of parameters for which to construct the confidence intervals. Possible values are "all" for all parameters, "var-cov" for the variance-covariance parameters only, and "fixed" for the fixed effects only. Defaults to "all".

`...`         some methods for this generic require additional arguments. None are used in this method.

**Value**

a list with components given by data frames with rows corresponding to parameters and columns `lower`, `est.`, and `upper` representing respectively lower confidence limits, the estimated values, and upper confidence limits for the parameters. Possible components are:

<code>fixed</code>	fixed effects, only present when <code>which</code> is not equal to <code>"var-cov"</code> .
<code>reStruct</code>	random effects variance-covariance parameters, only present when <code>which</code> is not equal to <code>"fixed"</code> .
<code>corStruct</code>	within-group correlation parameters, only present when <code>which</code> is not equal to <code>"fixed"</code> and a correlation structure is used in <code>object</code> .
<code>varFunc</code>	within-group variance function parameters, only present when <code>which</code> is not equal to <code>"fixed"</code> and a variance function structure is used in <code>object</code> .
<code>sigma</code>	within-group standard deviation.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[lme](#), [intervals](#), [print.intervals.lme](#), [pdNatural](#)

**Examples**

```
fml <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
intervals(fml)
```

---

`intervals.lmList`     *Confidence Intervals on lmList Coefficients*

---

**Description**

Confidence intervals on the linear model coefficients are obtained for each `lm` component of `object` and organized into a three dimensional array. The first dimension corresponding to the names of the `object` components. The second dimension is given by `lower`, `est.`, and `upper` corresponding, respectively, to the lower confidence limit, estimated coefficient, and upper confidence limit. The third dimension is given by the coefficients names.

**Usage**

```
## S3 method for class 'lmList':
intervals(object, level, pool, ...)
```



**Arguments**

<code>object</code>	an object inheriting from class <code>lmList</code> , representing a list of <code>lm</code> objects with a common model.
<code>level</code>	an optional numeric value with the confidence level for the intervals. Defaults to 0.95.
<code>pool</code>	an optional logical value indicating whether a pooled estimate of the residual standard error should be used. Default is <code>attr(object, "pool")</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a three dimensional array with the confidence intervals and estimates for the coefficients of each `lm` component of `object`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[lmList](#), [intervals](#), [plot.intervals.lmList](#)

**Examples**

```
fml <- lmList(distance ~ age | Subject, Orthodont)
intervals(fml)
```

---

isBalanced

*Check a Design for Balance*

---

**Description**

Check the design of the experiment or study for balance.

**Usage**

```
isBalanced(object, countOnly, level)
```

**Arguments**

object	A <code>groupedData</code> object containing a data frame and a formula that describes the roles of variables in the data frame. The object will have one or more nested grouping factors and a primary covariate.
countOnly	A logical value indicating if the check for balance should only consider the number of observations at each level of the grouping factor(s). Defaults to <code>FALSE</code> .
level	an optional integer vector specifying the desired prediction levels. Levels increase from outermost to innermost grouping, with level 0 representing the population (fixed effects) predictions. Defaults to the innermost level.

**Details**

A design is balanced with respect to the grouping factor(s) if there are the same number of observations at each distinct value of the grouping factor or each combination of distinct levels of the nested grouping factors. If `countOnly` is `FALSE` the design is also checked for balance with respect to the primary covariate, which is often the time of the observation. A design is balanced with respect to the grouping factor and the covariate if the number of observations at each distinct level (or combination of levels for nested factors) is constant and the times at which the observations are taken (in general, the values of the primary covariates) also are constant.

**Value**

`TRUE` or `FALSE` according to whether the data are balanced or not

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[table](#), [groupedData](#)

**Examples**

```
isBalanced(Orthodont)           # should return TRUE
isBalanced(Orthodont, countOnly = TRUE) # should return TRUE
isBalanced(Pixel)               # should return FALSE
isBalanced(Pixel, level = 1)    # should return FALSE
```

---

isInitialized      *Check if Object is Initialized*

---

**Description**

Checks if `object` has been initialized (generally through a call to `Initialize`), by searching for components and attributes which are modified during initialization.

**Usage**

```
isInitialized(object)
```

**Arguments**

`object` any object requiring initialization.

**Value**

a logical value indicating whether `object` has been initialized.

**Author(s)**

Jose Pinheiro and Douglas Bates

**See Also**

[Initialize](#)

**Examples**

```
pd1 <- pdDiag(~age)
isInitialized(pd1)
```

---

LDEsysMat

*Generate system matrix for LDEs*

---

**Description**

Generate the system matrix for the linear differential equations determined by a compartment model.

**Usage**

```
LDEsysMat(pars, incidence)
```

**Arguments**

`pars` a numeric vector of parameter values.

`incidence` an integer matrix with columns named `From`, `To`, and `Par`. Values in the `Par` column must be in the range 1 to `length(pars)`. Values in the `From` column must be between 1 and the number of compartments. Values in the `To` column must be between 0 and the number of compartments.

**Details**

A compartment model describes material transfer between  $k$  in a system of  $k$  compartments to a linear system of differential equations. Given a description of the system and a vector of parameter values this function returns the system matrix.

This function is intended for use in a general system for solving compartment models, as described in Bates and Watts (1988).

**Value**

A  $k$  by  $k$  numeric matrix.

**Author(s)**

Douglas Bates <bates@stat.wisc.edu>

**References**

Bates, D. M. and Watts, D. G. (1988), *Nonlinear Regression Analysis and Its Applications*, Wiley, New York.

**Examples**

```
# incidence matrix for a two compartment open system
incidence <-
  matrix(c(1,1,2,2,2,1,3,2,0), ncol = 3, byrow = TRUE,
        dimnames = list(NULL, c("Par", "From", "To")))
incidence
LDEsysMat(c(1.2, 0.3, 0.4), incidence)
```

---

lme

*Linear Mixed-Effects Models*


---

**Description**

This generic function fits a linear mixed-effects model in the formulation described in Laird and Ware (1982) but allowing for nested random effects. The within-group errors are allowed to be correlated and/or have unequal variances.

**Usage**

```
lme(fixed, data, random, correlation, weights, subset, method,
    na.action, control, contrasts = NULL, keep.data = TRUE)
## S3 method for class 'lme':
update(object, fixed., ..., evaluate = TRUE)
```

**Arguments**

object	an object inheriting from class <code>lme</code> , representing a fitted linear mixed-effects model.
fixed	a two-sided linear formula object describing the fixed-effects part of the model, with the response on the left of a <code>~</code> operator and the terms, separated by <code>+</code> operators, on the right, an <code>lmList</code> object, or a <code>groupedData</code> object. The method functions <code>lme.lmList</code> and <code>lme.groupedData</code> are documented separately.
fixed.	Changes to the fixed-effects formula – see <code>update.formula</code> for details.
data	an optional data frame containing the variables named in <code>fixed</code> , <code>random</code> , <code>correlation</code> , <code>weights</code> , and <code>subset</code> . By default the variables are taken from the environment from which <code>lme</code> is called.
random	optionally, any of the following: (i) a one-sided formula of the form <code>~x1+...+xn   g1/.../gm</code> , with <code>x1+...+xn</code> specifying the model for the random effects and <code>g1/.../gm</code> the grouping structure ( <code>m</code> may be equal to 1, in which case no <code>/</code> is required). The random effects formula will be repeated for all levels of grouping, in the case of multiple levels of grouping; (ii) a list

of one-sided formulas of the form  $\sim x_1 + \dots + x_n \mid g$ , with possibly different random effects models for each grouping level. The order of nesting will be assumed the same as the order of the elements in the list; (iii) a one-sided formula of the form  $\sim x_1 + \dots + x_n$ , or a `pdMat` object with a formula (i.e. a non-NULL value for `formula(object)`), or a list of such formulas or `pdMat` objects. In this case, the grouping structure formula will be derived from the data used to fit the linear mixed-effects model, which should inherit from class `groupedData`; (iv) a named list of formulas or `pdMat` objects as in (iii), with the grouping factors as names. The order of nesting will be assumed the same as the order of the elements in the list; (v) an `reStruct` object. See the documentation on `pdClasses` for a description of the available `pdMat` classes. Defaults to a formula consisting of the right hand side of `fixed`.

<code>correlation</code>	an optional <code>corStruct</code> object describing the within-group correlation structure. See the documentation of <code>corClasses</code> for a description of the available <code>corStruct</code> classes. Defaults to <code>NULL</code> , corresponding to no within-group correlations.
<code>weights</code>	an optional <code>varFunc</code> object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to <code>varFixed</code> , corresponding to fixed variance weights. See the documentation on <code>varClasses</code> for a description of the available <code>varFunc</code> classes. Defaults to <code>NULL</code> , corresponding to homoscedastic within-group errors.
<code>subset</code>	an optional expression indicating the subset of the rows of <code>data</code> that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
<code>method</code>	a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "REML".
<code>na.action</code>	a function that indicates what should happen when the data contain NAs. The default action ( <code>na.fail</code> ) causes <code>lme</code> to print an error message and terminate if there are any incomplete observations.
<code>control</code>	a list of control values for the estimation algorithm to replace the default values returned by the function <code>lmeControl</code> . Defaults to an empty list.
<code>contrasts</code>	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
<code>keep.data</code>	logical: should the <code>data</code> argument (if supplied and a data frame) be saved as part of the model object?
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.
<code>evaluate</code>	If <code>TRUE</code> evaluate the new call else return the call.

**Value**

an object of class `lme` representing the linear mixed-effects model fit. Generic functions such as `print`, `plot` and `summary` have methods to show the results of the fit. See `lmeObject` for the components of the fit. The functions `resid`, `coef`, `fitted`, `fixed.effects`, and `random.effects` can be used to extract some of its components.

**Author(s)**

Jose Pinheiro <jose.pinhoiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

## References

The computational methods follow the general framework of Lindstrom and Bates (1988). The model formulation is described in Laird and Ware (1982). The variance-covariance parametrizations are described in Pinheiro and Bates (1996). The different correlation structures available for the `correlation` argument are described in Box, Jenkins and Reinsel (1994), Littell *et al* (1996), and Venables and Ripley, (1997). The use of variance functions for linear and nonlinear mixed effects models is presented in detail in Davidian and Giltinan (1995).

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Venables, W.N. and Ripley, B.D. (2002) "Modern Applied Statistics with S", 4th Edition, Springer-Verlag.

## See Also

[corClasses](#), [lme.lmList](#), [lme.groupedData](#), [lmeControl](#), [lmeObject](#), [lmeStruct](#), [lmList](#), [pdClasses](#), [plot.lme](#), [predict.lme](#), [qqnorm.lme](#), [residuals.lme](#), [reStruct](#), [simulate.lme](#), [summary.lme](#), [varClasses](#), [varFunc](#)

## Examples

```
fm1 <- lme(distance ~ age, data = Orthodont) # random is ~ age
fm2 <- lme(distance ~ age + Sex, data = Orthodont, random = ~ 1)
summary(fm1)
summary(fm2)
```

---

`lme.groupedData`      *LME fit from groupedData Object*

---

## Description

The response variable and primary covariate in `formula` (`fixed`) are used to construct the fixed effects model formula. This formula and the `groupedData` object are passed as the `fixed` and `data` arguments to `lme.formula`, together with any other additional arguments in the function call. See the documentation on `lme.formula` for a description of that function.

**Usage**

```
## S3 method for class 'groupedData':
lme(fixed, data, random, correlation, weights,
    subset, method, na.action, control, contrasts, keep.data = TRUE)
```

**Arguments**

<code>fixed</code>	a data frame inheriting from class <code>groupedData</code> .
<code>data</code>	this argument is included for consistency with the generic function. It is ignored in this method function.
<code>random</code>	optionally, any of the following: (i) a one-sided formula of the form $\sim x_1 + \dots + x_n \mid g_1 / \dots / g_m$ , with $x_1 + \dots + x_n$ specifying the model for the random effects and $g_1 / \dots / g_m$ the grouping structure ( $m$ may be equal to 1, in which case no $/$ is required). The random effects formula will be repeated for all levels of grouping, in the case of multiple levels of grouping; (ii) a list of one-sided formulas of the form $\sim x_1 + \dots + x_n \mid g$ , with possibly different random effects models for each grouping level. The order of nesting will be assumed the same as the order of the elements in the list; (iii) a one-sided formula of the form $\sim x_1 + \dots + x_n$ , or a <code>pdMat</code> object with a formula (i.e. a non-NULL value for <code>formula(object)</code> ), or a list of such formulas or <code>pdMat</code> objects. In this case, the grouping structure formula will be derived from the data used to fit the linear mixed-effects model, which should inherit from class <code>groupedData</code> ; (iv) a named list of formulas or <code>pdMat</code> objects as in (iii), with the grouping factors as names. The order of nesting will be assumed the same as the order of the order of the elements in the list; (v) an <code>reStruct</code> object. See the documentation on <code>pdClasses</code> for a description of the available <code>pdMat</code> classes. Defaults to a formula consisting of the right hand side of <code>fixed</code> .
<code>correlation</code>	an optional <code>corStruct</code> object describing the within-group correlation structure. See the documentation of <code>corClasses</code> for a description of the available <code>corStruct</code> classes. Defaults to <code>NULL</code> , corresponding to no within-group correlations.
<code>weights</code>	an optional <code>varFunc</code> object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to <code>varFixed</code> , corresponding to fixed variance weights. See the documentation on <code>varClasses</code> for a description of the available <code>varFunc</code> classes. Defaults to <code>NULL</code> , corresponding to homoscedastic within-group errors.
<code>subset</code>	an optional expression indicating the subset of the rows of <code>data</code> that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
<code>method</code>	a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "REML".
<code>na.action</code>	a function that indicates what should happen when the data contain NAs. The default action ( <code>na.fail</code> ) causes <code>lme</code> to print an error message and terminate if there are any incomplete observations.
<code>control</code>	a list of control values for the estimation algorithm to replace the default values returned by the function <code>lmeControl</code> . Defaults to an empty list.
<code>contrasts</code>	an optional list. See the <code>contrasts.arg</code> of <code>model.matrix.default</code> .
<code>keep.data</code>	logical: should the <code>data</code> argument (if supplied and a data frame) be saved as part of the model object?

**Value**

an object of class `lme` representing the linear mixed-effects model fit. Generic functions such as `print`, `plot` and `summary` have methods to show the results of the fit. See `lmeObject` for the components of the fit. The functions `resid`, `coef`, `fitted`, `fixed.effects`, and `random.effects` can be used to extract some of its components.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

The computational methods follow on the general framework of Lindstrom, M.J. and Bates, D.M. (1988). The model formulation is described in Laird, N.M. and Ware, J.H. (1982). The variance-covariance parametrizations are described in Pinheiro, J.C. and Bates., D.M. (1996). The different correlation structures available for the `correlation` argument are described in Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994), Littell, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996), and Venables, W.N. and Ripley, B.D. (1997). The use of variance functions for linear and nonlinear mixed effects models is presented in detail in Davidian, M. and Giltinan, D.M. (1995).

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

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Laird, N.M. and Ware, J.H. (1982) "Random-Effects Models for Longitudinal Data", *Biometrics*, 38, 963-974.

Lindstrom, M.J. and Bates, D.M. (1988) "Newton-Raphson and EM Algorithms for Linear Mixed-Effects Models for Repeated-Measures Data", *Journal of the American Statistical Association*, 83, 1014-1022.

Littell, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996) "SAS Systems for Mixed Models", SAS Institute.

Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", *Statistics and Computing*, 6, 289-296.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

Venables, W.N. and Ripley, B.D. (1997) "Modern Applied Statistics with S-plus", 2nd Edition, Springer-Verlag.

**See Also**

[lme](#), [groupedData](#), [lmeObject](#)

**Examples**

```
fml <- lme(Orthodont)
summary(fml)
```



lme.lmList

*LME fit from lmList Object***Description**

If the random effects names defined in `random` are a subset of the `lmList` object coefficient names, initial estimates for the covariance matrix of the random effects are obtained (overwriting any values given in `random`). `formula(fixed)` and the `data` argument in the calling sequence used to obtain `fixed` are passed as the `fixed` and `data` arguments to `lme.formula`, together with any other additional arguments in the function call. See the documentation on `lme.formula` for a description of that function.

**Usage**

```
## S3 method for class 'lmList':
lme(fixed, data, random, correlation, weights, subset, method,
    na.action, control, contrasts, keep.data)
```

**Arguments**

<code>fixed</code>	an object inheriting from class <code>lmList</code> , representing a list of <code>lm</code> fits with a common model.
<code>data</code>	this argument is included for consistency with the generic function. It is ignored in this method function.
<code>random</code>	an optional one-sided linear formula with no conditioning expression, or a <code>pdMat</code> object with a <code>formula</code> attribute. Multiple levels of grouping are not allowed with this method function. Defaults to a formula consisting of the right hand side of <code>formula(fixed)</code> .
<code>correlation</code>	an optional <code>corStruct</code> object describing the within-group correlation structure. See the documentation of <code>corClasses</code> for a description of the available <code>corStruct</code> classes. Defaults to <code>NULL</code> , corresponding to no within-group correlations.
<code>weights</code>	an optional <code>varFunc</code> object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to <code>varFixed</code> , corresponding to fixed variance weights. See the documentation on <code>varClasses</code> for a description of the available <code>varFunc</code> classes. Defaults to <code>NULL</code> , corresponding to homoscedastic within-group errors.
<code>subset</code>	an optional expression indicating the subset of the rows of <code>data</code> that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
<code>method</code>	a character string. If <code>"REML"</code> the model is fit by maximizing the restricted log-likelihood. If <code>"ML"</code> the log-likelihood is maximized. Defaults to <code>"REML"</code> .
<code>na.action</code>	a function that indicates what should happen when the data contain <code>NA</code> s. The default action ( <code>na.fail</code> ) causes <code>lme</code> to print an error message and terminate if there are any incomplete observations.
<code>control</code>	a list of control values for the estimation algorithm to replace the default values returned by the function <code>lmeControl</code> . Defaults to an empty list.

`contrasts` an optional list. See the `contrasts.arg` of `model.matrix.default`.  
`keep.data` logical: should the data argument (if supplied and a data frame) be saved as part of the model object?

### Value

an object of class `lme` representing the linear mixed-effects model fit. Generic functions such as `print`, `plot` and `summary` have methods to show the results of the fit. See `lmeObject` for the components of the fit. The functions `resid`, `coef`, `fitted`, `fixed.effects`, and `random.effects` can be used to extract some of its components.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

The computational methods follow the general framework of Lindstrom and Bates (1988). The model formulation is described in Laird and Ware (1982). The variance-covariance parametrizations are described in Pinheiro and Bates (1996). The different correlation structures available for the `correlation` argument are described in Box, Jenkins and Reinsel (1994), Littell *et al* (1996), and Venables and Ripley, (1997). The use of variance functions for linear and nonlinear mixed effects models is presented in detail in Davidian and Giltinan (1995).

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Davidian, M. and Giltinan, D.M. (1995) "Nonlinear Mixed Effects Models for Repeated Measurement Data", Chapman and Hall.

Laird, N.M. and Ware, J.H. (1982) "Random-Effects Models for Longitudinal Data", *Biometrics*, 38, 963–974.

Lindstrom, M.J. and Bates, D.M. (1988) "Newton-Raphson and EM Algorithms for Linear Mixed-Effects Models for Repeated-Measures Data", *Journal of the American Statistical Association*, 83, 1014–1022.

Littell, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996) "SAS Systems for Mixed Models", SAS Institute.

Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", *Statistics and Computing*, 6, 289–296.

Venables, W.N. and Ripley, B.D. (2002) "Modern Applied Statistics with S", 4th Edition, Springer-Verlag.

### See Also

[lme](#), [lmList](#), [lmeObject](#)

### Examples

```
fm1 <- lmList(Orthodont)
fm2 <- lme(fm1)
summary(fm1)
summary(fm2)
```

---

lmeControl

*Control Values for lme Fit*


---

### Description

The values supplied in the function call replace the defaults and a list with all possible arguments is returned. The returned list is used as the `control` argument to the `lme` function.

### Usage

```
lmeControl(maxIter, msMaxIter, tolerance, niterEM, msMaxEval, msTol,
           msScale, msVerbose, returnObject, gradHess, apVar,
           .relStep, minAbsParApVar, nlmStepMax,
           opt = c("nlminb", "optim"), optimMethod,
           natural)
```

### Arguments

<code>maxIter</code>	maximum number of iterations for the <code>lme</code> optimization algorithm. Default is 50.
<code>msMaxIter</code>	maximum number of iterations for the <code>nlm</code> optimization step inside the <code>lme</code> optimization. Default is 50.
<code>tolerance</code>	tolerance for the convergence criterion in the <code>lme</code> algorithm. Default is 1e-6.
<code>niterEM</code>	number of iterations for the EM algorithm used to refine the initial estimates of the random effects variance-covariance coefficients. Default is 25.
<code>msMaxEval</code>	maximum number of evaluations of the objective function permitted for <code>nlminb</code> . Default is 200.
<code>msTol</code>	tolerance for the convergence criterion in <code>nlm</code> , passed as the <code>rel.tolerance</code> argument to the function (see documentation on <code>nlm</code> ). Default is 1e-7.
<code>msScale</code>	scale function passed as the <code>scale</code> argument to the <code>nlm</code> function (see documentation on that function). Default is <code>lmeScale</code> .
<code>msVerbose</code>	a logical value passed as the <code>trace</code> argument to <code>nlm</code> (see documentation on that function). Default is <code>FALSE</code> .
<code>returnObject</code>	a logical value indicating whether the fitted object should be returned when the maximum number of iterations is reached without convergence of the algorithm. Default is <code>FALSE</code> .
<code>gradHess</code>	a logical value indicating whether numerical gradient vectors and Hessian matrices of the log-likelihood function should be used in the <code>nlm</code> optimization. This option is only available when the correlation structure ( <code>corStruct</code> ) and the variance function structure ( <code>varFunc</code> ) have no "varying" parameters and the <code>pdMat</code> classes used in the random effects structure are <code>pdSymm</code> (general positive-definite), <code>pdDiag</code> (diagonal), <code>pdIdent</code> (multiple of the identity), or <code>pdCompSymm</code> (compound symmetry). Default is <code>TRUE</code> .
<code>apVar</code>	a logical value indicating whether the approximate covariance matrix of the variance-covariance parameters should be calculated. Default is <code>TRUE</code> .
<code>.relStep</code>	relative step for numerical derivatives calculations. Default is <code>.Machine\$double.eps^(1/3)</code> .

nlmStepMax	stepmax value to be passed to nlm. See <a href="#">nlm</a> for details. Default is 100.0
opt	the optimizer to be used, either <a href="#">nlminb</a> (the default since (R 2.2.0) or <a href="#">optim</a> (the previous default).
optimMethod	character - the optimization method to be used with the <a href="#">optim</a> optimizer. The default is "BFGS". An alternative is "L-BFGS-B".
minAbsParApVar	numeric value - minimum absolute parameter value in the approximate variance calculation. The default is 0.05.
natural	a logical value indicating whether the <code>pdNatural</code> parametrization should be used for general positive-definite matrices ( <code>pdSymm</code> ) in <code>reStruct</code> , when the approximate covariance matrix of the estimators is calculated. Default is <code>TRUE</code> .

**Value**

a list with components for each of the possible arguments.

**Author(s)**

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**See Also**

[lme](#), [nlm](#), [optim](#), [lmeScale](#)

**Examples**

```
# decrease the maximum number iterations in the ms call and
# request that information on the evolution of the ms iterations be printed
lmeControl(msMaxIter = 20, msVerbose = TRUE)
```

---

lmeObject

*Fitted lme Object*


---

**Description**

An object returned by the `lme` function, inheriting from class `lme` and representing a fitted linear mixed-effects model. Objects of this class have methods for the generic functions `anova`, `coef`, `fitted`, `fixed.effects`, `formula`, `getGroups`, `getResponse`, `intervals`, `logLik`, `pairs`, `plot`, `predict`, `print`, `random.effects`, `residuals`, `summary`, and `update`.

**Value**

The following components must be included in a legitimate `lme` object.

apVar	an approximate covariance matrix for the variance-covariance coefficients. If <code>apVar = FALSE</code> in the list of control values used in the call to <code>lme</code> , this component is equal to <code>NULL</code> .
call	a list containing an image of the <code>lme</code> call that produced the object.

<code>coefficients</code>	a list with two components, <code>fixed</code> and <code>random</code> , where the first is a vector containing the estimated fixed effects and the second is a list of matrices with the estimated random effects for each level of grouping. For each matrix in the <code>random</code> list, the columns refer to the random effects and the rows to the groups.
<code>contrasts</code>	a list with the contrasts used to represent factors in the fixed effects formula and/or random effects formula. This information is important for making predictions from a new data frame in which not all levels of the original factors are observed. If no factors are used in the lme model, this component will be an empty list.
<code>dims</code>	a list with basic dimensions used in the lme fit, including the components <code>N</code> - the number of observations in the data, <code>Q</code> - the number of grouping levels, <code>qvec</code> - the number of random effects at each level from innermost to outermost (last two values are equal to zero and correspond to the fixed effects and the response), <code>ngrps</code> - the number of groups at each level from innermost to outermost (last two values are one and correspond to the fixed effects and the response), and <code>ncol</code> - the number of columns in the model matrix for each level of grouping from innermost to outermost (last two values are equal to the number of fixed effects and one).
<code>fitted</code>	a data frame with the fitted values as columns. The leftmost column corresponds to the population fixed effects (corresponding to the fixed effects only) and successive columns from left to right correspond to increasing levels of grouping.
<code>fixDF</code>	a list with components <code>X</code> and <code>terms</code> specifying the denominator degrees of freedom for, respectively, t-tests for the individual fixed effects and F-tests for the fixed-effects terms in the models.
<code>groups</code>	a data frame with the grouping factors as columns. The grouping level increases from left to right.
<code>logLik</code>	the (restricted) log-likelihood at convergence.
<code>method</code>	the estimation method: either "ML" for maximum likelihood, or "REML" for restricted maximum likelihood.
<code>modelStruct</code>	an object inheriting from class <code>lmeStruct</code> , representing a list of mixed-effects model components, such as <code>reStruct</code> , <code>corStruct</code> , and <code>varFunc</code> objects.
<code>numIter</code>	the number of iterations used in the iterative algorithm.
<code>residuals</code>	a data frame with the residuals as columns. The leftmost column corresponds to the population residuals and successive columns from left to right correspond to increasing levels of grouping.
<code>sigma</code>	the estimated within-group error standard deviation.
<code>varFix</code>	an approximate covariance matrix of the fixed effects estimates.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[lme](#), `lmeStruct`

---

`lmeScale`*Scale for lme Optimization*

---

**Description**

This function calculates the scales to be used for each coefficient estimated through an `nlm` optimization in the `lme` function. If all initial values are zero, the scale is set to one for all coefficients; else, the scale for a coefficient with non-zero initial value is equal to the inverse of its initial value and the scale for the coefficients with initial value equal to zero is set to the median of the non-zero initial value coefficients.

**Usage**

```
lmeScale(start)
```

**Arguments**

`start`            the starting values for the coefficients to be estimated.

**Value**

a vector with the scales to be used in `nlm` for estimating the coefficients.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[nlm](#)

---

`lmeStruct`*Linear Mixed-Effects Structure*

---

**Description**

A linear mixed-effects structure is a list of model components representing different sets of parameters in the linear mixed-effects model. An `lmeStruct` list must contain at least a `reStruct` object, but may also contain `corStruct` and `varFunc` objects. `NULL` arguments are not included in the `lmeStruct` list.

**Usage**

```
lmeStruct(reStruct, corStruct, varStruct)
```

**Arguments**

reStruct	a reStruct representing a random effects structure.
corStruct	an optional corStruct object, representing a correlation structure. Default is NULL.
varStruct	an optional varFunc object, representing a variance function structure. Default is NULL.

**Value**

a list of model components determining the parameters to be estimated for the associated linear mixed-effects model.

**Author(s)**

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**See Also**

[corClasses](#), [lme](#), [residuals.lmeStruct](#), [reStruct](#), [varFunc](#)

**Examples**

```
lms1 <- lmeStruct(reStruct(~age), corAR1(), varPower())
```

---

lmList

---

*List of lm Objects with a Common Model*


---

**Description**

Data is partitioned according to the levels of the grouping factor `g` and individual `lm` fits are obtained for each data partition, using the model defined in `object`.

**Usage**

```
lmList(object, data, level, subset, na.action, pool)
## S3 method for class 'lmList':
update(object, formula., ..., evaluate = TRUE)
## S3 method for class 'lmList':
print(x, pool, ...)
```

**Arguments**

`object` For `lmList`, either a linear formula object of the form `y ~ x1+...+xn | g` or a `groupedData` object. In the formula object, `y` represents the response, `x1, ..., xn` the covariates, and `g` the grouping factor specifying the partitioning of the data according to which different `lm` fits should be performed. The grouping factor `g` may be omitted from the formula, in which case the grouping structure will be obtained from `data`, which must inherit from class `groupedData`. The method function `lmList.groupedData` is documented separately. For the method `update.lmList`, `object` is an object inheriting from class `lmList`.

<code>formula</code>	(used in <code>update.lmList</code> only) a two-sided linear formula with the common model for the individuals <code>lm</code> fits.
<code>formula.</code>	Changes to the formula – see <code>update.formula</code> for details.
<code>data</code>	a data frame in which to interpret the variables named in <code>object</code> .
<code>level</code>	an optional integer specifying the level of grouping to be used when multiple nested levels of grouping are present.
<code>subset</code>	an optional expression indicating which subset of the rows of <code>data</code> should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
<code>na.action</code>	a function that indicates what should happen when the data contain NAs. The default action ( <code>na.fail</code> ) causes <code>lmList</code> to print an error message and terminate if there are any incomplete observations.
<code>pool</code>	an optional logical value indicating whether a pooled estimate of the residual standard error should be used in calculations of standard deviations or standard errors for summaries.
<code>x</code>	an object inheriting from class <code>lmList</code> to be printed.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.
<code>evaluate</code>	If <code>TRUE</code> evaluate the new call else return the call.

### Value

a list of `lm` objects with as many components as the number of groups defined by the grouping factor. Generic functions such as `coef`, `fixed.effects`, `lme`, `pairs`, `plot`, `predict`, `random.effects`, `summary`, and `update` have methods that can be applied to an `lmList` object.

### References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

### See Also

[lm](#), [lme.lmList](#), [plot.lmList](#), [pooledSD](#), [predict.lmList](#), [residuals.lmList](#), [summary.lmList](#)

### Examples

```
fml <- lmList(distance ~ age | Subject, Orthodont)
summary(fml)
```



---

lmList.groupedData *lmList Fit from a groupedData Object*

---

### Description

The response variable and primary covariate in `formula(object)` are used to construct the linear model formula. This formula and the `groupedData` object are passed as the `object` and `data` arguments to `lmList.formula`, together with any other additional arguments in the function call. See the documentation on `lmList.formula` for a description of that function.

### Usage

```
## S3 method for class 'groupedData':
lmList(object, data, level, subset, na.action, pool)
```

### Arguments

<code>object</code>	a data frame inheriting from class <code>groupedData</code> .
<code>data</code>	this argument is included for consistency with the generic function. It is ignored in this method function.
<code>level</code>	an optional integer specifying the level of grouping to be used when multiple nested levels of grouping are present.
<code>subset</code>	an optional expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
<code>na.action</code>	a function that indicates what should happen when the data contain NAs. The default action ( <code>na.fail</code> ) causes <code>lmList</code> to print an error message and terminate if there are any incomplete observations.
<code>pool</code>	an optional logical value that is preserved as an attribute of the returned value. This will be used as the default for <code>pool</code> in calculations of standard deviations or standard errors for summaries.

### Value

a list of `lm` objects with as many components as the number of groups defined by the grouping factor. Generic functions such as `coef`, `fixed.effects`, `lme`, `pairs`, `plot`, `predict`, `random.effects`, `summary`, and `update` have methods that can be applied to an `lmList` object.

### See Also

[groupedData](#), [lm](#), [lme.lmList](#), [lmList](#), [lmList.formula](#)

### Examples

```
fml <- lmList(Orthodont)
summary(fml)
```

---

logDet

---

*Extract the Logarithm of the Determinant*


---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `corStruct`, several `pdMat` classes, and `reStruct`.

**Usage**

```
logDet(object, ...)
```

**Arguments**

<code>object</code>	any object from which a matrix, or list of matrices, can be extracted
<code>...</code>	some methods for this generic function require additional arguments.

**Value**

will depend on the method function used; see the appropriate documentation.

**Author(s)**

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**See Also**

[logLik](#), [logDet.corStruct](#), [logDet.pdMat](#), [logDet.reStruct](#)

**Examples**

```
## see the method function documentation
```

---

logDet.corStruct

---

*Extract corStruct Log-Determinant*


---

**Description**

This method function extracts the logarithm of the determinant of a square-root factor of the correlation matrix associated with `object`, or the sum of the log-determinants of square-root factors of the list of correlation matrices associated with `object`.

**Usage**

```
## S3 method for class 'corStruct':
logDet(object, covariate, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>corStruct</code> , representing a correlation structure.
<code>covariate</code>	an optional covariate vector (matrix), or list of covariate vectors (matrices), at which values the correlation matrix, or list of correlation matrices, are to be evaluated. Defaults to <code>getCovariate(object)</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

the log-determinant of a square-root factor of the correlation matrix associated with `object`, or the sum of the log-determinants of square-root factors of the list of correlation matrices associated with `object`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[logLik.corStruct](#), [corMatrix.corStruct](#), [logDet](#)

**Examples**

```
cs1 <- corAR1(0.3)
logDet(cs1, covariate = 1:4)
```

---

logDet.pdMat

*Extract Log-Determinant from a pdMat Object*

---

**Description**

This method function extracts the logarithm of the determinant of a square-root factor of the positive-definite matrix represented by `object`.

**Usage**

```
## S3 method for class 'pdMat':
logDet(object, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>pdMat</code> , representing a positive definite matrix.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

the log-determinant of a square-root factor of the positive-definite matrix represented by `object`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[pdMat](#), [logDet](#)

**Examples**

```
pd1 <- pdSymm(diag(1:3))
logDet(pd1)
```

---

logDet.reStruct      *Extract reStruct Log-Determinants*

---

**Description**

Calculates, for each of the `pdMat` components of `object`, the logarithm of the determinant of a square-root factor.

**Usage**

```
## S3 method for class 'reStruct':
logDet(object, ...)
```

**Arguments**

`object`      an object inheriting from class `reStruct`, representing a random effects structure and consisting of a list of `pdMat` objects.

`...`      some methods for this generic require additional arguments. None are used in this method.

**Value**

a vector with the log-determinants of square-root factors of the `pdMat` components of `object`.

**Author(s)**

Jose Pinheiro

**See Also**

[reStruct](#), [pdMat](#), [logDet](#)

**Examples**

```
rs1 <- reStruct(list(A = pdSymm(diag(1:3)), form = ~Score),
  B = pdDiag(2 * diag(4), form = ~Educ))
logDet(rs1)
```

---

logLik.corStruct    *Extract corStruct Log-Likelihood*

---

### Description

This method function extracts the component of a Gaussian log-likelihood associated with the correlation structure, which is equal to the negative of the logarithm of the determinant (or sum of the logarithms of the determinants) of the matrix (or matrices) represented by `object`.

### Usage

```
## S3 method for class 'corStruct':  
logLik(object, data, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>corStruct</code> , representing a correlation structure.
<code>data</code>	this argument is included to make this method function compatible with other <code>logLik</code> methods and will be ignored.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

the negative of the logarithm of the determinant (or sum of the logarithms of the determinants) of the correlation matrix (or matrices) represented by `object`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[logDet.corStruct](#), [logLik.lme](#),

### Examples

```
cs1 <- corAR1(0.2)  
cs1 <- Initialize(cs1, data = Orthodont)  
logLik(cs1)
```

---

logLik.glsStruct     *Log-Likelihood of a glsStruct Object*

---

### Description

`Pars` is used to update the coefficients of the model components of `object` and the individual (restricted) log-likelihood contributions of each component are added together. The type of log-likelihood (restricted or not) is determined by the `settings` attribute of `object`.

### Usage

```
## S3 method for class 'glsStruct':
logLik(object, Pars, conLin, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>glsStruct</code> , representing a list of linear model components, such as <code>corStruct</code> and <code>varFunc</code> objects.
<code>Pars</code>	the parameter values at which the (restricted) log-likelihood is to be evaluated.
<code>conLin</code>	an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying linear model. Defaults to <code>attr(object, "conLin")</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

the (restricted) log-likelihood for the linear model described by `object`, evaluated at `Pars`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[gls](#), [glsStruct](#), [logLik.lme](#)

---

logLik.gnls     *Log-Likelihood of a gnls Object*

---

### Description

Returns the log-likelihood value of the nonlinear model represented by `object` evaluated at the estimated coefficients.

**Usage**

```
## S3 method for class 'gnls':
logLik(object, REML, ...)
```

**Arguments**

object	an object inheriting from class <code>gnls</code> , representing a generalized nonlinear least squares fitted model.
REML	an logical value for consistency with <code>logLik, gls</code> , but only <code>FALSE</code> is accepted..
...	some methods for this generic require additional arguments. None are used in this method.

**Value**

the log-likelihood of the linear model represented by `object` evaluated at the estimated coefficients.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[gnls](#), [logLik.lme](#)

**Examples**

```
fm1 <- gnls(weight ~ SSlogis(Time, Asym, xmid, scal), Soybean,
            weights = varPower())
logLik(fm1)
```

---

logLik.gnlsStruct *Log-Likelihood of a gnlsStruct Object*

---

**Description**

`Pars` is used to update the coefficients of the model components of `object` and the individual log-likelihood contributions of each component are added together.

**Usage**

```
## S3 method for class 'gnlsStruct':
logLik(object, Pars, conLin, ...)
```

**Arguments**

object	an object inheriting from class <code>gnlsStruct</code> , representing a list of model components, such as <code>corStruct</code> and <code>varFunc</code> objects, and attributes specifying the underlying nonlinear model and the response variable.
Pars	the parameter values at which the log-likelihood is to be evaluated.
conLin	an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying nonlinear model. Defaults to <code>attr(object, "conLin")</code> .
...	some methods for this generic require additional arguments. None are used in this method.

**Value**

the log-likelihood for the linear model described by `object`, evaluated at `Pars`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[gnls](#), [gnlsStruct](#), [logLik.gnls](#)

---

logLik.lme

*Log-Likelihood of an lme Object*

---

**Description**

If `REML=FALSE`, returns the log-likelihood value of the linear mixed-effects model represented by `object` evaluated at the estimated coefficients; else, the restricted log-likelihood evaluated at the estimated coefficients is returned.

**Usage**

```
## S3 method for class 'lme':
logLik(object, REML, ...)
```

**Arguments**

object	an object inheriting from class <code>lme</code> , representing a fitted linear mixed-effects model.
REML	an optional logical value. If <code>TRUE</code> the restricted log-likelihood is returned, else, if <code>FALSE</code> , the log-likelihood is returned. Defaults to the method of estimation used, that is <code>TRUE</code> if and only <code>object</code> was fitted with <code>method = "REML"</code> (the default for these fitting functions).
...	some methods for this generic require additional arguments. None are used in this method.



**Value**

the (restricted) log-likelihood of the model represented by `object` evaluated at the estimated coefficients.

**Author(s)**

Jose Pinheiro and Douglas Bates

**References**

Harville, D.A. (1974) "Bayesian Inference for Variance Components Using Only Error Contrasts", *Biometrika*, **61**, 383–385.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

`lme.gls`, `logLik.corStruct`, `logLik.glsStruct`, `logLik.lmeStruct`, `logLik.lmList`, `logLik.reStruct`, `logLik.varFunc`,

**Examples**

```
fml <- lme(distance ~ Sex * age, Orthodont, random = ~ age, method = "ML")
logLik(fml)
logLik(fml, REML = TRUE)
```

---

`logLik.lmeStruct`    *Log-Likelihood of an lmeStruct Object*

---

**Description**

`Pars` is used to update the coefficients of the model components of `object` and the individual (restricted) log-likelihood contributions of each component are added together. The type of log-likelihood (restricted or not) is determined by the `settings` attribute of `object`.

**Usage**

```
## S3 method for class 'lmeStruct':
logLik(object, Pars, conLin, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>lmeStruct</code> , representing a list of linear mixed-effects model components, such as <code>reStruct</code> , <code>corStruct</code> , and <code>varFunc</code> objects.
<code>Pars</code>	the parameter values at which the (restricted) log-likelihood is to be evaluated.
<code>conLin</code>	an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying lme model. Defaults to <code>attr(object, "conLin")</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

the (restricted) log-likelihood for the linear mixed-effects model described by `object`, evaluated at `Pars`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[lme](#), [lmeStruct](#), [logLik.lme](#)

---

`logLik.lmList`*Log-Likelihood of an lmList Object*

---

**Description**

If `pool=FALSE`, the (restricted) log-likelihoods of the `lm` components of `object` are summed together. Else, the (restricted) log-likelihood of the `lm` fit with different coefficients for each level of the grouping factor associated with the partitioning of the `object` components is obtained.

**Usage**

```
## S3 method for class 'lmList':  
logLik(object, REML, pool, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>lmList</code> , representing a list of <code>lm</code> objects with a common model.
<code>REML</code>	an optional logical value. If <code>TRUE</code> the restricted log-likelihood is returned, else, if <code>FALSE</code> , the log-likelihood is returned. Defaults to <code>FALSE</code> .
<code>pool</code>	an optional logical value indicating whether all <code>lm</code> components of <code>object</code> may be assumed to have the same error variance. Default is <code>attr(object, "pool")</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

either the sum of the (restricted) log-likelihoods of each `lm` component in `object`, or the (restricted) log-likelihood for the `lm` fit with separate coefficients for each component of `object`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[lmList](#), [logLik.lme](#),

**Examples**

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
logLik(fm1) # returns NA when it should not
```

---

logLik.reStruct      *Calculate reStruct Log-Likelihood*

---

**Description**

Calculates the log-likelihood, or restricted log-likelihood, of the Gaussian linear mixed-effects model represented by `object` and `conLin` (assuming spherical within-group covariance structure), evaluated at `coef(object)`. The `settings` attribute of `object` determines whether the log-likelihood, or the restricted log-likelihood, is to be calculated. The computational methods are described in Bates and Pinheiro (1998).

**Usage**

```
## S3 method for class 'reStruct':
logLik(object, conLin, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>reStruct</code> , representing a random effects structure and consisting of a list of <code>pdMat</code> objects.
<code>conLin</code>	a condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying model.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

the log-likelihood, or restricted log-likelihood, of linear mixed-effects model represented by `object` and `conLin`, evaluated at `coef{object}`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[reStruct](#), [pdMat](#), [logLik.lme](#)

---

logLik.varFunc      *Extract varFunc logLik*

---

### Description

This method function extracts the component of a Gaussian log-likelihood associated with the variance function structure represented by `object`, which is equal to the sum of the logarithms of the corresponding weights.

### Usage

```
## S3 method for class 'varFunc':  
logLik(object, data, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>varFunc</code> , representing a variance function structure.
<code>data</code>	this argument is included to make this method function compatible with other <code>logLik</code> methods and will be ignored.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

the sum of the logarithms of the weights corresponding to the variance function structure represented by `object`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[logLik.lme](#)

### Examples

```
vf1 <- varPower(form = ~age)  
vf1 <- Initialize(vf1, Orthodont)  
coef(vf1) <- 0.1  
logLik(vf1)
```

---

Machines

*Productivity Scores for Machines and Workers*


---

**Description**

The `Machines` data frame has 54 rows and 3 columns.

**Format**

This data frame contains the following columns:

**Worker** an ordered factor giving the unique identifier for the worker.

**Machine** a factor with levels A, B, and C identifying the machine brand.

**score** a productivity score.

**Details**

Data on an experiment to compare three brands of machines used in an industrial process are presented in Milliken and Johnson (p. 285, 1992). Six workers were chosen randomly among the employees of a factory to operate each machine three times. The response is an overall productivity score taking into account the number and quality of components produced.

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.14)

Milliken, G. A. and Johnson, D. E. (1992), *Analysis of Messy Data, Volume I: Designed Experiments*, Chapman and Hall, London.

---

MathAchieve

*Mathematics achievement scores*


---

**Description**

The `MathAchieve` data frame has 7185 rows and 6 columns.

**Format**

This data frame contains the following columns:

**School** an ordered factor identifying the school that the student attends

**Minority** a factor with levels `No` `Yes` indicating if the student is a member of a minority racial group.

**Sex** a factor with levels `Male` `Female`

**SES** a numeric vector of socio-economic status.

**MathAch** a numeric vector of mathematics achievement scores.

**MEANSES** a numeric vector of the mean SES for the school.

**Details**

Each row in this data frame contains the data for one student.

**Examples**

```
summary(MathAchieve)
```

---

MathAchSchool	<i>School demographic data for MathAchieve</i>
---------------	--

---

**Description**

The `MathAchSchool` data frame has 160 rows and 7 columns.

**Format**

This data frame contains the following columns:

**School** a factor giving the school on which the measurement is made.

**Size** a numeric vector giving the number of students in the school

**Sector** a factor with levels `Public Catholic`

**PRACAD** a numeric vector giving the percentage of students on the academic track

**DISCLIM** a numeric vector measuring the discrimination climate

**HIMINTY** a factor with levels `0 1`

**MEANSES** a numeric vector giving the mean SES score.

**Details**

These variables give the school-level demographic data to accompany the `MathAchieve` data.

---

<code>Matrix</code>	<i>Assign Matrix Values</i>
---------------------	-----------------------------

---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `pdMat`, `pdBlocked`, and `reStruct`.

**Usage**

```
matrix(object) <- value
```

**Arguments**

`object` any object to which `as.matrix` can be applied.

`value` a matrix, or list of matrices, with the same dimensions as `as.matrix(object)` with the new values to be assigned to the matrix associated with `object`.

**Value**

will depend on the method function; see the appropriate documentation.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[as.matrix](#)

**Examples**

```
## see the method function documentation
```

---

Matrix.pdMat

*Assign Matrix to a pdMat Object*

---

**Description**

The positive-definite matrix represented by `object` is replaced by `value`. If the original matrix had row and/or column names, the corresponding names for `value` can either be `NULL`, or a permutation of the original names.

**Usage**

```
## S3 replacement method for class 'pdMat':  
matrix(object) <- value
```

**Arguments**

`object` an object inheriting from class `pdMat`, representing a positive definite matrix.  
`value` a matrix with the new values to be assigned to the positive-definite matrix represented by `object`. Must have the same dimensions as `as.matrix(object)`.

**Value**

a `pdMat` object similar to `object`, but with its coefficients modified to produce the matrix in `value`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[pdMat, "matrix<-"](#)

## Examples

```
pd1 <- pdSymm(diag(3))
matrix(pd1) <- diag(1:3)
pd1
```

---

Matrix.reStruct      *Assign reStruct Matrices*

---

## Description

The individual matrices in `value` are assigned to each `pdMat` component of `object`, in the order they are listed. The new matrices must have the same dimensions as the matrices they are meant to replace.

## Usage

```
## S3 replacement method for class 'reStruct':
matrix(object) <- value
```

## Arguments

<code>object</code>	an object inheriting from class <code>reStruct</code> , representing a random effects structure and consisting of a list of <code>pdMat</code> objects.
<code>value</code>	a matrix, or list of matrices, with the new values to be assigned to the matrices associated with the <code>pdMat</code> components of <code>object</code> .

## Value

an `reStruct` object similar to `object`, but with the coefficients of the individual `pdMat` components modified to produce the matrices listed in `value`.

## Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

## See Also

[reStruct](#), [pdMat](#), "[matrix<-](#)"

## Examples

```
rs1 <- reStruct(list(Dog = ~day, Side = ~1), data = Pixel)
matrix(rs1) <- list(diag(2), 3)
```



Meat

*Tenderness of meat***Description**

The `Meat` data frame has 30 rows and 4 columns.

**Format**

This data frame contains the following columns:

**Storage** an ordered factor specifying the storage treatment - 1 (0 days), 2 (1 day), 3 (2 days), 4 (4 days), 5 (9 days), and 6 (18 days)

**score** a numeric vector giving the tenderness score of beef roast.

**Block** an ordered factor identifying the muscle from which the roast was extracted with levels `II < V < I < III < IV`

**Pair** an ordered factor giving the unique identifier for each pair of beef roasts with levels `II-1 < ... < IV-1`

**Details**

Cochran and Cox (section 11.51, 1957) describe data from an experiment conducted at Iowa State College (Paul, 1943) to compare the effects of length of cold storage on the tenderness of beef roasts. Six storage periods ranging from 0 to 18 days were used. Thirty roasts were scored by four judges on a scale from 0 to 10, with the score increasing with tenderness. The response was the sum of all four scores. Left and right roasts from the same animal were grouped into pairs, which were further grouped into five blocks, according to the muscle from which they were extracted. Different storage periods were applied to each roast within a pair according to a balanced incomplete block design.

**Source**

Cochran, W. G. and Cox, G. M. (1957), *Experimental Designs*, Wiley, New York.

Milk

*Protein content of cows' milk***Description**

The `Milk` data frame has 1337 rows and 4 columns.

**Format**

This data frame contains the following columns:

**protein** a numeric vector giving the protein content of the milk.

**Time** a numeric vector giving the time since calving (weeks).

**Cow** an ordered factor giving a unique identifier for each cow.

**Diet** a factor with levels `barley`, `barley+lupins`, and `lupins` identifying the diet for each cow.

## Details

Diggle, Liang, and Zeger (1994) describe data on the protein content of cows' milk in the weeks following calving. The cattle are grouped according to whether they are fed a diet with barley alone, with barley and lupins, or with lupins alone.

## Source

Diggle, Peter J., Liang, Kung-Yee and Zeger, Scott L. (1994), *Analysis of longitudinal data*, Oxford University Press, Oxford.

---

```
model.matrix.reStruct  
      reStruct Model Matrix
```

---

## Description

The model matrices for each element of `formula(object)`, calculated using `data`, are bound together column-wise. When multiple grouping levels are present (i.e. when `length(object) > 1`), the individual model matrices are combined from innermost (at the leftmost position) to outermost (at the rightmost position).

## Usage

```
## S3 method for class 'reStruct':  
model.matrix(object, data, contrast, ...)
```

## Arguments

<code>object</code>	an object inheriting from class <code>reStruct</code> , representing a random effects structure and consisting of a list of <code>pdMat</code> objects.
<code>data</code>	a data frame in which to evaluate the variables defined in <code>formula(object)</code> .
<code>contrast</code>	an optional named list specifying the contrasts to be used for representing the factor variables in <code>data</code> . The components names should match the names of the variables in <code>data</code> for which the contrasts are to be specified. The components of this list will be used as the <code>contrasts</code> attribute of the corresponding factor. If missing, the default contrast specification is used.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

## Value

a matrix obtained by binding together, column-wise, the model matrices for each element of `formula(object)`.

## Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

`model.matrix`, `contrasts`, `reStruct`, `formula.reStruct`

**Examples**

```
rs1 <- reStruct(list(Dog = ~day, Side = ~1), data = Pixel)
model.matrix(rs1, Pixel)
```

---

Muscle

*Contraction of heart muscle sections*

---

**Description**

The `Muscle` data frame has 60 rows and 3 columns.

**Format**

This data frame contains the following columns:

**Strip** an ordered factor indicating the strip of muscle being measured.

**conc** a numeric vector giving the concentration of  $\text{CaCl}_2$

**length** a numeric vector giving the shortening of the heart muscle strip.

**Details**

Baumann and Waldvogel (1963) describe data on the shortening of heart muscle strips dipped in a  $\text{CaCl}_2$  solution. The muscle strips are taken from the left auricle of a rat's heart.

**Source**

Baumann, F. and Waldvogel, F. (1963), La restitution postsystolique de la contraction de l'oreillette gauche du rat. Effets de divers ions et de l'acetylcholine, *Helvetica Physiologica Acta*, **21**.

---

Names

*Names Associated with an Object*

---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `formula`, `modelStruct`, `pdBlocked`, `pdMat`, and `reStruct`.

**Usage**

```
Names(object, ...)
Names(object, ...) <- value
```

**Arguments**

object            any object for which names can be extracted and/or assigned.  
...                some methods for this generic function require additional arguments.  
value             names to be assigned to object.

**Value**

will depend on the method function used; see the appropriate documentation.

**SIDE EFFECTS**

On the left side of an assignment, sets the names associated with `object` to `value`, which must have an appropriate length.

**Note**

If names were generic, there would be no need for this generic function.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[Names.formula](#), [Names.pdMat](#)

**Examples**

```
## see the method function documentation
```

---

Names.formula            *Extract Names from a formula*

---

**Description**

This method function returns the names of the terms corresponding to the right hand side of `object` (treated as a linear formula), obtained as the column names of the corresponding `model.matrix`.

**Usage**

```
## S3 method for class 'formula':  
Names(object, data, exclude, ...)
```

**Arguments**

object	an object inheriting from class <code>formula</code> .
data	an optional data frame containing the variables specified in <code>object</code> . By default the variables are taken from the environment from which <code>Names.formula</code> is called.
exclude	an optional character vector with names to be excluded from the returned value. Default is <code>c("pi", ".")</code> .
...	some methods for this generic require additional arguments. None are used in this method.

**Value**

a character vector with the column names of the `model.matrix` corresponding to the right hand side of `object` which are not listed in `excluded`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[model.matrix](#), [terms](#), [Names](#)

**Examples**

```
Names(distance ~ Sex * age, data = Orthodont)
```

---

Names.pdBlocked      *Names of a pdBlocked Object*

---

**Description**

This method function extracts the first element of the `Dimnames` attribute, which contains the column names, for each block diagonal element in the matrix represented by `object`.

**Usage**

```
## S3 method for class 'pdBlocked':
Names(object, asList, ...)
```

**Arguments**

object	an object inheriting from class <code>pdBlocked</code> representing a positive-definite matrix with block diagonal structure
asList	a logical value. If <code>TRUE</code> a list with the names for each block diagonal element is returned. If <code>FALSE</code> a character vector with all column names is returned. Defaults to <code>FALSE</code> .
...	some methods for this generic require additional arguments. None are used in this method.

**Value**

if `asList` is `FALSE`, a character vector with column names of the matrix represented by `object`; otherwise, if `asList` is `TRUE`, a list with components given by the column names of the individual block diagonal elements in the matrix represented by `object`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[Names](#), [Names.pdMat](#)

**Examples**

```
pd1 <- pdBlocked(list(~Sex - 1, ~age - 1), data = Orthodont)
Names(pd1)
```

---

Names.pdMat

*Names of a pdMat Object*

---

**Description**

This method function returns the first element of the `Dimnames` attribute of `object`, which contains the column names of the matrix represented by `object`.

**Usage**

```
## S3 method for class 'pdMat':
Names(object, ...)
## S3 method for class 'pdMat':
Names(object, ...) <- value
```

**Arguments**

<code>object</code>	an object inheriting from class <code>pdMat</code> , representing a positive-definite matrix.
<code>value</code>	a character vector with the replacement values for the column and row names of the matrix represented by <code>object</code> . It must have length equal to the dimension of the matrix represented by <code>object</code> and, if names have been previously assigned to <code>object</code> , it must correspond to a permutation of the original names.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

if `object` has a `Dimnames` attribute then the first element of this attribute is returned; otherwise `NULL`.

**SIDE EFFECTS**

On the left side of an assignment, sets the `Dimnames` attribute of `object` to `list(value, value)`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[Names](#), [Names.pdBlocked](#)

**Examples**

```
pd1 <- pdSymm(~age, data = Orthodont)
Names(pd1)
```

---

Names.reStruct      *Names of an reStruct Object*

---

**Description**

This method function extracts the column names of each of the positive-definite matrices represented the `pdMat` elements of `object`.

**Usage**

```
## S3 method for class 'reStruct':
Names(object, ...)
## S3 method for class 'reStruct':
Names(object, ...) <- value
```

**Arguments**

<code>object</code>	an object inheriting from class <code>reStruct</code> , representing a random effects structure and consisting of a list of <code>pdMat</code> objects.
<code>value</code>	a list of character vectors with the replacement values for the names of the individual <code>pdMat</code> objects that form <code>object</code> . It must have the same length as <code>object</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a list containing the column names of each of the positive-definite matrices represented by the `pdMat` elements of `object`.

**SIDE EFFECTS**

On the left side of an assignment, sets the `Names` of the `pdMat` elements of `object` to the corresponding element of `value`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[reStruct](#), [pdMat](#), [Names.pdMat](#)

**Examples**

```
rs1 <- reStruct(list(Dog = ~day, Side = ~1), data = Pixel)
Names(rs1)
```

---

needUpdate	<i>Check if Update is Needed</i>
------------	----------------------------------

---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. By default, it tries to extract a `needUpdate` attribute of `object`. If this is `NULL` or `FALSE` it returns `FALSE`; else it returns `TRUE`. Updating of objects usually takes place in iterative algorithms in which auxiliary quantities associated with the object, and not being optimized over, may change.

**Usage**

```
needUpdate(object)
```

**Arguments**

`object` any object

**Value**

a logical value indicating whether `object` needs to be updated.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[needUpdate.modelStruct](#)

**Examples**

```
vf1 <- varExp()
vf1 <- Initialize(vf1, data = Orthodont)
needUpdate(vf1)
```



---

```
needUpdate.modelStruct
```

*Check if a modelStruct Object Needs Updating*

---

### Description

This method function checks if any of the elements of `object` needs to be updated. Updating of objects usually takes place in iterative algorithms in which auxiliary quantities associated with the object, and not being optimized over, may change.

### Usage

```
## S3 method for class 'modelStruct':  
needUpdate(object)
```

### Arguments

`object` an object inheriting from class `modelStruct`, representing a list of model components, such as `corStruct` and `varFunc` objects.

### Value

a logical value indicating whether any element of `object` needs to be updated.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

### See Also

[needUpdate](#)

### Examples

```
lms1 <- lmeStruct(reStruct = reStruct(pdDiag(diag(2), ~age)),  
varStruct = varPower(form = ~age))  
needUpdate(lms1)
```

---

Nitrendipene

*Assay of nitrendipene*

---

### Description

The Nitrendipene data frame has 89 rows and 4 columns.

**Format**

This data frame contains the following columns:

**activity** a numeric vector

**NIF** a numeric vector

**Tissue** an ordered factor with levels 2 < 1 < 3 < 4

**log.NIF** a numeric vector

**Source**

Bates, D. M. and Watts, D. G. (1988), *Nonlinear Regression Analysis and Its Applications*, Wiley, New York.

---

 nlme

*Nonlinear Mixed-Effects Models*


---

**Description**

This generic function fits a nonlinear mixed-effects model in the formulation described in Lindstrom and Bates (1990) but allowing for nested random effects. The within-group errors are allowed to be correlated and/or have unequal variances.

**Usage**

```
nlme(model, data, fixed, random, groups, start, correlation, weights,
      subset, method, na.action, naPattern, control, verbose)
```

**Arguments**

- |        |  |
|--------|--|
| model  | a nonlinear model formula, with the response on the left of a <code>~</code> operator and an expression involving parameters and covariates on the right, or an <code>nlsList</code> object. If <code>data</code> is given, all names used in the formula should be defined as parameters or variables in the data frame. The method function <code>nlme.nlsList</code> is documented separately.  |
| data   | an optional data frame containing the variables named in <code>model</code> , <code>fixed</code> , <code>random</code> , <code>correlation</code> , <code>weights</code> , <code>subset</code> , and <code>naPattern</code> . By default the variables are taken from the environment from which <code>nlme</code> is called.  |
| fixed  | a two-sided linear formula of the form <code>f1+...+fn~x1+...+xm</code> , or a list of two-sided formulas of the form <code>f1~x1+...+xm</code> , with possibly different models for different parameters. The <code>f1, ..., fn</code> are the names of parameters included on the right hand side of <code>model</code> and the <code>x1+...+xm</code> expressions define linear models for these parameters (when the left hand side of the formula contains several parameters, they all are assumed to follow the same linear model, described by the right hand side expression). A <code>1</code> on the right hand side of the formula(s) indicates a single fixed effects for the corresponding parameter(s). |
| random | optionally, any of the following: (i) a two-sided formula of the form <code>r1+...+rn~x1+...+xm   g1/.../gQ</code> , with <code>r1, ..., rn</code> naming parameters included on the right hand side of <code>model</code> , <code>x1+...+xm</code> specifying the random-effects model for these parameters and <code>g1/.../gQ</code> the  |

grouping structure ( $Q$  may be equal to 1, in which case no  $/$  is required). The random effects formula will be repeated for all levels of grouping, in the case of multiple levels of grouping; (ii) a two-sided formula of the form  $r_1 + \dots + r_n \sim x_1 + \dots + x_m$ , a list of two-sided formulas of the form  $r_1 \sim x_1 + \dots + x_m$ , with possibly different random-effects models for different parameters, a `pdMat` object with a two-sided formula, or list of two-sided formulas (i.e. a non-NULL value for `formula(random)`), or a list of `pdMat` objects with two-sided formulas, or lists of two-sided formulas. In this case, the grouping structure formula will be given in `groups`, or derived from the data used to fit the nonlinear mixed-effects model, which should inherit from class `groupedData`; (iii) a named list of formulas, lists of formulas, or `pdMat` objects as in (ii), with the grouping factors as names. The order of nesting will be assumed the same as the order of the elements in the list; (iv) an `reStruct` object. See the documentation on `pdClasses` for a description of the available `pdMat` classes. Defaults to `fixed`, resulting in all fixed effects having also random effects.

<code>groups</code>	an optional one-sided formula of the form $\sim g_1$ (single level of nesting) or $\sim g_1 / \dots / g_Q$ (multiple levels of nesting), specifying the partitions of the data over which the random effects vary. $g_1, \dots, g_Q$ must evaluate to factors in <code>data</code> . The order of nesting, when multiple levels are present, is taken from left to right (i.e. $g_1$ is the first level, $g_2$ the second, etc.).
<code>start</code>	an optional numeric vector, or list of initial estimates for the fixed effects and random effects. If declared as a numeric vector, it is converted internally to a list with a single component <code>fixed</code> , given by the vector. The <code>fixed</code> component is required, unless the model function inherits from class <code>selfStart</code> , in which case initial values will be derived from a call to <code>nlsList</code> . An optional <code>random</code> component is used to specify initial values for the random effects and should consist of a matrix, or a list of matrices with length equal to the number of grouping levels. Each matrix should have as many rows as the number of groups at the corresponding level and as many columns as the number of random effects in that level.
<code>correlation</code>	an optional <code>corStruct</code> object describing the within-group correlation structure. See the documentation of <code>corClasses</code> for a description of the available <code>corStruct</code> classes. Defaults to <code>NULL</code> , corresponding to no within-group correlations.
<code>weights</code>	an optional <code>varFunc</code> object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to <code>varFixed</code> , corresponding to fixed variance weights. See the documentation on <code>varClasses</code> for a description of the available <code>varFunc</code> classes. Defaults to <code>NULL</code> , corresponding to homoscedastic within-group errors.
<code>subset</code>	an optional expression indicating the subset of the rows of <code>data</code> that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
<code>method</code>	a character string. If "REML" the model is fit by maximizing the restricted log-likelihood. If "ML" the log-likelihood is maximized. Defaults to "ML".
<code>na.action</code>	a function that indicates what should happen when the data contain NAs. The default action ( <code>na.fail</code> ) causes <code>nlme</code> to print an error message and terminate if there are any incomplete observations.
<code>naPattern</code>	an expression or formula object, specifying which returned values are to be regarded as missing.

<code>control</code>	a list of control values for the estimation algorithm to replace the default values returned by the function <code>nlmeControl</code> . Defaults to an empty list.
<code>verbose</code>	an optional logical value. If <code>TRUE</code> information on the evolution of the iterative algorithm is printed. Default is <code>FALSE</code> .

### Value

an object of class `nlme` representing the nonlinear mixed-effects model fit. Generic functions such as `print`, `plot` and `summary` have methods to show the results of the fit. See `nlmeObject` for the components of the fit. The functions `resid`, `coef`, `fitted`, `fixed.effects`, and `random.effects` can be used to extract some of its components.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

The model formulation and computational methods are described in Lindstrom, M.J. and Bates, D.M. (1990). The variance-covariance parametrizations are described in Pinheiro, J.C. and Bates., D.M. (1996). The different correlation structures available for the `correlation` argument are described in Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994), Littell, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996), and Venables, W.N. and Ripley, B.D. (1997). The use of variance functions for linear and nonlinear mixed effects models is presented in detail in Davidian, M. and Giltinan, D.M. (1995).

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Davidian, M. and Giltinan, D.M. (1995) "Nonlinear Mixed Effects Models for Repeated Measurement Data", Chapman and Hall.

Laird, N.M. and Ware, J.H. (1982) "Random-Effects Models for Longitudinal Data", *Biometrics*, 38, 963-974.

Littell, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996) "SAS Systems for Mixed Models", SAS Institute.

Lindstrom, M.J. and Bates, D.M. (1990) "Nonlinear Mixed Effects Models for Repeated Measures Data", *Biometrics*, 46, 673-687.

Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", *Statistics and Computing*, 6, 289-296.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

Venables, W.N. and Ripley, B.D. (1997) "Modern Applied Statistics with S-plus", 2nd Edition, Springer-Verlag.

### See Also

[nlmeControl](#), [nlme.nlsList](#), [nlmeObject](#), [nlsList](#), [nlmeStruct](#), [pdClasses](#), [reStruct](#), [varFunc](#), [corClasses](#), [varClasses](#)

**Examples**

```

fm1 <- nlme(height ~ SSasym(age, Asym, R0, lrc),
            data = Loblolly,
            fixed = Asym + R0 + lrc ~ 1,
            random = Asym ~ 1,
            start = c(Asym = 103, R0 = -8.5, lrc = -3.3))
summary(fm1)
fm2 <- update(fm1, random = pdDiag(Asym + lrc ~ 1))
summary(fm2)

```

nlme.nlsList

*NLME fit from nlsList Object***Description**

If the random effects names defined in `random` are a subset of the `lmList` object coefficient names, initial estimates for the covariance matrix of the random effects are obtained (overwriting any values given in `random`). `formula(fixed)` and the `data` argument in the calling sequence used to obtain `fixed` are passed as the `fixed` and `data` arguments to `nlme.formula`, together with any other additional arguments in the function call. See the documentation on `nlme.formula` for a description of that function.

**Usage**

```

## S3 method for class 'nlsList':
nlme(model, data, fixed, random, groups, start, correlation, weights,
      subset, method, na.action, naPattern, control, verbose)

```

**Arguments**

<code>model</code>	an object inheriting from class <code>nlsList</code> , representing a list of <code>nls</code> fits with a common model.
<code>data</code>	this argument is included for consistency with the generic function. It is ignored in this method function.
<code>fixed</code>	this argument is included for consistency with the generic function. It is ignored in this method function.
<code>random</code>	an optional one-sided linear formula with no conditioning expression, or a <code>pdMat</code> object with a <code>formula</code> attribute. Multiple levels of grouping are not allowed with this method function. Defaults to a formula consisting of the right hand side of <code>formula(fixed)</code> .
<code>groups</code>	an optional one-sided formula of the form <code>~g1</code> (single level of nesting) or <code>~g1/.../gQ</code> (multiple levels of nesting), specifying the partitions of the data over which the random effects vary. <code>g1, ..., gQ</code> must evaluate to factors in <code>data</code> . The order of nesting, when multiple levels are present, is taken from left to right (i.e. <code>g1</code> is the first level, <code>g2</code> the second, etc.).
<code>start</code>	an optional numeric vector, or list of initial estimates for the fixed effects and random effects. If declared as a numeric vector, it is converted internally to a list with a single component <code>fixed</code> , given by the vector. The <code>fixed</code> component is required, unless the model function inherits from class <code>selfStart</code> , in which case initial values will be derived from a call to <code>nlsList</code> . An optional <code>random</code>

	component is used to specify initial values for the random effects and should consist of a matrix, or a list of matrices with length equal to the number of grouping levels. Each matrix should have as many rows as the number of groups at the corresponding level and as many columns as the number of random effects in that level.
<code>correlation</code>	an optional <code>corStruct</code> object describing the within-group correlation structure. See the documentation of <code>corClasses</code> for a description of the available <code>corStruct</code> classes. Defaults to <code>NULL</code> , corresponding to no within-group correlations.
<code>weights</code>	an optional <code>varFunc</code> object or one-sided formula describing the within-group heteroscedasticity structure. If given as a formula, it is used as the argument to <code>varFixed</code> , corresponding to fixed variance weights. See the documentation on <code>varClasses</code> for a description of the available <code>varFunc</code> classes. Defaults to <code>NULL</code> , corresponding to homoscedastic within-group errors.
<code>subset</code>	an optional expression indicating the subset of the rows of <code>data</code> that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
<code>method</code>	a character string. If <code>"REML"</code> the model is fit by maximizing the restricted log-likelihood. If <code>"ML"</code> the log-likelihood is maximized. Defaults to <code>"ML"</code> .
<code>na.action</code>	a function that indicates what should happen when the data contain <code>NA</code> s. The default action ( <code>na.fail</code> ) causes <code>nlme</code> to print an error message and terminate if there are any incomplete observations.
<code>naPattern</code>	an expression or formula object, specifying which returned values are to be regarded as missing.
<code>control</code>	a list of control values for the estimation algorithm to replace the default values returned by the function <code>nlmeControl</code> . Defaults to an empty list.
<code>verbose</code>	an optional logical value. If <code>TRUE</code> information on the evolution of the iterative algorithm is printed. Default is <code>FALSE</code> .

## Value

an object of class `nlme` representing the linear mixed-effects model fit. Generic functions such as `print`, `plot` and `summary` have methods to show the results of the fit. See `nlmeObject` for the components of the fit. The functions `resid`, `coef`, `fitted`, `fixed.effects`, and `random.effects` can be used to extract some of its components.

## Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

## References

The computational methods follow on the general framework of Lindstrom, M.J. and Bates, D.M. (1988). The model formulation is described in Laird, N.M. and Ware, J.H. (1982). The variance-covariance parametrizations are described in <Pinheiro, J.C. and Bates., D.M. (1996). The different correlation structures available for the `correlation` argument are described in Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994), Littell, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger,

R.D. (1996), and Venables, W.N. and Ripley, B.D. (1997). The use of variance functions for linear and nonlinear mixed effects models is presented in detail in Davidian, M. and Giltinan, D.M. (1995).

Box, G.E.P., Jenkins, G.M., and Reinsel G.C. (1994) "Time Series Analysis: Forecasting and Control", 3rd Edition, Holden-Day.

Davidian, M. and Giltinan, D.M. (1995) "Nonlinear Mixed Effects Models for Repeated Measurement Data", Chapman and Hall.

Laird, N.M. and Ware, J.H. (1982) "Random-Effects Models for Longitudinal Data", Biometrics, 38, 963-974.

Lindstrom, M.J. and Bates, D.M. (1988) "Newton-Raphson and EM Algorithms for Linear Mixed-Effects Models for Repeated-Measures Data", Journal of the American Statistical Association, 83, 1014-1022.

Littel, R.C., Milliken, G.A., Stroup, W.W., and Wolfinger, R.D. (1996) "SAS Systems for Mixed Models", SAS Institute.

Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", Statistics and Computing, 6, 289-296.

Venables, W.N. and Ripley, B.D. (1997) "Modern Applied Statistics with S-plus", 2nd Edition, Springer-Verlag.

### See Also

[nlme](#), [lmList](#), [nlmeObject](#)

### Examples

```
fml <- nlsList(SSasymp, data = Loblolly)
fm2 <- nlme(fml, random = Asym ~ 1)
summary(fml)
summary(fm2)
```

---

nlmeControl

*Control Values for nlme Fit*

---

### Description

The values supplied in the function call replace the defaults and a list with all possible arguments is returned. The returned list is used as the `control` argument to the `nlme` function.

### Usage

```
nlmeControl(maxIter, pnlsMaxIter, msMaxIter, minScale,
            tolerance, niterEM, pnlsTol, msTol, msScale,
            returnObject, msVerbose, gradHess, apVar, .relStep,
            nlmStepMax = 100.0, minAbsParApVar = 0.05,
            opt = c("nlminb", "nlm"), natural = TRUE)
```

**Arguments**

maxIter	maximum number of iterations for the <code>nlme</code> optimization algorithm. Default is 50.
pnlsMaxIter	maximum number of iterations for the PNLs optimization step inside the <code>nlme</code> optimization. Default is 7.
msMaxIter	maximum number of iterations for the <code>nlm</code> optimization step inside the <code>nlme</code> optimization. Default is 50.
minScale	minimum factor by which to shrink the default step size in an attempt to decrease the sum of squares in the PNLs step. Default 0.001.
tolerance	tolerance for the convergence criterion in the <code>nlme</code> algorithm. Default is 1e-6.
niterEM	number of iterations for the EM algorithm used to refine the initial estimates of the random effects variance-covariance coefficients. Default is 25.
pnlsTol	tolerance for the convergence criterion in PNLs step. Default is 1e-3.
msTol	tolerance for the convergence criterion in <code>nlm</code> , passed as the <code>rel.tolerance</code> argument to the function (see documentation on <code>nlm</code> ). Default is 1e-7.
msScale	scale function passed as the <code>scale</code> argument to the <code>nlm</code> function (see documentation on that function). Default is <code>lmeScale</code> .
returnObject	a logical value indicating whether the fitted object should be returned when the maximum number of iterations is reached without convergence of the algorithm. Default is <code>FALSE</code> .
msVerbose	a logical value passed as the <code>trace</code> argument to <code>nlm</code> (see documentation on that function). Default is <code>FALSE</code> .
gradHess	a logical value indicating whether numerical gradient vectors and Hessian matrices of the log-likelihood function should be used in the <code>nlm</code> optimization. This option is only available when the correlation structure ( <code>corStruct</code> ) and the variance function structure ( <code>varFunc</code> ) have no "varying" parameters and the <code>pdMat</code> classes used in the random effects structure are <code>pdSymm</code> (general positive-definite), <code>pdDiag</code> (diagonal), <code>pdIdent</code> (multiple of the identity), or <code>pdCompSymm</code> (compound symmetry). Default is <code>TRUE</code> .
apVar	a logical value indicating whether the approximate covariance matrix of the variance-covariance parameters should be calculated. Default is <code>TRUE</code> .
.relStep	relative step for numerical derivatives calculations. Default is <code>.Machine\$double.eps^(1/3)</code> .
nlmStepMax	stepmax value to be passed to <code>nlm</code> . See <code>nlm</code> for details. Default is 100.0
minAbsParApVar	numeric value - minimum absolute parameter value in the approximate variance calculation. The default is 0.05.
opt	the optimizer to be used, either <code>nlminb</code> (the default since (R 2.2.0) or <code>nlm</code> (the previous default).
natural	a logical value indicating whether the <code>pdNatural</code> parametrization should be used for general positive-definite matrices ( <code>pdSymm</code> ) in <code>reStruct</code> , when the approximate covariance matrix of the estimators is calculated. Default is <code>TRUE</code> .

**Value**

a list with components for each of the possible arguments.



**Author(s)**

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<bates@stat.wisc.edu>

**See Also**

[nlme](#), [nlm](#), [optim](#), [nlmeStruct](#)

**Examples**

```
# decrease the maximum number iterations in the ms call and
# request that information on the evolution of the ms iterations be printed
nlmeControl(msMaxIter = 20, msVerbose = TRUE)
```

---

nlmeObject

*Fitted nlme Object*


---

**Description**

An object returned by the `nlme` function, inheriting from class `nlme`, also inheriting from class `lme`, and representing a fitted nonlinear mixed-effects model. Objects of this class have methods for the generic functions `anova`, `coef`, `fitted`, `fixed.effects`, `formula`, `getGroups`, `getResponse`, `intervals`, `logLik`, `pairs`, `plot`, `predict`, `print`, `random.effects`, `residuals`, `summary`, and `update`.

**Value**

The following components must be included in a legitimate `nlme` object.

<code>apVar</code>	an approximate covariance matrix for the variance-covariance coefficients. If <code>apVar = FALSE</code> in the list of control values used in the call to <code>nlme</code> , this component is equal to <code>NULL</code> .
<code>call</code>	a list containing an image of the <code>nlme</code> call that produced the object.
<code>coefficients</code>	a list with two components, <code>fixed</code> and <code>random</code> , where the first is a vector containing the estimated fixed effects and the second is a list of matrices with the estimated random effects for each level of grouping. For each matrix in the <code>random</code> list, the columns refer to the random effects and the rows to the groups.
<code>contrasts</code>	a list with the contrasts used to represent factors in the fixed effects formula and/or random effects formula. This information is important for making predictions from a new data frame in which not all levels of the original factors are observed. If no factors are used in the <code>nlme</code> model, this component will be an empty list.
<code>dims</code>	a list with basic dimensions used in the <code>nlme</code> fit, including the components <code>N</code> - the number of observations in the data, <code>Q</code> - the number of grouping levels, <code>qvec</code> - the number of random effects at each level from innermost to outermost (last two values are equal to zero and correspond to the fixed effects and the response), <code>ngrps</code> - the number of groups at each level from innermost to outermost (last two values are one and correspond to the fixed effects and the response), and <code>ncol</code> - the number of columns in the model matrix for each level of grouping from innermost to outermost (last two values are equal to the number of fixed effects and one).

fitted	a data frame with the fitted values as columns. The leftmost column corresponds to the population fixed effects (corresponding to the fixed effects only) and successive columns from left to right correspond to increasing levels of grouping.
fixDF	a list with components <code>X</code> and <code>terms</code> specifying the denominator degrees of freedom for, respectively, t-tests for the individual fixed effects and F-tests for the fixed-effects terms in the models.
groups	a data frame with the grouping factors as columns. The grouping level increases from left to right.
logLik	the (restricted) log-likelihood at convergence.
map	a list with components <code>fmap</code> , <code>rmap</code> , <code>rmapRel</code> , and <code>bmap</code> , specifying various mappings for the fixed and random effects, used to generate predictions from the fitted object.
method	the estimation method: either "ML" for maximum likelihood, or "REML" for restricted maximum likelihood.
modelStruct	an object inheriting from class <code>nlmeStruct</code> , representing a list of mixed-effects model components, such as <code>reStruct</code> , <code>corStruct</code> , and <code>varFunc</code> objects.
numIter	the number of iterations used in the iterative algorithm.
residuals	a data frame with the residuals as columns. The leftmost column corresponds to the population residuals and successive columns from left to right correspond to increasing levels of grouping.
sigma	the estimated within-group error standard deviation.
varFix	an approximate covariance matrix of the fixed effects estimates.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[nlme](#), `nlmeStruct`

---

nlmeStruct

*Nonlinear Mixed-Effects Structure*

---

**Description**

A nonlinear mixed-effects structure is a list of model components representing different sets of parameters in the nonlinear mixed-effects model. An `nlmeStruct` list must contain at least a `reStruct` object, but may also contain `corStruct` and `varFunc` objects. NULL arguments are not included in the `nlmeStruct` list.

**Usage**

```
nlmeStruct(reStruct, corStruct, varStruct)
```

**Arguments**

<code>reStruct</code>	a <code>reStruct</code> representing a random effects structure.
<code>corStruct</code>	an optional <code>corStruct</code> object, representing a correlation structure. Default is <code>NULL</code> .
<code>varStruct</code>	an optional <code>varFunc</code> object, representing a variance function structure. Default is <code>NULL</code> .

**Value**

a list of model components determining the parameters to be estimated for the associated nonlinear mixed-effects model.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[corClasses](#), [nlme](#), [residuals.nlmeStruct](#), [reStruct](#), [varFunc](#)

**Examples**

```
nlms1 <- nlmeStruct(reStruct(~age), corAR1(), varPower())
```

---

nlsList

*List of nls Objects with a Common Model*

---

**Description**

Data is partitioned according to the levels of the grouping factor defined in `model` and individual `nls` fits are obtained for each data partition, using the model defined in `model`.

**Usage**

```
nlsList(model, data, start, control, level, subset, na.action, pool)
## S3 method for class 'nlsList':
update(object, model., ..., evaluate = TRUE)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>nlsList</code> , representing a list of fitted <code>nls</code> objects.
<code>model</code>	either a nonlinear model formula, with the response on the left of a <code>~</code> operator and an expression involving parameters, covariates, and a grouping factor separated by the <code> </code> operator on the right, or a <code>selfStart</code> function. The method function <code>nlsList.selfStart</code> is documented separately.
<code>model.</code>	Changes to the model – see <code>update.formula</code> for details.
<code>data</code>	a data frame in which to interpret the variables named in <code>model</code> .

start	an optional named list with initial values for the parameters to be estimated in <code>model</code> . It is passed as the <code>start</code> argument to each <code>nls</code> call and is required when the nonlinear function in <code>model</code> does not inherit from class <code>selfStart</code> .
control	a list of control values passed as the <code>control</code> argument to <code>nls</code> . Defaults to an empty list.
level	an optional integer specifying the level of grouping to be used when multiple nested levels of grouping are present.
subset	an optional expression indicating the subset of the rows of <code>data</code> that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
na.action	a function that indicates what should happen when the data contain NAs. The default action ( <code>na.fail</code> ) causes <code>nlsList</code> to print an error message and terminate if there are any incomplete observations.
pool	an optional logical value that is preserved as an attribute of the returned value. This will be used as the default for <code>pool</code> in calculations of standard deviations or standard errors for summaries.
...	some methods for this generic require additional arguments. None are used in this method.
evaluate	If <code>TRUE</code> evaluate the new call else return the call.

### Value

a list of `nls` objects with as many components as the number of groups defined by the grouping factor. Generic functions such as `coef`, `fixed.effects`, `lme`, `pairs`, `plot`, `predict`, `random.effects`, `summary`, and `update` have methods that can be applied to an `nlsList` object.

### References

Pinheiro, J.C., and Bates, D.M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer.

### See Also

[nls](#), [nlme.nlsList](#), [nlsList.selfStart](#), [summary.nlsList](#)

### Examples

```
fml <- nlsList(uptake ~ SSasymOff(conc, Asym, lrc, c0),
  data = CO2, start = c(Asym = 30, lrc = -4.5, c0 = 52))
summary(fml)
```

---

`nlsList.selfStart` *nlsList Fit from a selfStart Function*

---

### Description

The response variable and primary covariate in `formula(data)` are used together with `model` to construct the nonlinear model formula. This is used in the `nls` calls and, because a selfStarting model function can calculate initial estimates for its parameters from the data, no starting estimates need to be provided.

## Usage

```
## S3 method for class 'selfStart':  
nlsList(model, data, start, control, level, subset, na.action, pool)
```

## Arguments

<code>model</code>	a <code>selfStart</code> model function, which calculates initial estimates for the model parameters from <code>data</code> .
<code>data</code>	a data frame in which to interpret the variables in <code>model</code> . Because no grouping factor can be specified in <code>model</code> , <code>data</code> must inherit from class <code>groupedData</code> .
<code>start</code>	an optional named list with initial values for the parameters to be estimated in <code>model</code> . It is passed as the <code>start</code> argument to each <code>nls</code> call and is required when the nonlinear function in <code>model</code> does not inherit from class <code>selfStart</code> .
<code>control</code>	a list of control values passed as the <code>control</code> argument to <code>nls</code> . Defaults to an empty list.
<code>level</code>	an optional integer specifying the level of grouping to be used when multiple nested levels of grouping are present.
<code>subset</code>	an optional expression indicating the subset of the rows of <code>data</code> that should be used in the fit. This can be a logical vector, or a numeric vector indicating which observation numbers are to be included, or a character vector of the row names to be included. All observations are included by default.
<code>na.action</code>	a function that indicates what should happen when the data contain NAs. The default action ( <code>na.fail</code> ) causes <code>nlsList</code> to print an error message and terminate if there are any incomplete observations.
<code>pool</code>	an optional logical value that is preserved as an attribute of the returned value. This will be used as the default for <code>pool</code> in calculations of standard deviations or standard errors for summaries.

## Value

a list of `nls` objects with as many components as the number of groups defined by the grouping factor. A `NULL` value is assigned to the components corresponding to clusters for which the `nls` algorithm failed to converge. Generic functions such as `coef`, `fixed.effects`, `lme`, `pairs`, `plot`, `predict`, `random.effects`, `summary`, and `update` have methods that can be applied to an `nlsList` object.

## See Also

[selfStart](#), [groupedData](#), [nls](#), [nlsList](#), [nlme.nlsList](#), [nlsList.formula](#)

## Examples

```
fm1 <- nlsList(SSasymptOff, CO2)  
summary(fm1)
```

Oats

*Split-plot Experiment on Varieties of Oats***Description**

The `Oats` data frame has 72 rows and 4 columns.

**Format**

This data frame contains the following columns:

**Block** an ordered factor with levels VI < V < III < IV < II < I

**Variety** a factor with levels Golden Rain Marvellous Victory

**nitro** a numeric vector

**yield** a numeric vector

**Details**

These data have been introduced by Yates (1935) as an example of a split-plot design. The treatment structure used in the experiment was a  $3 \times 4$  full factorial, with three varieties of oats and four concentrations of nitrogen. The experimental units were arranged into six blocks, each with three whole-plots subdivided into four subplots. The varieties of oats were assigned randomly to the whole-plots and the concentrations of nitrogen to the subplots. All four concentrations of nitrogen were used on each whole-plot.

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.15)

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS (3rd ed)*, Springer, New York.

Orthodont

*Growth curve data on an orthodontic measurement***Description**

The `Orthodont` data frame has 108 rows and 4 columns of the change in an orthodontic measurement over time for several young subjects.

**Format**

This data frame contains the following columns:

**distance** a numeric vector of distances from the pituitary to the pterygomaxillary fissure (mm). These distances are measured on x-ray images of the skull.

**age** a numeric vector of ages of the subject (yr).

**Subject** an ordered factor indicating the subject on which the measurement was made. The levels are labelled M01 to M16 for the males and F01 to F13 for the females. The ordering is by increasing average distance within sex.

**Sex** a factor with levels Male and Female

**Details**

Investigators at the University of North Carolina Dental School followed the growth of 27 children (16 males, 11 females) from age 8 until age 14. Every two years they measured the distance between the pituitary and the pterygomaxillary fissure, two points that are easily identified on x-ray exposures of the side of the head.

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.17)

Potthoff, R. F. and Roy, S. N. (1964), "A generalized multivariate analysis of variance model useful especially for growth curve problems", *Biometrika*, **51**, 313–326.

**Examples**

```
formula(Orthodont)
plot(Orthodont)
```

---

 Ovary

---

*Counts of Ovarian Follicles*


---

**Description**

The Ovary data frame has 308 rows and 3 columns.

**Format**

This data frame contains the following columns:

**Mare** an ordered factor indicating the mare on which the measurement is made.

**Time** time in the estrus cycle. The data were recorded daily from 3 days before ovulation until 3 days after the next ovulation. The measurement times for each mare are scaled so that the ovulations for each mare occur at times 0 and 1.

**follicles** the number of ovarian follicles greater than 10 mm in diameter.

**Details**

Pierson and Ginther (1987) report on a study of the number of large ovarian follicles detected in different mares at several times in their estrus cycles.

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.18)

Pierson, R. A. and Ginther, O. J. (1987), Follicular population dynamics during the estrus cycle of the mare, *Animal Reproduction Science*, **14**, 219-231.

---

Oxboys

*Heights of Boys in Oxford*

---

### Description

The Oxboys data frame has 234 rows and 4 columns.

### Format

This data frame contains the following columns:

**Subject** an ordered factor giving a unique identifier for each boy in the experiment

**age** a numeric vector giving the standardized age (dimensionless)

**height** a numeric vector giving the height of the boy (cm)

**Occasion** an ordered factor - the result of converting age from a continuous variable to a count so these slightly unbalanced data can be analyzed as balanced.

### Details

These data are described in Goldstein (1987) as data on the height of a selection of boys from Oxford, England versus a standardized age.

### Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.19)

---

Oxide

*Variability in Semiconductor Manufacturing*

---

### Description

The Oxide data frame has 72 rows and 5 columns.

### Format

This data frame contains the following columns:

**Source** a factor with levels 1 and 2

**Lot** a factor giving a unique identifier for each lot.

**Wafer** a factor giving a unique identifier for each wafer within a lot.

**Site** a factor with levels 1, 2, and 3

**Thickness** a numeric vector giving the thickness of the oxide layer.



**Details**

These data are described in Littell et al. (1996, p. 155) as coming “from a passive data collection study in the semiconductor industry where the objective is to estimate the variance components to determine the assignable causes of the observed variability.” The observed response is the thickness of the oxide layer on silicon wafers, measured at three different sites of each of three wafers selected from each of eight lots sampled from the population of lots.

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.20)

Littell, R. C., Milliken, G. A., Stroup, W. W. and Wolfinger, R. D. (1996), *SAS System for Mixed Models*, SAS Institute, Cary, NC.

---

pairs.compareFits *Pairs Plot of compareFits Object*

---

**Description**

Scatter plots of the values being compared are generated for each pair of coefficients in  $x$ . Different symbols (colors) are used for each object being compared and values corresponding to the same group are joined by a line, to facilitate comparison of fits. If only two coefficients are present, the `trellis` function `xyplot` is used; otherwise the `trellis` function `splom` is used.

**Usage**

```
## S3 method for class 'compareFits':
pairs(x, subset, key, ...)
```

**Arguments**

<code>x</code>	an object of class <code>compareFits</code> .
<code>subset</code>	an optional logical or integer vector specifying which rows of <code>x</code> should be used in the plots. If missing, all rows are used.
<code>key</code>	an optional logical value, or list. If <code>TRUE</code> , a legend is included at the top of the plot indicating which symbols (colors) correspond to which objects being compared. If <code>FALSE</code> , no legend is included. If given as a list, <code>key</code> is passed down as an argument to the <code>trellis</code> function generating the plots ( <code>splom</code> or <code>xyplot</code> ). Defaults to <code>TRUE</code> .
<code>...</code>	optional arguments passed down to the <code>trellis</code> function generating the plots.

**Value**

Pairwise scatter plots of the values being compared, with different symbols (colors) used for each object under comparison.

**Author(s)**

Jose Pinheiro and Douglas Bates

**See Also**

`compareFits`, `plot.compareFits`, `pairs.lme`, `pairs.lmList`, `xyplot`, `spIom`

**Examples**

```
fm1 <- lmList(Orthodont)
fm2 <- lme(Orthodont)
pairs(compareFits(coef(fm1), coef(fm2)))
```

---

pairs.lme

*Pairs Plot of an lme Object*

---

**Description**

Diagnostic plots for the linear mixed-effects fit are obtained. The `form` argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a `|` operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. The expression on the right hand side of the formula, before a `|` operator, must evaluate to a data frame with at least two columns. If the data frame has two columns, a scatter plot of the two variables is displayed (the Trellis function `xyplot` is used). Otherwise, if more than two columns are present, a scatter plot matrix with pairwise scatter plots of the columns in the data frame is displayed (the Trellis function `spIom` is used).

**Usage**

```
## S3 method for class 'lme':
pairs(x, form, label, id, idLabels, grid, ...)
```

**Arguments**

<code>x</code>	an object inheriting from class <code>lme</code> , representing a fitted linear mixed-effects model.
<code>form</code>	an optional one-sided formula specifying the desired type of plot. Any variable present in the original data frame used to obtain <code>x</code> can be referenced. In addition, <code>x</code> itself can be referenced in the formula using the symbol <code>"."</code> . Conditional expressions on the right of a <code> </code> operator can be used to define separate panels in a Trellis display. The expression on the right hand side of <code>form</code> , and to the left of the <code> </code> operator, must evaluate to a data frame with at least two columns. Default is <code>~ coef(.)</code> , corresponding to a pairs plot of the coefficients evaluated at the innermost level of nesting.
<code>label</code>	an optional character vector of labels for the variables in the pairs plot.
<code>id</code>	an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for an outlier test based on the Mahalanobis distances of the estimated random effects. Groups with random effects distances greater than the $1 - \text{value}$ percentile of the appropriate chi-square distribution are identified in the plot using <code>idLabels</code> . If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify points in the plot. If missing, no points are identified.

`idLabels` an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the points identified according to `id`. If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified points. Default is the innermost grouping factor.

`grid` an optional logical value indicating whether a grid should be added to plot. Default is `FALSE`.

`...` optional arguments passed to the Trellis plot function.

**Value**

a diagnostic Trellis plot.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[lme](#), [pairs.compareFits](#), [pairs.lmList](#), [xyplot](#), [splom](#)

**Examples**

```
fml <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
# scatter plot of coefficients by gender, identifying unusual subjects
pairs(fml, ~coef(., augFrame = TRUE) | Sex, id = 0.1, adj = -0.5)
# scatter plot of estimated random effects
## Not run:
pairs(fml, ~ranef(.))

## End(Not run)
```

---

`pairs.lmList`

*Pairs Plot of an lmList Object*

---

**Description**

Diagnostic plots for the linear model fits corresponding to the  $x$  components are obtained. The `form` argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a `|` operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. The expression on the right hand side of the formula, before a `|` operator, must evaluate to a data frame with at least two columns. If the data frame has two columns, a scatter plot of the two variables is displayed (the Trellis function `xyplot` is used). Otherwise, if more than two columns are present, a scatter plot matrix with pairwise scatter plots of the columns in the data frame is displayed (the Trellis function `splom` is used).

**Usage**

```
## S3 method for class 'lmList':
pairs(x, form, label, id, idLabels, grid, ...)
```

**Arguments**

<code>x</code>	an object inheriting from class <code>lmList</code> , representing a list of <code>lm</code> objects with a common model.
<code>form</code>	an optional one-sided formula specifying the desired type of plot. Any variable present in the original data frame used to obtain <code>x</code> can be referenced. In addition, <code>x</code> itself can be referenced in the formula using the symbol <code>"."</code> . Conditional expressions on the right of a <code> </code> operator can be used to define separate panels in a Trellis display. The expression on the right hand side of <code>form</code> , and to the left of the <code> </code> operator, must evaluate to a data frame with at least two columns. Default is <code>~ coef(.)</code> , corresponding to a pairs plot of the coefficients of <code>x</code> .
<code>label</code>	an optional character vector of labels for the variables in the pairs plot.
<code>id</code>	an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for an outlier test based on the Mahalanobis distances of the estimated random effects. Groups with random effects distances greater than the $1 - \text{value}$ percentile of the appropriate chi-square distribution are identified in the plot using <code>idLabels</code> . If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify points in the plot. If missing, no points are identified.
<code>idLabels</code>	an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the points identified according to <code>id</code> . If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified points. Default is the innermost grouping factor.
<code>grid</code>	an optional logical value indicating whether a grid should be added to plot. Default is <code>FALSE</code> .
<code>...</code>	optional arguments passed to the Trellis plot function.

**Value**

a diagnostic Trellis plot.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[lmList](#), [pairs.lme](#), [pairs.compareFits](#), [xyplot](#), [splom](#)

**Examples**

```
fml <- lmList(distance ~ age | Subject, Orthodont)
# scatter plot of coefficients by gender, identifying unusual subjects
pairs(fml, ~coef(.) | Sex, id = 0.1, adj = -0.5)
# scatter plot of estimated random effects
## Not run:
pairs(fml, ~ranef(.))

## End(Not run)
```

PBG

*Effect of Phenylbiguanide on Blood Pressure***Description**

The PBG data frame has 60 rows and 5 columns.

**Format**

This data frame contains the following columns:

**deltaBP** a numeric vector

**dose** a numeric vector

**Run** an ordered factor with levels T5 < T4 < T3 < T2 < T1 < P5 < P3 < P2 < P4 < P1

**Treatment** a factor with levels MDL 72222 Placebo

**Rabbit** an ordered factor with levels 5 < 3 < 2 < 4 < 1

**Details**

Data on an experiment to examine the effect of a antagonist MDL 72222 on the change in blood pressure experienced with increasing dosage of phenylbiguanide are described in Ludbrook (1994) and analyzed in Venables and Ripley (1999, section 8.8). Each of five rabbits was exposed to increasing doses of phenylbiguanide after having either a placebo or the HD5-antagonist MDL 72222 administered.

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.21)

Venables, W. N. and Ripley, B. D. (1999) *Modern Applied Statistics with S-PLUS (3rd ed)*, Springer, New York.

Ludbrook, J. (1994), Repeated measurements and multiple comparisons in cardiovascular research, *Cardiovascular Research*, **28**, 303-311.

pdBlocked

*Positive-Definite Block Diagonal Matrix***Description**

This function is a constructor for the pdBlocked class, representing a positive-definite block-diagonal matrix. Each block-diagonal element of the underlying matrix is itself a positive-definite matrix and is represented internally as an individual pdMat object. When value is numeric(0), a list of uninitialized pdMat objects, a list of one-sided formulas, or a list of vectors of character strings, object is returned as an uninitialized pdBlocked object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the coef or matrix replacement functions. If value is a list of initialized pdMat objects, object will be constructed from the list obtained by applying as.matrix to each of the pdMat elements of value. Finally, if value is a list of numeric vectors, they are assumed to represent the unrestricted coefficients of the block-diagonal elements of the underlying positive-definite matrix.

## Usage

```
pdBlocked(value, form, nam, data, pdClass)
```

## Arguments

- |         |  |
|---------|--|
| value   | an optional list with elements to be used as the <code>value</code> argument to other <code>pdMat</code> constructors. These include: <code>pdMat</code> objects, positive-definite matrices, one-sided linear formulas, vectors of character strings, or numeric vectors. All elements in the list must be similar (e.g. all one-sided formulas, or all numeric vectors). Defaults to <code>numeric(0)</code> , corresponding to an uninitialized object. |
| form    | an optional list of one-sided linear formulas specifying the row/column names for the block-diagonal elements of the matrix represented by <code>object</code> . Because factors may be present in <code>form</code> , the formulas needs to be evaluated on a <code>data.frame</code> to resolve the names they define. This argument is ignored when <code>value</code> is a list of one-sided formulas. Defaults to <code>NULL</code> .                 |
| nam     | an optional list of vector of character strings specifying the row/column names for the block-diagonal elements of the matrix represented by <code>object</code> . Each of its components must have length equal to the dimension of the corresponding block-diagonal element and unreplicated elements. This argument is ignored when <code>value</code> is a list of vector of character strings. Defaults to <code>NULL</code> .                        |
| data    | an optional data frame in which to evaluate the variables named in <code>value</code> and <code>form</code> . It is used to obtain the levels for <code>factors</code> , which affect the dimensions and the row/column names of the underlying matrix. If <code>NULL</code> , no attempt is made to obtain information on any <code>factors</code> appearing in the formulas. Defaults to the parent frame from which the function was called.            |
| pdClass | an optional vector of character strings naming the <code>pdMat</code> classes to be assigned to the individual blocks in the underlying matrix. If a single class is specified, it is used for all block-diagonal elements. This argument will only be used when <code>value</code> is missing, or its elements are not <code>pdMat</code> objects. Defaults to <code>"pdSymm"</code> .  |

## Value

a `pdBlocked` object representing a positive-definite block-diagonal matrix, also inheriting from class `pdMat`.

## Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

## References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. p. 162.

## See Also

[as.matrix.pdMat](#), [coef.pdMat](#), [pdClasses](#), [matrix<-pdMat](#)

**Examples**

```
pd1 <- pdBlocked(list(diag(1:2), diag(c(0.1, 0.2, 0.3))),
                 nam = list(c("A", "B"), c("a1", "a2", "a3")))
pd1
```

---

 pdClasses

*Positive-Definite Matrix Classes*


---

**Description**

Standard classes of positive-definite matrices (pdMat) structures available in the nlme library.

**Value**

Available standard classes:

pdSymm	general positive-definite matrix, with no additional structure
pdLogChol	general positive-definite matrix, with no additional structure, using a log-Cholesky parameterization
pdDiag	diagonal
pdIdent	multiple of an identity
pdCompSymm	compound symmetry structure (constant diagonal and constant off-diagonal elements)
pdBlocked	block-diagonal matrix, with diagonal blocks of any "atomic" pdMat class
pdNatural	general positive-definite matrix in natural parametrization (i.e. parametrized in terms of standard deviations and correlations). The underlying coefficients are not unrestricted, so this class should NOT be used for optimization.

**Note**

Users may define their own pdMat classes by specifying a constructor function and, at a minimum, methods for the functions pdConstruct, pdMatrix and coef. For examples of these functions, see the methods for classes pdSymm and pdDiag.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[pdBlocked](#), [pdCompSymm](#), [pdDiag](#), [pdFactor](#), [pdIdent](#), [pdMat](#), [pdMatrix](#), [pdNatural](#), [pdSymm](#), [pdLogChol](#)

---

`pdCompSymm`*Positive-Definite Matrix with Compound Symmetry Structure*

---

### Description

This function is a constructor for the `pdCompSymm` class, representing a positive-definite matrix with compound symmetry structure (constant diagonal and constant off-diagonal elements). The underlying matrix is represented by 2 unrestricted parameters. When `value` is `numeric(0)`, an uninitialized `pdMat` object, a one-sided formula, or a vector of character strings, `object` is returned as an uninitialized `pdCompSymm` object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the `coef` or `matrix` replacement functions. If `value` is an initialized `pdMat` object, `object` will be constructed from `as.matrix(value)`. Finally, if `value` is a numeric vector of length 2, it is assumed to represent the unrestricted coefficients of the underlying positive-definite matrix.

### Usage

```
pdCompSymm(value, form, nam, data)
```

### Arguments

<code>value</code>	an optional initialization value, which can be any of the following: a <code>pdMat</code> object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric vector of length 2. Defaults to <code>numeric(0)</code> , corresponding to an uninitialized object.
<code>form</code>	an optional one-sided linear formula specifying the row/column names for the matrix represented by <code>object</code> . Because factors may be present in <code>form</code> , the formula needs to be evaluated on a <code>data.frame</code> to resolve the names it defines. This argument is ignored when <code>value</code> is a one-sided formula. Defaults to <code>NULL</code> .
<code>nam</code>	an optional vector of character strings specifying the row/column names for the matrix represented by <code>object</code> . It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when <code>value</code> is a vector of character strings. Defaults to <code>NULL</code> .
<code>data</code>	an optional data frame in which to evaluate the variables named in <code>value</code> and <code>form</code> . It is used to obtain the levels for <code>factors</code> , which affect the dimensions and the row/column names of the underlying matrix. If <code>NULL</code> , no attempt is made to obtain information on <code>factors</code> appearing in the formulas. Defaults to the parent frame from which the function was called.

### Value

a `pdCompSymm` object representing a positive-definite matrix with compound symmetry structure, also inheriting from class `pdMat`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>



## References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. p. 161.

## See Also

[as.matrix.pdMat](#), [coef.pdMat](#), [matrix<- .pdMat](#), [pdClasses](#)

## Examples

```
pd1 <- pdCompSymm(diag(3) + 1, nam = c("A", "B", "C"))
pd1
```

---

pdConstruct

*Construct pdMat Objects*

---

## Description

This function is an alternative constructor for the `pdMat` class associated with `object` and is mostly used internally in other functions. See the documentation on the principal constructor function, generally with the same name as the `pdMat` class of `object`.

## Usage

```
pdConstruct(object, value, form, nam, data, ...)
```

## Arguments

<code>object</code>	an object inheriting from class <code>pdMat</code> , representing a positive definite matrix.
<code>value</code>	an optional initialization value, which can be any of the following: a <code>pdMat</code> object, a positive-definite matrix, a one-sided linear formula (with variables separated by <code>+</code> ), a vector of character strings, or a numeric vector. Defaults to <code>numeric(0)</code> , corresponding to an uninitialized object.
<code>form</code>	an optional one-sided linear formula specifying the row/column names for the matrix represented by <code>object</code> . Because factors may be present in <code>form</code> , the formula needs to be evaluated on a <code>data.frame</code> to resolve the names it defines. This argument is ignored when <code>value</code> is a one-sided formula. Defaults to <code>NULL</code> .
<code>nam</code>	an optional vector of character strings specifying the row/column names for the matrix represented by <code>object</code> . It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when <code>value</code> is a vector of character strings. Defaults to <code>NULL</code> .
<code>data</code>	an optional data frame in which to evaluate the variables named in <code>value</code> and <code>form</code> . It is used to obtain the levels for <code>factors</code> , which affect the dimensions and the row/column names of the underlying matrix. If <code>NULL</code> , no attempt is made to obtain information on <code>factors</code> appearing in the formulas. Defaults to the parent frame from which the function was called.
<code>...</code>	optional arguments for some methods.

**Value**

a `pdMat` object representing a positive-definite matrix, inheriting from the same classes as `object`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[pdCompSymm](#), [pdDiag](#), [pdIdent](#), [pdNatural](#), [pdSymm](#)

**Examples**

```
pd1 <- pdSymm()
pdConstruct(pd1, diag(1:4))
```

---

`pdConstruct.pdBlocked`

*Construct pdBlocked Objects*

---

**Description**

This function give an alternative constructor for the `pdBlocked` class, representing a positive-definite block-diagonal matrix. Each block-diagonal element of the underlying matrix is itself a positive-definite matrix and is represented internally as an individual `pdMat` object. When `value` is `numeric(0)`, a list of uninitialized `pdMat` objects, a list of one-sided formulas, or a list of vectors of character strings, `object` is returned as an uninitialized `pdBlocked` object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the `coef` or `matrix` replacement functions. If `value` is a list of initialized `pdMat` objects, `object` will be constructed from the list obtained by applying `as.matrix` to each of the `pdMat` elements of `value`. Finally, if `value` is a list of numeric vectors, they are assumed to represent the unrestricted coefficients of the block-diagonal elements of the underlying positive-definite matrix.

**Usage**

```
## S3 method for class 'pdBlocked':
pdConstruct(object, value, form, nam, data, pdClass,
...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>pdBlocked</code> , representing a positive definite block-diagonal matrix.
<code>value</code>	an optional list with elements to be used as the <code>value</code> argument to other <code>pdMat</code> constructors. These include: <code>pdMat</code> objects, positive-definite matrices, one-sided linear formulas, vectors of character strings, or numeric vectors. All elements in the list must be similar (e.g. all one-sided formulas, or all numeric vectors). Defaults to <code>numeric(0)</code> , corresponding to an uninitialized object.

<code>form</code>	an optional list of one-sided linear formula specifying the row/column names for the block-diagonal elements of the matrix represented by <code>object</code> . Because factors may be present in <code>form</code> , the formulas needs to be evaluated on a <code>data.frame</code> to resolve the names they defines. This argument is ignored when <code>value</code> is a list of one-sided formulas. Defaults to <code>NULL</code> .
<code>nam</code>	an optional list of vector of character strings specifying the row/column names for the block-diagonal elements of the matrix represented by <code>object</code> . Each of its components must have length equal to the dimension of the corresponding block-diagonal element and unreplicated elements. This argument is ignored when <code>value</code> is a list of vector of character strings. Defaults to <code>NULL</code> .
<code>data</code>	an optional data frame in which to evaluate the variables named in <code>value</code> and <code>form</code> . It is used to obtain the levels for <code>factors</code> , which affect the dimensions and the row/column names of the underlying matrix. If <code>NULL</code> , no attempt is made to obtain information on <code>factors</code> appearing in the formulas. Defaults to the parent frame from which the function was called.
<code>pdClass</code>	an optional vector of character strings naming the <code>pdMat</code> classes to be assigned to the individual blocks in the underlying matrix. If a single class is specified, it is used for all block-diagonal elements. This argument will only be used when <code>value</code> is missing, or its elements are not <code>pdMat</code> objects. Defaults to <code>"pdSymm"</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

a `pdBlocked` object representing a positive-definite block-diagonal matrix, also inheriting from class `pdMat`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

### See Also

[as.matrix.pdMat](#), [coef.pdMat](#), [pdBlocked](#), [pdClasses](#), [pdConstruct](#), [matrix<-.pdMat](#)

### Examples

```
pd1 <- pdBlocked(list(c("A","B"), c("a1", "a2", "a3")))
pdConstruct(pd1, list(diag(1:2), diag(c(0.1, 0.2, 0.3))))
```

---

`pdDiag`*Diagonal Positive-Definite Matrix*

---

### Description

This function is a constructor for the `pdDiag` class, representing a diagonal positive-definite matrix. If the matrix associated with `object` is of dimension  $n$ , it is represented by  $n$  unrestricted parameters, given by the logarithm of the square-root of the diagonal values. When `value` is `numeric(0)`, an uninitialized `pdMat` object, a one-sided formula, or a vector of character strings, `object` is returned as an uninitialized `pdDiag` object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the `coef` or `matrix` replacement functions. If `value` is an initialized `pdMat` object, `object` will be constructed from `as.matrix(value)`. Finally, if `value` is a numeric vector, it is assumed to represent the unrestricted coefficients of the underlying positive-definite matrix.

### Usage

```
pdDiag(value, form, nam, data)
```

### Arguments

<code>value</code>	an optional initialization value, which can be any of the following: a <code>pdMat</code> object, a positive-definite matrix, a one-sided linear formula (with variables separated by <code>+</code> ), a vector of character strings, or a numeric vector of length equal to the dimension of the underlying positive-definite matrix. Defaults to <code>numeric(0)</code> , corresponding to an uninitialized object.
<code>form</code>	an optional one-sided linear formula specifying the row/column names for the matrix represented by <code>object</code> . Because factors may be present in <code>form</code> , the formula needs to be evaluated on a <code>data.frame</code> to resolve the names it defines. This argument is ignored when <code>value</code> is a one-sided formula. Defaults to <code>NULL</code> .
<code>nam</code>	an optional vector of character strings specifying the row/column names for the matrix represented by <code>object</code> . It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when <code>value</code> is a vector of character strings. Defaults to <code>NULL</code> .
<code>data</code>	an optional data frame in which to evaluate the variables named in <code>value</code> and <code>form</code> . It is used to obtain the levels for <code>factors</code> , which affect the dimensions and the row/column names of the underlying matrix. If <code>NULL</code> , no attempt is made to obtain information on <code>factors</code> appearing in the formulas. Defaults to the parent frame from which the function was called.

### Value

a `pdDiag` object representing a diagonal positive-definite matrix, also inheriting from class `pdMat`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[as.matrix.pdMat](#), [coef.pdMat](#), [pdClasses](#), [matrix<-pdMat](#)

**Examples**

```
pd1 <- pdDiag(diag(1:3), nam = c("A", "B", "C"))
pd1
```

---

pdFactor

*Square-Root Factor of a Positive-Definite Matrix*

---

**Description**

A square-root factor of the positive-definite matrix represented by `object` is obtained. Letting  $\Sigma$  denote a positive-definite matrix, a square-root factor of  $\Sigma$  is any square matrix  $L$  such that  $\Sigma = L'L$ . This function extracts  $L$ .

**Usage**

```
pdFactor(object)
```

**Arguments**

`object` an object inheriting from class `pdMat`, representing a positive definite matrix, which must have been initialized (i.e. `length(coef(object)) > 0`).

**Value**

a vector with a square-root factor of the positive-definite matrix associated with `object` stacked column-wise.

**Note**

This function is used intensively in optimization algorithms and its value is returned as a vector for efficiency reasons. The `pdMatrix` function can be used to obtain square-root factors in matrix form.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[pdMatrix](#)

**Examples**

```
pd1 <- pdCompSymm(4 * diag(3) + 1)
pdFactor(pd1)
```

---

pdFactor.reStruct *Extract Square-Root Factor from Components of an reStruct Object*

---

**Description**

This method function extracts square-root factors of the positive-definite matrices corresponding to the pdMat elements of object.

**Usage**

```
## S3 method for class 'reStruct':
pdFactor(object)
```

**Arguments**

object            an object inheriting from class reStruct, representing a random effects structure and consisting of a list of pdMat objects.

**Value**

a vector with square-root factors of the positive-definite matrices corresponding to the elements of object stacked column-wise.

**Note**

This function is used intensively in optimization algorithms and its value is returned as a vector for efficiency reasons. The pdMatrix function can be used to obtain square-root factors in matrix form.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[pdFactor](#), [pdMatrix.reStruct](#), [pdFactor.pdMat](#)

**Examples**

```
rs1 <- reStruct(pdSymm(diag(3), ~age+Sex, data = Orthodont))
pdFactor(rs1)
```

pdIdent

*Multiple of the Identity Positive-Definite Matrix***Description**

This function is a constructor for the `pdIdent` class, representing a multiple of the identity positive-definite matrix. The matrix associated with `object` is represented by 1 unrestricted parameter, given by the logarithm of the square-root of the diagonal value. When `value` is `numeric(0)`, an uninitialized `pdMat` object, a one-sided formula, or a vector of character strings, `object` is returned as an uninitialized `pdIdent` object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the `coef` or `matrix` replacement functions. If `value` is an initialized `pdMat` object, `object` will be constructed from `as.matrix(value)`. Finally, if `value` is a numeric value, it is assumed to represent the unrestricted coefficient of the underlying positive-definite matrix.

**Usage**

```
pdIdent(value, form, nam, data)
```

**Arguments**

<code>value</code>	an optional initialization value, which can be any of the following: a <code>pdMat</code> object, a positive-definite matrix, a one-sided linear formula (with variables separated by <code>+</code> ), a vector of character strings, or a numeric value. Defaults to <code>numeric(0)</code> , corresponding to an uninitialized object.
<code>form</code>	an optional one-sided linear formula specifying the row/column names for the matrix represented by <code>object</code> . Because factors may be present in <code>form</code> , the formula needs to be evaluated on a <code>data.frame</code> to resolve the names it defines. This argument is ignored when <code>value</code> is a one-sided formula. Defaults to <code>NULL</code> .
<code>nam</code>	an optional vector of character strings specifying the row/column names for the matrix represented by <code>object</code> . It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when <code>value</code> is a vector of character strings. Defaults to <code>NULL</code> .
<code>data</code>	an optional data frame in which to evaluate the variables named in <code>value</code> and <code>form</code> . It is used to obtain the levels for <code>factors</code> , which affect the dimensions and the row/column names of the underlying matrix. If <code>NULL</code> , no attempt is made to obtain information on <code>factors</code> appearing in the formulas. Defaults to the parent frame from which the function was called.

**Value**

a `pdIdent` object representing a multiple of the identity positive-definite matrix, also inheriting from class `pdMat`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

`as.matrix.pdMat`, `coef.pdMat`, `pdClasses`, `matrix<- .pdMat`

**Examples**

```
pd1 <- pdIdent(4 * diag(3), nam = c("A", "B", "C"))
pd1
```

---

pdLogChol

*General Positive-Definite Matrix*

---

**Description**

This function is a constructor for the `pdLogChol` class, representing a general positive-definite matrix. If the matrix associated with `object` is of dimension  $n$ , it is represented by  $n(n + 1)/2$  unrestricted parameters, using the log-Cholesky parametrization described in Pinheiro and Bates (1996). When `value` is `numeric(0)`, an uninitialized `pdMat` object, a one-sided formula, or a vector of character strings, `object` is returned as an uninitialized `pdLogChol` object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the `coef` or `matrix` replacement functions. If `value` is an initialized `pdMat` object, `object` will be constructed from `as.matrix(value)`. Finally, if `value` is a numeric vector, it is assumed to represent the unrestricted coefficients of the matrix-logarithm parametrization of the underlying positive-definite matrix.

**Usage**

```
pdLogChol(value, form, nam, data)
```

**Arguments**

<code>value</code>	an optional initialization value, which can be any of the following: a <code>pdMat</code> object, a positive-definite matrix, a one-sided linear formula (with variables separated by <code>+</code> ), a vector of character strings, or a numeric vector. Defaults to <code>numeric(0)</code> , corresponding to an uninitialized object.
<code>form</code>	an optional one-sided linear formula specifying the row/column names for the matrix represented by <code>object</code> . Because factors may be present in <code>form</code> , the formula needs to be evaluated on a <code>data.frame</code> to resolve the names it defines. This argument is ignored when <code>value</code> is a one-sided formula. Defaults to <code>NULL</code> .
<code>nam</code>	an optional vector of character strings specifying the row/column names for the matrix represented by <code>object</code> . It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when <code>value</code> is a vector of character strings. Defaults to <code>NULL</code> .
<code>data</code>	an optional data frame in which to evaluate the variables named in <code>value</code> and <code>form</code> . It is used to obtain the levels for <code>factors</code> , which affect the dimensions and the row/column names of the underlying matrix. If <code>NULL</code> , no attempt is made to obtain information on <code>factors</code> appearing in the formulas. Defaults to the parent frame from which the function was called.



**Value**

a `pdLogChol` object representing a general positive-definite matrix, also inheriting from class `pdMat`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", *Statistics and Computing*, 6, 289-296.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[as.matrix.pdMat](#), [coef.pdMat](#), [pdClasses](#), [matrix<-pdMat](#)

**Examples**

```
pd1 <- pdLogChol(diag(1:3), nam = c("A", "B", "C"))
pd1
```

---

pdMat

*Positive-Definite Matrix*

---

**Description**

This function gives an alternative way of constructing an object inheriting from the `pdMat` class named in `pdClass`, or from `data.class(object)` if `object` inherits from `pdMat`, and is mostly used internally in other functions. See the documentation on the principal constructor function, generally with the same name as the `pdMat` class of object.

**Usage**

```
pdMat(value, form, nam, data, pdClass)
```

**Arguments**

<code>value</code>	an optional initialization value, which can be any of the following: a <code>pdMat</code> object, a positive-definite matrix, a one-sided linear formula (with variables separated by +), a vector of character strings, or a numeric vector. Defaults to <code>numeric(0)</code> , corresponding to an uninitialized object.
<code>form</code>	an optional one-sided linear formula specifying the row/column names for the matrix represented by <code>object</code> . Because factors may be present in <code>form</code> , the formula needs to be evaluated on a <code>data.frame</code> to resolve the names it defines. This argument is ignored when <code>value</code> is a one-sided formula. Defaults to <code>NULL</code> .

nam	an optional vector of character strings specifying the row/column names for the matrix represented by object. It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when value is a vector of character strings. Defaults to NULL.
data	an optional data frame in which to evaluate the variables named in value and form. It is used to obtain the levels for factors, which affect the dimensions and the row/column names of the underlying matrix. If NULL, no attempt is made to obtain information on factors appearing in the formulas. Defaults to the parent frame from which the function was called.
pdClass	an optional character string naming the pdMat class to be assigned to the returned object. This argument will only be used when value is not a pdMat object. Defaults to "pdSymm".

**Value**

a pdMat object representing a positive-definite matrix, inheriting from the class named in pdClass, or from class(object), if object inherits from pdMat.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[pdClasses](#), [pdCompSymm](#), [pdDiag](#), [pdIdent](#), [pdNatural](#), [pdSymm](#), [reStruct](#), [solve.pdMat](#), [summary.pdMat](#)

**Examples**

```
pd1 <- pdMat(diag(1:4), pdClass = "pdDiag")
pd1
```

---

pdMatrix

*Extract Matrix or Square-Root Factor from a pdMat Object*

---

**Description**

The positive-definite matrix represented by object, or a square-root factor of it is obtained. Letting  $\Sigma$  denote a positive-definite matrix, a square-root factor of  $\Sigma$  is any square matrix  $L$  such that  $\Sigma = L'L$ . This function extracts  $S$  or  $L$ .

**Usage**

```
pdMatrix(object, factor)
```

**Arguments**

`object` an object inheriting from class `pdMat`, representing a positive definite matrix.

`factor` an optional logical value. If `TRUE`, a square-root factor of the positive-definite matrix represented by `object` is returned; else, if `FALSE`, the positive-definite matrix is returned. Defaults to `FALSE`.

**Value**

if `fact` is `FALSE` the positive-definite matrix represented by `object` is returned; else a square-root of the positive-definite matrix is returned.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. p. 162.

**See Also**

[as.matrix.pdMat](#), [pdClasses](#), [pdFactor](#), [pdMat](#), [pdMatrix.reStruct](#), [corMatrix](#)

**Examples**

```
pd1 <- pdSymm(diag(1:4))
pdMatrix(pd1)
```

---

`pdMatrix.reStruct` *Extract Matrix or Square-Root Factor from Components of an reStruct Object*

---

**Description**

This method function extracts the positive-definite matrices corresponding to the `pdMat` elements of `object`, or square-root factors of the positive-definite matrices.

**Usage**

```
## S3 method for class 'reStruct':
pdMatrix(object, factor)
```

**Arguments**

`object` an object inheriting from class `reStruct`, representing a random effects structure and consisting of a list of `pdMat` objects.

`factor` an optional logical value. If `TRUE`, square-root factors of the positive-definite matrices represented by the elements of `object` are returned; else, if `FALSE`, the positive-definite matrices are returned. Defaults to `FALSE`.

**Value**

a list with components given by the positive-definite matrices corresponding to the elements of `object`, or square-root factors of the positive-definite matrices.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. p. 162.

**See Also**

[as.matrix.reStruct](#), [reStruct](#), [pdMat](#), [pdMatrix](#), [pdMatrix.pdMat](#)

**Examples**

```
rs1 <- reStruct(pdSymm(diag(3), ~age+Sex, data = Orthodont))
pdMatrix(rs1)
```

---

pdNatural

*General Positive-Definite Matrix in Natural Parametrization*

---

**Description**

This function is a constructor for the `pdNatural` class, representing a general positive-definite matrix, using a natural parametrization. If the matrix associated with `object` is of dimension  $n$ , it is represented by  $n(n+1)/2$  parameters. Letting  $\sigma_{ij}$  denote the  $ij$ -th element of the underlying positive definite matrix and  $\rho_{ij} = \sigma_{ij} / \sqrt{\sigma_{ii}\sigma_{jj}}$ ,  $i \neq j$  denote the associated "correlations", the "natural" parameters are given by  $\sqrt{\sigma_{ii}}$ ,  $i = 1, \dots, n$  and  $\log((1 + \rho_{ij}) / (1 - \rho_{ij}))$ ,  $i \neq j$ . Note that all natural parameters are individually unrestricted, but not jointly unrestricted (meaning that not all unrestricted vectors would give positive-definite matrices). Therefore, this parametrization should NOT be used for optimization. It is mostly used for deriving approximate confidence intervals on parameters following the optimization of an objective function. When `value` is `numeric(0)`, an uninitialized `pdMat` object, a one-sided formula, or a vector of character strings, `object` is returned as an uninitialized `pdSymm` object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the `coef` or `matrix` replacement functions. If `value` is an initialized `pdMat` object, `object` will be constructed from `as.matrix(value)`. Finally, if `value` is a numeric vector, it is assumed to represent the natural parameters of the underlying positive-definite matrix.

**Usage**

```
pdNatural(value, form, nam, data)
```

**Arguments**

value	an optional initialization value, which can be any of the following: a <code>pdMat</code> object, a positive-definite matrix, a one-sided linear formula (with variables separated by <code>+</code> ), a vector of character strings, or a numeric vector. Defaults to <code>numeric(0)</code> , corresponding to an uninitialized object.
form	an optional one-sided linear formula specifying the row/column names for the matrix represented by <code>object</code> . Because factors may be present in <code>form</code> , the formula needs to be evaluated on a <code>data.frame</code> to resolve the names it defines. This argument is ignored when <code>value</code> is a one-sided formula. Defaults to <code>NULL</code> .
nam	an optional vector of character strings specifying the row/column names for the matrix represented by <code>object</code> . It must have length equal to the dimension of the underlying positive-definite matrix and unrepliated elements. This argument is ignored when <code>value</code> is a vector of character strings. Defaults to <code>NULL</code> .
data	an optional data frame in which to evaluate the variables named in <code>value</code> and <code>form</code> . It is used to obtain the levels for <code>factors</code> , which affect the dimensions and the row/column names of the underlying matrix. If <code>NULL</code> , no attempt is made to obtain information on <code>factors</code> appearing in the formulas. Defaults to the parent frame from which the function was called.

**Value**

a `pdNatural` object representing a general positive-definite matrix in natural parametrization, also inheriting from class `pdMat`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. p. 162.

**See Also**

[as.matrix.pdMat](#), [coef.pdMat](#), [pdClasses](#), [matrix<-pdMat](#)

**Examples**

```
pdNatural(diag(1:3))
```

---

`pdSymm`*General Positive-Definite Matrix*

---

**Description**

This function is a constructor for the `pdSymm` class, representing a general positive-definite matrix. If the matrix associated with `object` is of dimension  $n$ , it is represented by  $n(n+1)/2$  unrestricted parameters, using the matrix-logarithm parametrization described in Pinheiro and Bates (1996). When `value` is `numeric(0)`, an uninitialized `pdMat` object, a one-sided formula, or a vector of character strings, `object` is returned as an uninitialized `pdSymm` object (with just some of its attributes and its class defined) and needs to have its coefficients assigned later, generally using the `coef` or `matrix` replacement functions. If `value` is an initialized `pdMat` object, `object` will be constructed from `as.matrix(value)`. Finally, if `value` is a numeric vector, it is assumed to represent the unrestricted coefficients of the matrix-logarithm parametrization of the underlying positive-definite matrix.

**Usage**

```
pdSymm(value, form, nam, data)
```

**Arguments**

<code>value</code>	an optional initialization value, which can be any of the following: a <code>pdMat</code> object, a positive-definite matrix, a one-sided linear formula (with variables separated by <code>+</code> ), a vector of character strings, or a numeric vector. Defaults to <code>numeric(0)</code> , corresponding to an uninitialized object.
<code>form</code>	an optional one-sided linear formula specifying the row/column names for the matrix represented by <code>object</code> . Because factors may be present in <code>form</code> , the formula needs to be evaluated on a <code>data.frame</code> to resolve the names it defines. This argument is ignored when <code>value</code> is a one-sided formula. Defaults to <code>NULL</code> .
<code>nam</code>	an optional vector of character strings specifying the row/column names for the matrix represented by <code>object</code> . It must have length equal to the dimension of the underlying positive-definite matrix and unreplicated elements. This argument is ignored when <code>value</code> is a vector of character strings. Defaults to <code>NULL</code> .
<code>data</code>	an optional data frame in which to evaluate the variables named in <code>value</code> and <code>form</code> . It is used to obtain the levels for <code>factors</code> , which affect the dimensions and the row/column names of the underlying matrix. If <code>NULL</code> , no attempt is made to obtain information on <code>factors</code> appearing in the formulas. Defaults to the parent frame from which the function was called.

**Value**

a `pdSymm` object representing a general positive-definite matrix, also inheriting from class `pdMat`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

## References

- Pinheiro, J.C. and Bates., D.M. (1996) "Unconstrained Parametrizations for Variance-Covariance Matrices", *Statistics and Computing*, 6, 289-296.
- Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

## See Also

[as.matrix.pdMat](#), [coef.pdMat](#), [pdClasses](#), [matrix<-pdMat](#)

## Examples

```
pd1 <- pdSymm(diag(1:3), nam = c("A", "B", "C"))
pd1
```

---

Phenobarb

*Phenobarbital Kinetics*

---

## Description

The `Phenobarb` data frame has 744 rows and 7 columns.

## Format

This data frame contains the following columns:

**Subject** an ordered factor identifying the infant.

**Wt** a numeric vector giving the birth weight of the infant (kg).

**Apgar** an ordered factor giving the 5-minute Apgar score for the infant. This is an indication of health of the newborn infant.

**ApgarInd** a factor indicating whether the 5-minute Apgar score is  $< 5$  or  $\geq 5$ .

**time** a numeric vector giving the time when the sample is drawn or drug administered (hr).

**dose** a numeric vector giving the dose of drug administered (*ug/kg*).

**conc** a numeric vector giving the phenobarbital concentration in the serum (*ug/L*).

## Details

Data from a pharmacokinetics study of phenobarbital in neonatal infants. During the first few days of life the infants receive multiple doses of phenobarbital for prevention of seizures. At irregular intervals blood samples are drawn and serum phenobarbital concentrations are determined. The data were originally given in Grasela and Donn(1985) and are analyzed in Boeckmann, Sheiner and Beal (1994), in Davidian and Giltinan (1995), and in Littell et al. (1996).

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.23)

Davidian, M. and Giltinan, D. M. (1995), *Nonlinear Models for Repeated Measurement Data*, Chapman and Hall, London. (section 6.6)

Grasela and Donn (1985), Neonatal population pharmacokinetics of phenobarbital derived from routine clinical data, *Developmental Pharmacology and Therapeutics*, **8**, 374-383.

Boeckmann, A. J., Sheiner, L. B., and Beal, S. L. (1994), *NONMEM Users Guide: Part V*, University of California, San Francisco.

Littell, R. C., Milliken, G. A., Stroup, W. W. and Wolfinger, R. D. (1996), *SAS System for Mixed Models*, SAS Institute, Cary, NC.

---

 phenoModel

---

*Model function for the Phenobarb data*


---

**Description**

A model function for a model used with the Phenobarb data. This function uses compiled C code to improve execution speed.

**Usage**

```
phenoModel(Subject, time, dose, lCl, lV)
```

**Arguments**

Subject	an integer vector of subject identifiers. These should be sorted in increasing order.
time	numeric. A vector of the times at which the sample was drawn or the drug administered (hr).
dose	numeric. A vector of doses of drug administered (ug/kg).
lCl	numeric. A vector of values of the natural log of the clearance parameter according to Subject and time.
lV	numeric. A vector of values of the natural log of the effective volume of distribution according to Subject and time.

**Details**

See the details section of [Phenobarb](#) for a description of the model function that phenoModel evaluates.

**Value**

a numeric vector of predicted phenobarbital concentrations.

**Author(s)**

Jose Pinheiro <jose.pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>



## References

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer. (section 6.4)

---

Pixel	<i>X-ray pixel intensities over time</i>
-------	--

---

## Description

The `Pixel` data frame has 102 rows and 4 columns of data on the pixel intensities of CT scans of dogs over time

## Format

This data frame contains the following columns:

**Dog** a factor with levels 1 to 10 designating the dog on which the scan was made

**Side** a factor with levels L and R designating the side of the dog being scanned

**day** a numeric vector giving the day post injection of the contrast on which the scan was made

**pixel** a numeric vector of pixel intensities

## Source

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer.

## Examples

```
fml <- lme(pixel ~ day + I(day^2), data = Pixel,
          random = list(Dog = ~ day, Side = ~ 1))
summary(fml)
VarCorr(fml)
```

---

plot.ACF	<i>Plot an ACF Object</i>
----------	---------------------------

---

## Description

an `xyplot` of the autocorrelations versus the lags, with `type = "h"`, is produced. If `alpha > 0`, curves representing the critical limits for a two-sided test of level `alpha` for the autocorrelations are added to the plot.

## Usage

```
## S3 method for class 'ACF':
plot(x, alpha, xlab, ylab, grid, ...)
```

**Arguments**

x	an object inheriting from class <code>ACF</code> , consisting of a data frame with two columns named <code>lag</code> and <code>ACF</code> , representing the autocorrelation values and the corresponding lags.
alpha	an optional numeric value with the significance level for testing if the autocorrelations are zero. Lines corresponding to the lower and upper critical values for a test of level <code>alpha</code> are added to the plot. Default is 0, in which case no lines are plotted.
xlab, ylab	optional character strings with the x- and y-axis labels. Default respectively to "Lag" and "Autocorrelation".
grid	an optional logical value indicating whether a grid should be added to plot. Default is <code>FALSE</code> .
...	optional arguments passed to the <code>xyplot</code> function.

**Value**

an `xyplot` Trellis plot.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[ACF](#), [xyplot](#)

**Examples**

```
fml <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary)
plot(ACF(fml, maxLag = 10), alpha = 0.01)
```

---

plot.augPred

*Plot an augPred Object*

---

**Description**

A Trellis `xyplot` of predictions versus the primary covariate is generated, with a different panel for each value of the grouping factor. Predicted values are joined by lines, with different line types (colors) being used for each level of grouping. Original observations are represented by circles.

**Usage**

```
## S3 method for class 'augPred':
plot(x, key, grid, ...)
```

**Arguments**

<code>x</code>	an object of class <code>augPred</code> .
<code>key</code>	an optional logical value, or list. If <code>TRUE</code> , a legend is included at the top of the plot indicating which symbols (colors) correspond to which prediction levels. If <code>FALSE</code> , no legend is included. If given as a list, <code>key</code> is passed down as an argument to the <code>trellis</code> function generating the plots ( <code>xyplot</code> ). Defaults to <code>TRUE</code> .
<code>grid</code>	an optional logical value indicating whether a grid should be added to plot. Default is <code>FALSE</code> .
<code>...</code>	optional arguments passed down to the <code>trellis</code> function generating the plots.

**Value**

A Trellis plot of predictions versus the primary covariate, with panels determined by the grouping factor.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[augPred](#), [xyplot](#)

**Examples**

```
fml <- lme(Orthodont)
plot(augPred(fml, level = 0:1, length.out = 2))
```

---

`plot.compareFits` *Plot a compareFits Object*

---

**Description**

A Trellis `dotplot` of the values being compared, with different rows per group, is generated, with a different panel for each coefficient. Different symbols (colors) are used for each object being compared.

**Usage**

```
## S3 method for class 'compareFits':
plot(x, subset, key, mark, ...)
```

**Arguments**

<code>x</code>	an object of class <code>compareFits</code> .
<code>subset</code>	an optional logical or integer vector specifying which rows of <code>x</code> should be used in the plots. If missing, all rows are used.
<code>key</code>	an optional logical value, or list. If <code>TRUE</code> , a legend is included at the top of the plot indicating which symbols (colors) correspond to which objects being compared. If <code>FALSE</code> , no legend is included. If given as a list, <code>key</code> is passed down as an argument to the <code>trellis</code> function generating the plots ( <code>dotplot</code> ). Defaults to <code>TRUE</code> .
<code>mark</code>	an optional numeric vector, of length equal to the number of coefficients being compared, indicating where vertical lines should be drawn in the plots. If missing, no lines are drawn.
<code>...</code>	optional arguments passed down to the <code>trellis</code> function generating the plots.

**Value**

A Trellis `dotplot` of the values being compared, with rows determined by the groups and panels by the coefficients.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[compareFits](#), [pairs.compareFits](#), [dotplot](#)

**Examples**

```
## Not run:
fm1 <- lmList(Orthodont)
fm2 <- lme(Orthodont)
plot(compareFits(coef(fm1), coef(fm2)))

## End(Not run)
```

---

plot.gls

*Plot a gls Object*

---

**Description**

Diagnostic plots for the linear model fit are obtained. The `form` argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a `|` operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. If `form` is a one-sided formula, histograms of the variable on the right hand side of the formula, before a `|` operator, are displayed (the Trellis function `histogram` is used). If `form` is two-sided and both its left and right hand side variables are numeric, scatter plots are displayed (the Trellis function `xyplot` is used). Finally, if `form` is two-sided and its left hand side variable is a factor, box-plots of the right hand side variable by the levels of the left hand side variable are displayed (the Trellis function `bwplot` is used).

**Usage**

```
## S3 method for class 'glms':
plot(x, form, abline, id, idLabels, idResType, grid, ...)
```

**Arguments**

<code>x</code>	an object inheriting from class <code>glms</code> , representing a generalized least squares fitted linear model.
<code>form</code>	an optional formula specifying the desired type of plot. Any variable present in the original data frame used to obtain <code>x</code> can be referenced. In addition, <code>x</code> itself can be referenced in the formula using the symbol <code>"."</code> . Conditional expressions on the right of a <code> </code> operator can be used to define separate panels in a Trellis display. Default is <code>resid(., type = "p") ~ fitted(.)</code> , corresponding to a plot of the standardized residuals versus fitted values, both evaluated at the innermost level of nesting.
<code>abline</code>	an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.
<code>id</code>	an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized residuals. Observations with absolute standardized residuals greater than the $1 - value/2$ quantile of the standard normal distribution are identified in the plot using <code>idLabels</code> . If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.
<code>idLabels</code>	an optional vector, or one-sided formula. If given as a vector, it is converted to character mode and used to label the observations identified according to <code>id</code> . If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character mode and used to label the identified observations. Default is the innermost grouping factor.
<code>idResType</code>	an optional character string specifying the type of residuals to be used in identifying outliers, when <code>id</code> is a numeric value. If <code>"pearson"</code> , the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if <code>"normalized"</code> , the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to <code>"pearson"</code> .
<code>grid</code>	an optional logical value indicating whether a grid should be added to plot. Default depends on the type of Trellis plot used: if <code>xyplot</code> defaults to <code>TRUE</code> , else defaults to <code>FALSE</code> .
<code>...</code>	optional arguments passed to the Trellis plot function.

**Value**

a diagnostic Trellis plot.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[gls](#), [xyplot](#), [bwplot](#), [histogram](#)

**Examples**

```
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
          correlation = corAR1(form = ~ 1 | Mare))
# standardized residuals versus fitted values by Mare
plot(fm1, resid(., type = "p") ~ fitted(.) | Mare, abline = 0)
# box-plots of residuals by Mare
plot(fm1, Mare ~ resid(.))
# observed versus fitted values by Mare
plot(fm1, follicles ~ fitted(.) | Mare, abline = c(0,1))
```

---

```
plot.intervals.lmList
```

*Plot lmList Confidence Intervals*

---

**Description**

A Trellis dot-plot of the confidence intervals on the linear model coefficients is generated, with a different panel for each coefficient. Rows in the dot-plot correspond to the names of the `lm` components of the `lmList` object used to produce `x`. The lower and upper confidence limits are connected by a line segment and the estimated coefficients are marked with a "+". The Trellis function `dotplot` is used in this method function.

**Usage**

```
## S3 method for class 'intervals.lmList':
plot(x, ...)
```

**Arguments**

`x` an object inheriting from class `intervals.lmList`, representing confidence intervals and estimates for the coefficients in the `lm` components of the `lmList` object used to produce `x`.

`...` optional arguments passed to the Trellis `dotplot` function.

**Value**

a Trellis plot with the confidence intervals on the coefficients of the individual `lm` components of the `lmList` that generated `x`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[intervals.lmList](#), [lmList](#), [dotplot](#)

**Examples**

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
plot(intervals(fm1))
```

plot.lme

*Plot an lme or nls object***Description**

Diagnostic plots for the linear mixed-effects fit are obtained. The `form` argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a `|` operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. If `form` is a one-sided formula, histograms of the variable on the right hand side of the formula, before a `|` operator, are displayed (the Trellis function `histogram` is used). If `form` is two-sided and both its left and right hand side variables are numeric, scatter plots are displayed (the Trellis function `xyplot` is used). Finally, if `form` is two-sided and its left hand side variable is a factor, box-plots of the right hand side variable by the levels of the left hand side variable are displayed (the Trellis function `bwplot` is used).

**Usage**

```
## S3 method for class 'lme':
plot(x, form, abline, id, idLabels, idResType, grid, ...)
## S3 method for class 'nls':
plot(x, form, abline, id, idLabels, idResType, grid, ...)
```

**Arguments**

- |                     |   |
|---------------------|---|
| <code>x</code>      | an object inheriting from class <code>lme</code> , representing a fitted linear mixed-effects model, or from <code>nls</code> , representing an fitted nonlinear least squares model.   |
| <code>form</code>   | an optional formula specifying the desired type of plot. Any variable present in the original data frame used to obtain <code>x</code> can be referenced. In addition, <code>x</code> itself can be referenced in the formula using the symbol <code>". "</code> . Conditional expressions on the right of a <code> </code> operator can be used to define separate panels in a Trellis display. Default is <code>resid(., type = "p") ~ fitted(.)</code> , corresponding to a plot of the standardized residuals versus fitted values, both evaluated at the innermost level of nesting.                     |
| <code>abline</code> | an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.  |
| <code>id</code>     | an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized, or normalized residuals. Observations with absolute standardized (normalized) residuals greater than the $1 - \text{value}/2$ quantile of the standard normal distribution are identified in the plot using <code>idLabels</code> . If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified. |

<code>idLabels</code>	an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the observations identified according to <code>id</code> . If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified observations. Default is the innermost grouping factor.
<code>idResType</code>	an optional character string specifying the type of residuals to be used in identifying outliers, when <code>id</code> is a numeric value. If "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".
<code>grid</code>	an optional logical value indicating whether a grid should be added to plot. Default depends on the type of Trellis plot used: if <code>xyplot</code> defaults to TRUE, else defaults to FALSE.
<code>...</code>	optional arguments passed to the Trellis plot function.

**Value**

a diagnostic Trellis plot.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[lme](#), [xyplot](#), [bwplot](#), [histogram](#)

**Examples**

```
fml <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
# standardized residuals versus fitted values by gender
plot(fml, resid(., type = "p") ~ fitted(.) | Sex, abline = 0)
# box-plots of residuals by Subject
plot(fml, Subject ~ resid(.))
# observed versus fitted values by Subject
plot(fml, distance ~ fitted(.) | Subject, abline = c(0,1))
```

---

plot.lmList

*Plot an lmList Object*

---

**Description**

Diagnostic plots for the linear model fits corresponding to the  $x$  components are obtained. The `form` argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a `|` operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display. If `form` is a one-sided formula, histograms of the variable on the right hand side of the formula, before a `|` operator, are displayed (the Trellis function `histogram` is used). If `form` is two-sided and both its left and right hand side



variables are numeric, scatter plots are displayed (the Trellis function `xyplot` is used). Finally, if `form` is two-sided and its left hand side variable is a factor, box-plots of the right hand side variable by the levels of the left hand side variable are displayed (the Trellis function `bwplot` is used).

### Usage

```
## S3 method for class 'lmList':
plot(x, form, abline, id, idLabels, grid, ...)
```

### Arguments

<code>x</code>	an object inheriting from class <code>lmList</code> , representing a list of <code>lm</code> objects with a common model.
<code>form</code>	an optional formula specifying the desired type of plot. Any variable present in the original data frame used to obtain <code>x</code> can be referenced. In addition, <code>x</code> itself can be referenced in the formula using the symbol <code>"."</code> . Conditional expressions on the right of a <code> </code> operator can be used to define separate panels in a Trellis display. Default is <code>resid(., type = "pool") ~ fitted(.)</code> , corresponding to a plot of the standardized residuals (using a pooled estimate for the residual standard error) versus fitted values.
<code>abline</code>	an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.
<code>id</code>	an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized residuals. Observations with absolute standardized residuals greater than the $1 - value/2$ quantile of the standard normal distribution are identified in the plot using <code>idLabels</code> . If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.
<code>idLabels</code>	an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the observations identified according to <code>id</code> . If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified observations. Default is <code>getGroups(x)</code> .
<code>grid</code>	an optional logical value indicating whether a grid should be added to plot. Default depends on the type of Trellis plot used: if <code>xyplot</code> defaults to <code>TRUE</code> , else defaults to <code>FALSE</code> .
<code>...</code>	optional arguments passed to the Trellis plot function.

### Value

a diagnostic Trellis plot.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[lmList](#), [predict.lm](#), [xyplot](#), [bwplot](#), [histogram](#)

**Examples**

```
fml <- lmList(distance ~ age | Subject, Orthodont)
# standardized residuals versus fitted values by gender
plot(fml, resid(., type = "pool") ~ fitted(.) | Sex, abline = 0, id = 0.05)
# box-plots of residuals by Subject
plot(fml, Subject ~ resid(.))
# observed versus fitted values by Subject
plot(fml, distance ~ fitted(.) | Subject, abline = c(0,1))
```

---

```
plot.nffGroupedData
```

*Plot an nffGroupedData Object*

---

**Description**

A Trellis dot-plot of the response by group is generated. If outer variables are specified, the combination of their levels are used to determine the panels of the Trellis display. The Trellis function `dotplot` is used.

**Usage**

```
## S3 method for class 'nffGroupedData':
plot(x, outer, inner, innerGroups, xlab, ylab, strip, panel, key,
      grid, ...)
```

**Arguments**

<code>x</code>	an object inheriting from class <code>nffGroupedData</code> , representing a <code>groupedData</code> object with a factor primary covariate and a single grouping level.
<code>outer</code>	an optional logical value or one-sided formula, indicating covariates that are outer to the grouping factor, which are used to determine the panels of the Trellis plot. If equal to <code>TRUE</code> , <code>attr(object, "outer")</code> is used to indicate the outer covariates. An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. Defaults to <code>NULL</code> , meaning that no outer covariates are to be used.
<code>inner</code>	an optional logical value or one-sided formula, indicating a covariate that is inner to the grouping factor, which is used to associate points within each panel of the Trellis plot. If equal to <code>TRUE</code> , <code>attr(object, "inner")</code> is used to indicate the inner covariate. An inner covariate can change within the sets of rows defined by the grouping factor. Defaults to <code>NULL</code> , meaning that no inner covariate is present.
<code>innerGroups</code>	an optional one-sided formula specifying a factor to be used for grouping the levels of the inner covariate. Different colors, or symbols, are used for each level of the <code>innerGroups</code> factor. Default is <code>NULL</code> , meaning that no <code>innerGroups</code> covariate is present.

<code>xlab</code>	an optional character string with the label for the horizontal axis. Default is the <code>y</code> elements of <code>attr(object, "labels")</code> and <code>attr(object, "units")</code> pasted together.
<code>ylab</code>	an optional character string with the label for the vertical axis. Default is the grouping factor name.
<code>strip</code>	an optional function passed as the <code>strip</code> argument to the <code>dotplot</code> function. Default is <code>strip.default(..., style = 1)</code> (see <code>trellis.args</code> ).
<code>panel</code>	an optional function used to generate the individual panels in the Trellis display, passed as the <code>panel</code> argument to the <code>dotplot</code> function.
<code>key</code>	an optional logical function or function. If <code>TRUE</code> and either <code>inner</code> or <code>innerGroups</code> are non-NULL, a legend for the different inner ( <code>innerGroups</code> ) levels is included at the top of the plot. If given as a function, it is passed as the <code>key</code> argument to the <code>dotplot</code> function. Default is <code>TRUE</code> is either <code>inner</code> or <code>innerGroups</code> are non-NULL and <code>FALSE</code> otherwise.
<code>grid</code>	this argument is included for consistency with the <code>plot.nfnGroupedData</code> method calling sequence. It is ignored in this method function.
<code>...</code>	optional arguments passed to the <code>dotplot</code> function.

**Value**

a Trellis dot-plot of the response by group.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Bates, D.M. and Pinheiro, J.C. (1997), "Software Design for Longitudinal Data", in "Modelling Longitudinal and Spatially Correlated Data: Methods, Applications and Future Directions", T.G. Gregoire (ed.), Springer-Verlag, New York.

**See Also**

[groupedData](#), [dotplot](#)

**Examples**

```
plot(Machines)
plot(Machines, inner = TRUE)
```

---

```
plot.nfnGroupedData
```

*Plot an nfnGroupedData Object*

---

### Description

A Trellis plot of the response versus the primary covariate is generated. If outer variables are specified, the combination of their levels are used to determine the panels of the Trellis display. Otherwise, the levels of the grouping variable determine the panels. A scatter plot of the response versus the primary covariate is displayed in each panel, with observations corresponding to same inner group joined by line segments. The Trellis function `xyplot` is used.

### Usage

```
## S3 method for class 'nfnGroupedData':
plot(x, outer, inner, innerGroups, xlab, ylab, strip, aspect, panel,
      key, grid, ...)
```

### Arguments

<code>x</code>	an object inheriting from class <code>nfnGroupedData</code> , representing a <code>groupedData</code> object with a numeric primary covariate and a single grouping level.
<code>outer</code>	an optional logical value or one-sided formula, indicating covariates that are outer to the grouping factor, which are used to determine the panels of the Trellis plot. If equal to <code>TRUE</code> , <code>attr(object, "outer")</code> is used to indicate the outer covariates. An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. Defaults to <code>NULL</code> , meaning that no outer covariates are to be used.
<code>inner</code>	an optional logical value or one-sided formula, indicating a covariate that is inner to the grouping factor, which is used to associate points within each panel of the Trellis plot. If equal to <code>TRUE</code> , <code>attr(object, "inner")</code> is used to indicate the inner covariate. An inner covariate can change within the sets of rows defined by the grouping factor. Defaults to <code>NULL</code> , meaning that no inner covariate is present.
<code>innerGroups</code>	an optional one-sided formula specifying a factor to be used for grouping the levels of the <code>inner</code> covariate. Different colors, or line types, are used for each level of the <code>innerGroups</code> factor. Default is <code>NULL</code> , meaning that no <code>innerGroups</code> covariate is present.
<code>xlab, ylab</code>	optional character strings with the labels for the plot. Default is the corresponding elements of <code>attr(object, "labels")</code> and <code>attr(object, "units")</code> pasted together.
<code>strip</code>	an optional function passed as the <code>strip</code> argument to the <code>xyplot</code> function. Default is <code>strip.default(..., style = 1)</code> (see <code>trellis.args</code> ).
<code>aspect</code>	an optional character string indicating the aspect ratio for the plot passed as the <code>aspect</code> argument to the <code>xyplot</code> function. Default is <code>"xy"</code> (see <code>trellis.args</code> ).

panel	an optional function used to generate the individual panels in the Trellis display, passed as the <code>panel</code> argument to the <code>xyplot</code> function.
key	an optional logical function or function. If <code>TRUE</code> and <code>innerGroups</code> is non-NULL, a legend for the different <code>innerGroups</code> levels is included at the top of the plot. If given as a function, it is passed as the <code>key</code> argument to the <code>xyplot</code> function. Default is <code>TRUE</code> if <code>innerGroups</code> is non-NULL and <code>FALSE</code> otherwise.
grid	an optional logical value indicating whether a grid should be added to plot. Default is <code>TRUE</code> .
...	optional arguments passed to the <code>xyplot</code> function.

**Value**

a Trellis plot of the response versus the primary covariate.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Bates, D.M. and Pinheiro, J.C. (1997), "Software Design for Longitudinal Data", in "Modelling Longitudinal and Spatially Correlated Data: Methods, Applications and Future Directions", T.G. Gregoire (ed.), Springer-Verlag, New York.

**See Also**

[groupedData](#), [xyplot](#)

**Examples**

```
# different panels per Subject
plot(Orthodont)
# different panels per gender
plot(Orthodont, outer = TRUE)
```

---

`plot.nmGroupedData` *Plot an nmGroupedData Object*

---

**Description**

The `groupedData` object is summarized by the values of the `displayLevel` grouping factor (or the combination of its values and the values of the covariate indicated in `preserve`, if any is present). The collapsed data is used to produce a new `groupedData` object, with grouping factor given by the `displayLevel` factor, which is plotted using the appropriate `plot` method for `groupedData` objects with single level of grouping.

**Usage**

```
## S3 method for class 'nmGroupedData':
plot(x, collapseLevel, displayLevel, outer, inner,
     preserve, FUN, subset, key, grid, ...)
```

**Arguments**

- x** an object inheriting from class `nmGroupedData`, representing a `groupedData` object with multiple grouping factors.
- collapseLevel** an optional positive integer or character string indicating the grouping level to use when collapsing the data. Level values increase from outermost to innermost grouping. Default is the highest or innermost level of grouping.
- displayLevel** an optional positive integer or character string indicating the grouping level to use for determining the panels in the Trellis display, when `outer` is missing. Default is `collapseLevel`.
- outer** an optional logical value or one-sided formula, indicating covariates that are outer to the `displayLevel` grouping factor, which are used to determine the panels of the Trellis plot. If equal to `TRUE`, the `displayLevel` element `attr(object, "outer")` is used to indicate the outer covariates. An outer covariate is invariant within the sets of rows defined by the grouping factor. Ordering of the groups is done in such a way as to preserve adjacency of groups with the same value of the outer variables. Defaults to `NULL`, meaning that no outer covariates are to be used.
- inner** an optional logical value or one-sided formula, indicating a covariate that is inner to the `displayLevel` grouping factor, which is used to associate points within each panel of the Trellis plot. If equal to `TRUE`, `attr(object, "outer")` is used to indicate the inner covariate. An inner covariate can change within the sets of rows defined by the grouping factor. Defaults to `NULL`, meaning that no inner covariate is present.
- preserve** an optional one-sided formula indicating a covariate whose levels should be preserved when collapsing the data according to the `collapseLevel` grouping factor. The collapsing factor is obtained by pasting together the levels of the `collapseLevel` grouping factor and the values of the covariate to be preserved. Default is `NULL`, meaning that no covariates need to be preserved.
- FUN** an optional summary function or a list of summary functions to be used for collapsing the data. The function or functions are applied only to variables in `object` that vary within the groups defined by `collapseLevel`. Invariant variables are always summarized by group using the unique value that they assume within that group. If `FUN` is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If `FUN` is a list of functions, the names in the list should designate classes of variables in the data such as `ordered`, `factor`, or `numeric`. The indicated function will be applied to any non-invariant variables of that class. The default functions to be used are `mean` for numeric factors, and `Mode` for both `factor` and `ordered`. The `Mode` function, defined internally in `gsummary`, returns the modal or most popular value of the variable. It is different from the `mode` function that returns the S-language mode of the variable.
- subset** an optional named list. Names can be either positive integers representing grouping levels, or names of grouping factors. Each element in the list is a vector indicating the levels of the corresponding grouping factor to be used for plotting the data. Default is `NULL`, meaning that all levels are used.
- key** an optional logical value, or list. If `TRUE`, a legend is included at the top of the plot indicating which symbols (colors) correspond to which prediction levels. If `FALSE`, no legend is included. If given as a list, `key` is passed down as an

	argument to the <code>trellis</code> function generating the plots ( <code>xyplot</code> ). Defaults to <code>TRUE</code> .
<code>grid</code>	an optional logical value indicating whether a grid should be added to plot. Default is <code>TRUE</code> .
<code>...</code>	optional arguments passed to the Trellis plot function.

**Value**

a Trellis display of the data collapsed over the values of the `collapseLevel` grouping factor and grouped according to the `displayLevel` grouping factor.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Bates, D.M. and Pinheiro, J.C. (1997), "Software Design for Longitudinal Data", in "Modelling Longitudinal and Spatially Correlated Data: Methods, Applications and Future Directions", T.G. Gregoire (ed.), Springer-Verlag, New York.

**See Also**

[groupedData](#), [collapse.groupedData](#), [plot.nfnGroupedData](#),  
[plot.nffGroupedData](#)

**Examples**

```
# no collapsing, panels by Dog
plot(Pixel, display = "Dog", inner = ~Side)
# collapsing by Dog, preserving day
plot(Pixel, collapse = "Dog", preserve = ~day)
```

---

`plot.ranef.lme`      *Plot a ranef.lme Object*

---

**Description**

If `form` is missing, or is given as a one-sided formula, a Trellis dot-plot of the random effects is generated, with a different panel for each random effect (coefficient). Rows in the dot-plot are determined by the `form` argument (if not missing) or by the row names of the random effects (coefficients). If a single factor is specified in `form`, its levels determine the dot-plot rows (with possibly multiple dots per row); otherwise, if `form` specifies a crossing of factors, the dot-plot rows are determined by all combinations of the levels of the individual factors in the formula. The Trellis function `dotplot` is used in this method function.

If `form` is a two-sided formula, a Trellis display is generated, with a different panel for each variable listed in the right hand side of `form`. Scatter plots are generated for numeric variables and boxplots are generated for categorical (`factor` or `ordered`) variables.

**Usage**

```
## S3 method for class 'ranef.lme':
plot(x, form, omitFixed, level, grid, control, ...)
```

**Arguments**

**x** an object inheriting from class `ranef.lme`, representing the estimated coefficients or estimated random effects for the `lme` object from which it was produced.

**form** an optional formula specifying the desired type of plot. If given as a one-sided formula, a `dotplot` of the estimated random effects (coefficients) grouped according to all combinations of the levels of the factors named in `form` is returned. Single factors (`~g`) or crossed factors (`~g1*g2`) are allowed. If given as a two-sided formula, the left hand side must be a single random effects (coefficient) and the right hand side is formed by covariates in `x` separated by `+`. A Trellis display of the random effect (coefficient) versus the named covariates is returned in this case. Default is `NULL`, in which case the row names of the random effects (coefficients) are used.

**omitFixed** an optional logical value indicating whether columns with values that are constant across groups should be omitted. Default is `TRUE`.

**level** an optional integer value giving the level of grouping to be used for `x`. Only used when `x` is a list with different components for each grouping level. Defaults to the highest or innermost level of grouping.

**grid** an optional logical value indicating whether a grid should be added to plot. Only applies to plots associated with two-sided formulas in `form`. Default is `FALSE`.

**control** an optional list with control values for the plot, when `form` is given as a two-sided formula. The control values are referenced by name in the `control` list and only the ones to be modified from the default need to be specified. Available values include: `drawLine`, a logical value indicating whether a loess smoother should be added to the scatter plots and a line connecting the medians should be added to the boxplots (default is `TRUE`); `span.loess`, used as the `span` argument in the call to `panel.loess` (default is `2/3`); `degree.loess`, used as the `degree` argument in the call to `panel.loess` (default is `1`); `cex.axis`, the character expansion factor for the x-axis (default is `0.8`); `srt.axis`, the rotation factor for the x-axis (default is `0`); and `mgp.axis`, the margin parameters for the x-axis (default is `c(2, 0.5, 0)`).

**...** optional arguments passed to the Trellis `dotplot` function.

**Value**

a Trellis plot of the estimated random-effects (coefficients) versus covariates, or groups.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[ranef.lme](#), [lme](#), [dotplot](#)



**Examples**

```
## Not run:
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
plot(ranef(fm1))
fm1RE <- ranef(fm1, aug = TRUE)
plot(fm1RE, form = ~ Sex)
plot(fm1RE, form = age ~ Sex)

## End(Not run)
```

---

plot.ranef.lmList *Plot a ranef.lmList Object*

---

**Description**

If `form` is missing, or is given as a one-sided formula, a Trellis dot-plot of the random effects is generated, with a different panel for each random effect (coefficient). Rows in the dot-plot are determined by the `form` argument (if not missing) or by the row names of the random effects (coefficients). If a single factor is specified in `form`, its levels determine the dot-plot rows (with possibly multiple dots per row); otherwise, if `form` specifies a crossing of factors, the dot-plot rows are determined by all combinations of the levels of the individual factors in the formula. The Trellis function `dotplot` is used in this method function.

If `form` is a two-sided formula, a Trellis display is generated, with a different panel for each variable listed in the right hand side of `form`. Scatter plots are generated for numeric variables and boxplots are generated for categorical (`factor` or `ordered`) variables.

**Usage**

```
## S3 method for class 'ranef.lmList':
plot(x, form, grid, control, ...)
```

**Arguments**

- |                      |  |
|----------------------|--|
| <code>x</code>       | an object inheriting from class <code>ranef.lmList</code> , representing the estimated coefficients or estimated random effects for the <code>lmList</code> object from which it was produced.   |
| <code>form</code>    | an optional formula specifying the desired type of plot. If given as a one-sided formula, a <code>dotplot</code> of the estimated random effects (coefficients) grouped according to all combinations of the levels of the factors named in <code>form</code> is returned. Single factors ( <code>~g</code> ) or crossed factors ( <code>~g1*g2</code> ) are allowed. If given as a two-sided formula, the left hand side must be a single random effects (coefficient) and the right hand side is formed by covariates in <code>x</code> separated by <code>+</code> . A Trellis display of the random effect (coefficient) versus the named covariates is returned in this case. Default is <code>NULL</code> , in which case the row names of the random effects (coefficients) are used. |
| <code>grid</code>    | an optional logical value indicating whether a grid should be added to plot. Only applies to plots associated with two-sided formulas in <code>form</code> . Default is <code>FALSE</code> .   |
| <code>control</code> | an optional list with control values for the plot, when <code>form</code> is given as a two-sided formula. The control values are referenced by name in the <code>control</code> list and only the ones to be modified from the default need to be specified.  |

Available values include: `drawLine`, a logical value indicating whether a loess smoother should be added to the scatter plots and a line connecting the medians should be added to the boxplots (default is `TRUE`); `span.loess`, used as the `span` argument in the call to `panel.loess` (default is `2/3`); `degree.loess`, used as the `degree` argument in the call to `panel.loess` (default is `1`); `cex.axis`, the character expansion factor for the x-axis (default is `0.8`); `srt.axis`, the rotation factor for the x-axis (default is `0`); and `mgp.axis`, the margin parameters for the x-axis (default is `c(2, 0.5, 0)`).

... optional arguments passed to the Trellis `dotplot` function.

### Value

a Trellis plot of the estimated random-effects (coefficients) versus covariates, or groups.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[lmList](#), [dotplot](#)

### Examples

```
fml <- lmList(distance ~ age | Subject, Orthodont)
plot(ranef(fml))
fmlRE <- ranef(fml, aug = TRUE)
plot(fmlRE, form = ~ Sex)
## Not run: plot(fmlRE, form = age ~ Sex)
```

---

plot.Variogram      *Plot a Variogram Object*

---

### Description

an xyplot of the semi-variogram versus the distances is produced. If `smooth = TRUE`, a loess smoother is added to the plot. If `showModel = TRUE` and `x` includes an "modelVariog" attribute, the corresponding semi-variogram is added to the plot.

### Usage

```
## S3 method for class 'Variogram':
plot(x, smooth, showModel, sigma, span, xlab,
     ylab, type, ylim, grid, ...)
```

**Arguments**

<code>x</code>	an object inheriting from class <code>Variogram</code> , consisting of a data frame with two columns named <code>variog</code> and <code>dist</code> , representing the semi-variogram values and the corresponding distances.
<code>smooth</code>	an optional logical value controlling whether a <code>loess</code> smoother should be added to the plot. Defaults to <code>TRUE</code> , when <code>showModel</code> is <code>FALSE</code> .
<code>showModel</code>	an optional logical value controlling whether the semi-variogram corresponding to an <code>"modelVariog"</code> attribute of <code>x</code> , if any is present, should be added to the plot. Defaults to <code>TRUE</code> , when the <code>"modelVariog"</code> attribute is present.
<code>sigma</code>	an optional numeric value used as the height of a horizontal line displayed in the plot. Can be used to represent the process standard deviation. Default is <code>NULL</code> , implying that no horizontal line is drawn.
<code>span</code>	an optional numeric value with the smoothing parameter for the <code>loess</code> fit. Default is 0.6.
<code>xlab, ylab</code>	optional character strings with the x- and y-axis labels. Default respectively to <code>"Distance"</code> and <code>"SemiVariogram"</code> .
<code>type</code>	an optional character indicating the type of plot. Defaults to <code>"p"</code> .
<code>ylim</code>	an optional numeric vector with the limits for the y-axis. Defaults to <code>c(0, max(x\$variog))</code> .
<code>grid</code>	an optional logical value indicating whether a grid should be added to plot. Default is <code>FALSE</code> .
<code>...</code>	optional arguments passed to the Trellis <code>xyplot</code> function.

**Value**

an `xyplot` Trellis plot.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[Variogram](#), [xyplot](#), [loess](#)

**Examples**

```
fm1 <- lme(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary)
plot(Variogram(fm1, form = ~ Time | Mare, maxDist = 0.7))
```

---

pooledSD

*Extract Pooled Standard Deviation*

---

### Description

The pooled estimated standard deviation is obtained by adding together the residual sum of squares for each non-null element of `object`, dividing by the sum of the corresponding residual degrees-of-freedom, and taking the square-root.

### Usage

```
pooledSD(object)
```

### Arguments

`object` an object inheriting from class `lmList`.

### Value

the pooled standard deviation for the non-null elements of `object`, with an attribute `df` with the number of degrees-of-freedom used in the estimation.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[lmList](#), [lm](#)

### Examples

```
fm1 <- lmList(Orthodont)
pooledSD(fm1)
```

---

predict.gls

*Predictions from a gls Object*

---

### Description

The predictions for the linear model represented by `object` are obtained at the covariate values defined in `newdata`.

### Usage

```
## S3 method for class 'glms':
predict(object, newdata, na.action, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>gls</code> , representing a generalized least squares fitted linear model.
<code>newdata</code>	an optional data frame to be used for obtaining the predictions. All variables used in the linear model must be present in the data frame. If missing, the fitted values are returned.
<code>na.action</code>	a function that indicates what should happen when <code>newdata</code> contains NAs. The default action ( <code>na.fail</code> ) causes the function to print an error message and terminate if there are any incomplete observations.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a vector with the predicted values.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[gls](#)

**Examples**

```
fml <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
          correlation = corAR1(form = ~ 1 | Mare))
newOvary <- data.frame(Time = c(-0.75, -0.5, 0, 0.5, 0.75))
predict(fml, newOvary)
```

---

predict.gnls

*Predictions from a gnls Object*

---

**Description**

The predictions for the nonlinear model represented by `object` are obtained at the covariate values defined in `newdata`.

**Usage**

```
## S3 method for class 'gnls':
predict(object, newdata, na.action, naPattern, ...)
```

**Arguments**

object	an object inheriting from class <code>gnls</code> , representing a generalized nonlinear least squares fitted model.
newdata	an optional data frame to be used for obtaining the predictions. All variables used in the nonlinear model must be present in the data frame. If missing, the fitted values are returned.
na.action	a function that indicates what should happen when <code>newdata</code> contains NAs. The default action ( <code>na.fail</code> ) causes the function to print an error message and terminate if there are any incomplete observations.
naPattern	an expression or formula object, specifying which returned values are to be regarded as missing.
...	some methods for this generic require additional arguments. None are used in this method.

**Value**

a vector with the predicted values.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[gnls](#)

**Examples**

```
fml <- gnls(weight ~ SSlogis(Time, Asym, xmid, scal), Soybean,
           weights = varPower())
newSoybean <- data.frame(Time = c(10, 30, 50, 80, 100))
predict(fml, newSoybean)
```

---

predict.lme

*Predictions from an lme Object*

---

**Description**

The predictions at level  $i$  are obtained by adding together the population predictions (based only on the fixed effects estimates) and the estimated contributions of the random effects to the predictions at grouping levels less or equal to  $i$ . The resulting values estimate the best linear unbiased predictions (BLUPs) at level  $i$ . If group values not included in the original grouping factors are present in `newdata`, the corresponding predictions will be set to NA for levels greater or equal to the level at which the unknown groups occur.

**Usage**

```
## S3 method for class 'lme':
predict(object, newdata, level, asList, na.action, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>lme</code> , representing a fitted linear mixed-effects model.
<code>newdata</code>	an optional data frame to be used for obtaining the predictions. All variables used in the fixed and random effects models, as well as the grouping factors, must be present in the data frame. If missing, the fitted values are returned.
<code>level</code>	an optional integer vector giving the level(s) of grouping to be used in obtaining the predictions. Level values increase from outermost to innermost grouping, with level zero corresponding to the population predictions. Defaults to the highest or innermost level of grouping.
<code>asList</code>	an optional logical value. If <code>TRUE</code> and a single value is given in <code>level</code> , the returned object is a list with the predictions split by groups; else the returned value is either a vector or a data frame, according to the length of <code>level</code> .
<code>na.action</code>	a function that indicates what should happen when <code>newdata</code> contains NAs. The default action ( <code>na.fail</code> ) causes the function to print an error message and terminate if there are any incomplete observations.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

if a single level of grouping is specified in `level`, the returned value is either a list with the predictions split by groups (`asList = TRUE`) or a vector with the predictions (`asList = FALSE`); else, when multiple grouping levels are specified in `level`, the returned object is a data frame with columns given by the predictions at different levels and the grouping factors.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[lme](#), [fitted.lme](#)

**Examples**

```
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
newOrth <- data.frame(Sex = c("Male", "Male", "Female", "Female", "Male", "Male"),
                    age = c(15, 20, 10, 12, 2, 4),
                    Subject = c("M01", "M01", "F30", "F30", "M04", "M04"))
predict(fm1, newOrth, level = 0:1)
```

---

predict.lmList      *Predictions from an lmList Object*

---

### Description

If the grouping factor corresponding to `object` is included in `newdata`, the data frame is partitioned according to the grouping factor levels; else, `newdata` is repeated for all `lm` components. The predictions and, optionally, the standard errors for the predictions, are obtained for each `lm` component of `object`, using the corresponding element of the partitioned `newdata`, and arranged into a list with as many components as `object`, or combined into a single vector or data frame (if `se.fit=TRUE`).

### Usage

```
## S3 method for class 'lmList':  
predict(object, newdata, subset, pool, asList, se.fit, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>lmList</code> , representing a list of <code>lm</code> objects with a common model.
<code>newdata</code>	an optional data frame to be used for obtaining the predictions. All variables used in the <code>object</code> model formula must be present in the data frame. If missing, the same data frame used to produce <code>object</code> is used.
<code>subset</code>	an optional character or integer vector naming the <code>lm</code> components of <code>object</code> from which the predictions are to be extracted. Default is <code>NULL</code> , in which case all components are used.
<code>asList</code>	an optional logical value. If <code>TRUE</code> , the returned object is a list with the predictions split by groups; else the returned value is a vector. Defaults to <code>FALSE</code> .
<code>pool</code>	an optional logical value indicating whether a pooled estimate of the residual standard error should be used. Default is <code>attr(object, "pool")</code> .
<code>se.fit</code>	an optional logical value indicating whether pointwise standard errors should be computed along with the predictions. Default is <code>FALSE</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

a list with components given by the predictions (and, optionally, the standard errors for the predictions) from each `lm` component of `object`, a vector with the predictions from all `lm` components of `object`, or a data frame with columns given by the predictions and their corresponding standard errors.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>



**See Also**

[lmList](#), [predict.lm](#)

**Examples**

```
fml <- lmList(distance ~ age | Subject, Orthodont)
predict(fml, se.fit = TRUE)
```

---

predict.nlme

*Predictions from an nlme Object*

---

**Description**

The predictions at level  $i$  are obtained by adding together the contributions from the estimated fixed effects and the estimated random effects at levels less or equal to  $i$  and evaluating the model function at the resulting estimated parameters. If group values not included in the original grouping factors are present in `newdata`, the corresponding predictions will be set to NA for levels greater or equal to the level at which the unknown groups occur.

**Usage**

```
## S3 method for class 'nlme':
predict(object, newdata, level, asList, na.action,
naPattern, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>nlme</code> , representing a fitted nonlinear mixed-effects model.
<code>newdata</code>	an optional data frame to be used for obtaining the predictions. All variables used in the nonlinear model, the fixed and the random effects models, as well as the grouping factors, must be present in the data frame. If missing, the fitted values are returned.
<code>level</code>	an optional integer vector giving the level(s) of grouping to be used in obtaining the predictions. Level values increase from outermost to innermost grouping, with level zero corresponding to the population predictions. Defaults to the highest or innermost level of grouping.
<code>asList</code>	an optional logical value. If <code>TRUE</code> and a single value is given in <code>level</code> , the returned object is a list with the predictions split by groups; else the returned value is either a vector or a data frame, according to the length of <code>level</code> .
<code>na.action</code>	a function that indicates what should happen when <code>newdata</code> contains NAs. The default action ( <code>na.fail</code> ) causes the function to print an error message and terminate if there are any incomplete observations.
<code>naPattern</code>	an expression or formula object, specifying which returned values are to be regarded as missing.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

if a single level of grouping is specified in `level`, the returned value is either a list with the predictions split by groups (`asList = TRUE`) or a vector with the predictions (`asList = FALSE`); else, when multiple grouping levels are specified in `level`, the returned object is a data frame with columns given by the predictions at different levels and the grouping factors.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[nlme](#), [fitted.lme](#)

**Examples**

```
fml <- nlme(height ~ SSasym(age, Asym, R0, lrc),
            data = Loblolly,
            fixed = Asym + R0 + lrc ~ 1,
            random = Asym ~ 1,
            start = c(Asym = 103, R0 = -8.5, lrc = -3.3))
newLoblolly <- data.frame(age = c(5,10,15,20,25,30),
                        Seed = rep(301,6))
predict(fml, newLoblolly, level = 0:1)
```

---

```
print.summary.pdMat
```

*Print a summary.pdMat Object*

---

**Description**

The standard deviations and correlations associated with the positive-definite matrix represented by `object` (considered as a variance-covariance matrix) are printed, together with the formula and the grouping level associated `object`, if any are present.

**Usage**

```
## S3 method for class 'summary.pdMat':
print(x, sigma, rdiag, Level, resid, ...)
```

**Arguments**

<code>x</code>	an object inheriting from class <code>summary.pdMat</code> , generally resulting from applying <code>summary</code> to an object inheriting from class <code>pdMat</code> .
<code>sigma</code>	an optional numeric value used as a multiplier for the square-root factor of the positive-definite matrix represented by <code>object</code> (usually the estimated within-group standard deviation from a mixed-effects model). Defaults to 1.
<code>rdig</code>	an optional integer value with the number of significant digits to be used in printing correlations. Defaults to 3.

Level	an optional character string with a description of the grouping level associated with <code>object</code> (generally corresponding to levels of grouping in a mixed-effects model). Defaults to <code>NULL</code> .
resid	an optional logical value. If <code>TRUE</code> an extra row with the "residual" standard deviation given in <code>sigma</code> will be included in the output. Defaults to <code>FALSE</code> .
...	optional arguments passed to <code>print.default</code> ; see the documentation on that method function.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[summary.pdMat,pdMat](#)

**Examples**

```
pd1 <- pdCompSymm(3 * diag(2) + 1, form = ~age + age^2,
  data = Orthodont)
print(summary(pd1), sigma = 1.2, resid = TRUE)
```

---

`print.varFunc`      *Print a varFunc Object*

---

**Description**

The class and the coefficients associated with `x` are printed.

**Usage**

```
## S3 method for class 'varFunc':
print(x, ...)
```

**Arguments**

<code>x</code>	an object inheriting from class <code>varFunc</code> , representing a variance function structure.
...	optional arguments passed to <code>print.default</code> ; see the documentation on that method function.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[summary.varFunc](#)

**Examples**

```
vf1 <- varPower(0.3, form = ~age)
vf1 <- Initialize(vf1, Orthodont)
print(vf1)
```

qqnorm.gls

*Normal Plot of Residuals from a gls Object***Description**

Diagnostic plots for assessing the normality of residuals the generalized least squares fit are obtained. The `form` argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a `|` operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display.

**Usage**

```
## S3 method for class 'gls':
qqnorm(y, form, abline, id, idLabels, grid, ...)
```

**Arguments**

<code>y</code>	an object inheriting from class <code>gls</code> , representing a generalized least squares fitted model.
<code>form</code>	an optional one-sided formula specifying the desired type of plot. Any variable present in the original data frame used to obtain <code>y</code> can be referenced. In addition, <code>y</code> itself can be referenced in the formula using the symbol <code>"."</code> . Conditional expressions on the right of a <code> </code> operator can be used to define separate panels in a Trellis display. The expression on the right hand side of <code>form</code> and to the left of a <code> </code> operator must evaluate to a residuals vector. Default is <code>~ resid(., type = "p")</code> , corresponding to a normal plot of the standardized residuals.
<code>abline</code>	an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.
<code>id</code>	an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized residuals (random effects). Observations with absolute standardized residuals (random effects) greater than the $1 - value/2$ quantile of the standard normal distribution are identified in the plot using <code>idLabels</code> . If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.
<code>idLabels</code>	an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the observations identified according to <code>id</code> . If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified observations. Default is the innermost grouping factor.

`grid` an optional logical value indicating whether a grid should be added to plot. Default depends on the type of Trellis plot used: if `xypplot` defaults to `TRUE`, else defaults to `FALSE`.

`...` optional arguments passed to the Trellis plot function.

**Value**

a diagnostic Trellis plot for assessing normality of residuals.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[gls](#), [plot.gls](#)

**Examples**

```
fml <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
          correlation = corAR1(form = ~ 1 | Mare))
qqnorm(fml, abline = c(0,1))
```

---

qqnorm.lme

*Normal Plot of Residuals or Random Effects from an lme Object*

---

**Description**

Diagnostic plots for assessing the normality of residuals and random effects in the linear mixed-effects fit are obtained. The `form` argument gives considerable flexibility in the type of plot specification. A conditioning expression (on the right side of a `|` operator) always implies that different panels are used for each level of the conditioning factor, according to a Trellis display.

**Usage**

```
## S3 method for class 'lme':
qqnorm(y, form, abline, id, idLabels, grid, ...)
```

**Arguments**

`y` an object inheriting from class `lme`, representing a fitted linear mixed-effects model or from class `lmList`, representing a list of `lm` objects, or from class `lm`, representing a fitted linear model, or from class `nls`, representing a nonlinear least squares fitted model.

`form` an optional one-sided formula specifying the desired type of plot. Any variable present in the original data frame used to obtain `y` can be referenced. In addition, `y` itself can be referenced in the formula using the symbol `"."`. Conditional expressions on the right of a `|` operator can be used to define separate panels in a Trellis display. The expression on the right hand side of `form` and to the left of a `|` operator must evaluate to a residuals vector, or a random effects matrix. Default is `~ resid(., type = "p")`, corresponding to a normal plot of the standardized residuals evaluated at the innermost level of nesting.

abline	an optional numeric value, or numeric vector of length two. If given as a single value, a horizontal line will be added to the plot at that coordinate; else, if given as a vector, its values are used as the intercept and slope for a line added to the plot. If missing, no lines are added to the plot.
id	an optional numeric value, or one-sided formula. If given as a value, it is used as a significance level for a two-sided outlier test for the standardized residuals (random effects). Observations with absolute standardized residuals (random effects) greater than the $1 - value/2$ quantile of the standard normal distribution are identified in the plot using <code>idLabels</code> . If given as a one-sided formula, its right hand side must evaluate to a logical, integer, or character vector which is used to identify observations in the plot. If missing, no observations are identified.
idLabels	an optional vector, or one-sided formula. If given as a vector, it is converted to character and used to label the observations identified according to <code>id</code> . If given as a one-sided formula, its right hand side must evaluate to a vector which is converted to character and used to label the identified observations. Default is the innermost grouping factor.
grid	an optional logical value indicating whether a grid should be added to plot. Default is <code>FALSE</code> .
...	optional arguments passed to the Trellis plot function.

**Value**

a diagnostic Trellis plot for assessing normality of residuals or random effects.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[lme](#), [plot.lme](#)

**Examples**

```
## Not run:
fml <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
# normal plot of standardized residuals by gender
qqnorm(fml, ~ resid(., type = "p") | Sex, abline = c(0, 1))
# normal plots of random effects
qqnorm(fml, ~ ranef(.))

## End(Not run)
```

---

Quinidine

*Quinidine Kinetics*

---

### Description

The `Quinidine` data frame has 1471 rows and 14 columns.

### Format

This data frame contains the following columns:

**Subject** a factor identifying the patient on whom the data were collected.

**time** a numeric vector giving the time (hr) at which the drug was administered or the blood sample drawn. This is measured from the time the patient entered the study.

**conc** a numeric vector giving the serum quinidine concentration (mg/L).

**dose** a numeric vector giving the dose of drug administered (mg). Although there were two different forms of quinidine administered, the doses were adjusted for differences in salt content by conversion to milligrams of quinidine base.

**interval** a numeric vector giving the when the drug has been given at regular intervals for a sufficiently long period of time to assume steady state behavior, the interval is recorded.

**Age** a numeric vector giving the age of the subject on entry to the study (yr).

**Height** a numeric vector giving the height of the subject on entry to the study (in.).

**Weight** a numeric vector giving the body weight of the subject (kg).

**Race** a factor with levels `Caucasian`, `Latin`, and `Black` identifying the race of the subject.

**Smoke** a factor with levels `no` and `yes` giving smoking status at the time of the measurement.

**Ethanol** a factor with levels `none`, `current`, `former` giving ethanol (alcohol) abuse status at the time of the measurement.

**Heart** a factor with levels `No/Mild`, `Moderate`, and `Severe` indicating congestive heart failure for the subject.

**Creatinine** an ordered factor with levels `< 50` `< = 50` indicating the creatine clearance (mg/min).

**glyco** a numeric vector giving the alpha-1 acid glycoprotein concentration (mg/dL). Often measured at the same time as the quinidine concentration.

### Details

Verme et al. (1992) analyze routine clinical data on patients receiving the drug quinidine as a treatment for cardiac arrhythmia (atrial fibrillation of ventricular arrhythmias). All patients were receiving oral quinidine doses. At irregular intervals blood samples were drawn and serum concentrations of quinidine were determined. These data are analyzed in several publications, including Davidian and Giltinan (1995, section 9.3).

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.25)

Davidian, M. and Giltinan, D. M. (1995), *Nonlinear Models for Repeated Measurement Data*, Chapman and Hall, London.

Verme, C. N., Ludden, T. M., Clementi, W. A. and Harris, S. C. (1992), Pharmacokinetics of quinine in male patients: A population analysis, *Clinical Pharmacokinetics*, **22**, 468-480.

---

 quinModel

---

*Model function for the Quinidine data*


---

**Description**

A model function for a model used with the `Quinidine` data. This function calls compiled C code.

**Usage**

```
quinModel(Subject, time, conc, dose, interval, lV, lKa, lCl)
```

**Arguments**

<code>Subject</code>	a factor identifying the patient on whom the data were collected.
<code>time</code>	a numeric vector giving the time (hr) at which the drug was administered or the blood sample drawn. This is measured from the time the patient entered the study.
<code>conc</code>	a numeric vector giving the serum quinidine concentration (mg/L).
<code>dose</code>	a numeric vector giving the dose of drug administered (mg). Although there were two different forms of quinidine administered, the doses were adjusted for differences in salt content by conversion to milligrams of quinidine base.
<code>interval</code>	a numeric vector giving the when the drug has been given at regular intervals for a sufficiently long period of time to assume steady state behavior, the interval is recorded.
<code>lV</code>	numeric. A vector of values of the natural log of the effective volume of distribution according to <code>Subject</code> and <code>time</code> .
<code>lKa</code>	numeric. A vector of values of the natural log of the absorption rate constant according to <code>Subject</code> and <code>time</code> .
<code>lCl</code>	numeric. A vector of values of the natural log of the clearance parameter according to <code>Subject</code> and <code>time</code> .

**Details**

See the details section of [Quinidine](#) for a description of the model function that `quinModel` evaluates.

**Value**

a numeric vector of predicted quinidine concentrations.



**Author(s)**

Jose Pinheiro <jose.pinhoero@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**References**

Pinheiro, J. C. and Bates, D. M. (2000) *Mixed-effects Models in S and S-PLUS*, Springer. (section 8.2)

---

 Rail

*Evaluation of Stress in Railway Rails*


---

**Description**

The Rail data frame has 18 rows and 2 columns.

**Format**

This data frame contains the following columns:

**Rail** an ordered factor identifying the rail on which the measurement was made.

**travel** a numeric vector giving the travel time for ultrasonic head-waves in the rail (nanoseconds).  
The value given is the original travel time minus 36,100 nanoseconds.

**Details**

Devore (2000, Example 10.10, p. 427) cites data from an article in *Materials Evaluation* on “a study of travel time for a certain type of wave that results from longitudinal stress of rails used for railroad track.”

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.26)

Devore, J. L. (2000), *Probability and Statistics for Engineering and the Sciences (5th ed)*, Duxbury, Boston, MA.

---

 random.effects

*Extract Random Effects*


---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `lmList` and `lme`.

**Usage**

```
random.effects(object, ...)
ranef(object, ...)
```

**Arguments**

object any fitted model object from which random effects estimates can be extracted.  
 ... some methods for this generic function require additional arguments.

**Value**

will depend on the method function used; see the appropriate documentation.

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 100, 461.

**See Also**

[ranef.lmList](#), [ranef.lme](#)

**Examples**

```
## see the method function documentation
```

---

<code>ranef.lme</code>	<i>Extract lme Random Effects</i>
------------------------	-----------------------------------

---

**Description**

The estimated random effects at level  $i$  are represented as a data frame with rows given by the different groups at that level and columns given by the random effects. If a single level of grouping is specified, the returned object is a data frame; else, the returned object is a list of such data frames. Optionally, the returned data frame(s) may be augmented with covariates summarized over groups.

**Usage**

```
## S3 method for class 'lme':
ranef(object, augFrame, level, data, which, FUN,
       standard, omitGroupingFactor, subset, ...)
```

**Arguments**

object an object inheriting from class `lme`, representing a fitted linear mixed-effects model.

augFrame an optional logical value. If `TRUE`, the returned data frame is augmented with variables defined in `data`; else, if `FALSE`, only the coefficients are returned. Defaults to `FALSE`.

level an optional vector of positive integers giving the levels of grouping to be used in extracting the random effects from an object with multiple nested grouping levels. Defaults to all levels of grouping.

data an optional data frame with the variables to be used for augmenting the returned data frame when `augFrame = TRUE`. Defaults to the data frame used to fit `object`.

which	an optional positive integer vector specifying which columns of data should be used in the augmentation of the returned data frame. Defaults to all columns in data.
FUN	an optional summary function or a list of summary functions to be applied to group-varying variables, when collapsing data by groups. Group-invariant variables are always summarized by the unique value that they assume within that group. If FUN is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If FUN is a list of functions, the names in the list should designate classes of variables in the frame such as <code>ordered</code> , <code>factor</code> , or <code>numeric</code> . The indicated function will be applied to any group-varying variables of that class. The default functions to be used are <code>mean</code> for numeric factors, and <code>Mode</code> for both <code>factor</code> and <code>ordered</code> . The <code>Mode</code> function, defined internally in <code>gsummary</code> , returns the modal or most popular value of the variable. It is different from the <code>mode</code> function that returns the S-language mode of the variable.
standard	an optional logical value indicating whether the estimated random effects should be "standardized" (i.e. divided by the estimate of the standard deviation of that group of random effects). Defaults to <code>FALSE</code> .
omitGroupingFactor	an optional logical value. When <code>TRUE</code> the grouping factor itself will be omitted from the group-wise summary of data but the levels of the grouping factor will continue to be used as the row names for the returned data frame. Defaults to <code>FALSE</code> .
subset	an optional expression indicating for which rows the random effects should be extracted.
...	some methods for this generic require additional arguments. None are used in this method.

### Value

a data frame, or list of data frames, with the estimated random effects at the grouping level(s) specified in `level` and, optionally, other covariates summarized over groups. The returned object inherits from classes `random.effects.lme` and `data.frame`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 100, 461.

### See Also

[coef.lme](#), [gsummary](#), [lme](#), [plot.ranef.lme](#), [random.effects](#)

### Examples

```
fml <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
ranef(fml)
```

```

random.effects(fml)           # same as above
random.effects(fml, augFrame = TRUE)

```

---

```

ranef.lmList           Extract lmList Random Effects

```

---

## Description

The difference between the individual `lm` components coefficients and their average is calculated.

## Usage

```

## S3 method for class 'lmList':
ranef(object, augFrame, data, which, FUN, standard,
       omitGroupingFactor, ...)

```

## Arguments

<code>object</code>	an object inheriting from class <code>lmList</code> , representing a list of <code>lm</code> objects with a common model.
<code>augFrame</code>	an optional logical value. If <code>TRUE</code> , the returned data frame is augmented with variables defined in <code>data</code> ; else, if <code>FALSE</code> , only the coefficients are returned. Defaults to <code>FALSE</code> .
<code>data</code>	an optional data frame with the variables to be used for augmenting the returned data frame when <code>augFrame = TRUE</code> . Defaults to the data frame used to fit <code>object</code> .
<code>which</code>	an optional positive integer vector specifying which columns of <code>data</code> should be used in the augmentation of the returned data frame. Defaults to all columns in <code>data</code> .
<code>FUN</code>	an optional summary function or a list of summary functions to be applied to group-varying variables, when collapsing <code>data</code> by groups. Group-invariant variables are always summarized by the unique value that they assume within that group. If <code>FUN</code> is a single function it will be applied to each non-invariant variable by group to produce the summary for that variable. If <code>FUN</code> is a list of functions, the names in the list should designate classes of variables in the frame such as <code>ordered</code> , <code>factor</code> , or <code>numeric</code> . The indicated function will be applied to any group-varying variables of that class. The default functions to be used are <code>mean</code> for numeric factors, and <code>Mode</code> for both <code>factor</code> and <code>ordered</code> . The <code>Mode</code> function, defined internally in <code>gsummary</code> , returns the modal or most popular value of the variable. It is different from the <code>mode</code> function that returns the S-language mode of the variable.
<code>standard</code>	an optional logical value indicating whether the estimated random effects should be "standardized" (i.e. divided by the corresponding estimated standard error). Defaults to <code>FALSE</code> .
<code>omitGroupingFactor</code>	an optional logical value. When <code>TRUE</code> the grouping factor itself will be omitted from the group-wise summary of <code>data</code> but the levels of the grouping factor will continue to be used as the row names for the returned data frame. Defaults to <code>FALSE</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a vector with the differences between the individual `lm` coefficients in `object` and their average.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 100, 461.

**See Also**

[fixed.effects.lmList](#), [lmList](#), [random.effects](#)

**Examples**

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
ranef(fm1)
random.effects(fm1)           # same as above
```

---

RatPupWeight	<i>The weight of rat pups</i>
--------------	-------------------------------

---

**Description**

The `RatPupWeight` data frame has 322 rows and 5 columns.

**Format**

This data frame contains the following columns:

**weight** a numeric vector

**sex** a factor with levels `Male` `Female`

**Litter** an ordered factor with levels `9 < 8 < 7 < 4 < 2 < 10 < 1 < 3 < 5 < 6 < 21 < 22 < 24 < 27 < 26 < 25 < 23 < 17 < 11 < 14 < 13 < 15 < 16 < 20 < 19 < 18 < 12`

**Lsize** a numeric vector

**Treatment** an ordered factor with levels `Control < Low < High`

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

---

`recalc`*Recalculate Condensed Linear Model Object*

---

**Description**

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include: `corStruct`, `modelStruct`, `reStruct`, and `varFunc`.

**Usage**

```
recalc(object, conLin, ...)
```

**Arguments**

<code>object</code>	any object which induces a recalculation of the condensed linear model object <code>conLin</code> .
<code>conLin</code>	a condensed linear model object, consisting of a list with components " <code>Xy</code> ", corresponding to a regression matrix ( $X$ ) combined with a response vector ( $y$ ), and " <code>logLik</code> ", corresponding to the log-likelihood of the underlying model.
<code>...</code>	some methods for this generic can take additional arguments.

**Value**

the recalculated condensed linear model object.

**Note**

This function is only used inside model fitting functions, such as `lme` and `gls`, that require recalculation of a condensed linear model object.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[recalc.corStruct](#), [recalc.modelStruct](#), [recalc.reStruct](#), [recalc.varFunc](#)

**Examples**

```
## see the method function documentation
```

---

recalc.corStruct     *Recalculate for corStruct Object*

---

### Description

This method function pre-multiplies the "Xy" component of `conLin` by the transpose square-root factor(s) of the correlation matrix (matrices) associated with `object` and adds the log-likelihood contribution of `object`, given by `logLik(object)`, to the "logLik" component of `conLin`.

### Usage

```
## S3 method for class 'corStruct':
recalc(object, conLin, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>corStruct</code> , representing a correlation structure.
<code>conLin</code>	a condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying model.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

the recalculated condensed linear model object.

### Note

This method function is only used inside model fitting functions, such as `lme` and `gls`, that allow correlated error terms.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

### See Also

[corFactor](#), [logLik.corStruct](#)

---

`recalc.modelStruct` *Recalculate for a modelStruct Object*

---

**Description**

This method function recalculates the condensed linear model object using each element of `object` sequentially from last to first.

**Usage**

```
## S3 method for class 'modelStruct':  
recalc(object, conLin, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>modelStruct</code> , representing a list of model components, such as <code>corStruct</code> and <code>varFunc</code> objects.
<code>conLin</code>	an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying model. Defaults to <code>attr(object, "conLin")</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

the recalculated condensed linear model object.

**Note**

This method function is generally only used inside model fitting functions, such as `lme` and `gls`, that allow model components, such as correlated error terms and variance functions.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[recalc.corStruct](#), [recalc.reStruct](#), [recalc.varFunc](#)



---

recalc.reStruct      *Recalculate for an reStruct Object*

---

### Description

The log-likelihood, or restricted log-likelihood, of the Gaussian linear mixed-effects model represented by `object` and `conLin` (assuming spherical within-group covariance structure), evaluated at `coef(object)` is calculated and added to the `logLik` component of `conLin`. The `settings` attribute of `object` determines whether the log-likelihood, or the restricted log-likelihood, is to be calculated. The computational methods for the (restricted) log-likelihood calculations are described in Bates and Pinheiro (1998).

### Usage

```
## S3 method for class 'reStruct':
recalc(object, conLin, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>reStruct</code> , representing a random effects structure and consisting of a list of <code>pdMat</code> objects.
<code>conLin</code>	a condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying model.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

the condensed linear model with its `logLik` component updated.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[logLik](#), [lme](#), [recalc](#), [reStruct](#)

---

recalc.varFunc      *Recalculate for varFunc Object*

---

### Description

This method function pre-multiplies the "Xy" component of `conLin` by a diagonal matrix with diagonal elements given by the weights corresponding to the variance structure represented by `object` and adds the log-likelihood contribution of `object`, given by `logLik(object)`, to the "logLik" component of `conLin`.

**Usage**

```
## S3 method for class 'varFunc':
recalc(object, conLin, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>varFunc</code> , representing a variance function structure.
<code>conLin</code>	a condensed linear model object, consisting of a list with components " <code>Xy</code> ", corresponding to a regression matrix ( <code>X</code> ) combined with a response vector ( <code>y</code> ), and " <code>logLik</code> ", corresponding to the log-likelihood of the underlying model.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

the recalculated condensed linear model object.

**Note**

This method function is only used inside model fitting functions, such as `lme` and `gls`, that allow heteroscedastic error terms.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

`recalc`, `varWeights`, `logLik.varFunc`

---

Relaxin

*Assay for Relaxin*

---

**Description**

The `Relaxin` data frame has 198 rows and 3 columns.

**Format**

This data frame contains the following columns:

**Run** an ordered factor with levels 5 < 8 < 9 < 3 < 4 < 2 < 7 < 1 < 6

**conc** a numeric vector

**cAMP** a numeric vector

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

---

`Remifentanil`*Pharmacokinetics of remifentanil*

---

**Description**

The `Remifentanil` data frame has 2107 rows and 12 columns.

**Format**

This data frame contains the following columns:

**ID** a numeric vector

**Subject** an ordered factor

**Time** a numeric vector

**conc** a numeric vector

**Rate** a numeric vector

**Amt** a numeric vector

**Age** a numeric vector

**Sex** a factor with levels `Female Male`

**Ht** a numeric vector

**Wt** a numeric vector

**BSA** a numeric vector

**LBM** a numeric vector

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

---

`residuals.gls`*Extract gls Residuals*

---

**Description**

The residuals for the linear model represented by `object` are extracted.

**Usage**

```
## S3 method for class 'gls':  
residuals(object, type, ...)
```

**Arguments**

object	an object inheriting from class <code>gls</code> , representing a generalized least squares fitted linear model, or from class <code>gnls</code> , representing a generalized nonlinear least squares fitted linear model.
type	an optional character string specifying the type of residuals to be used. If "response", the "raw" residuals (observed - fitted) are used; else, if "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".
...	some methods for this generic function require additional arguments. None are used in this method.

**Value**

a vector with the residuals for the linear model represented by `object`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[gls](#)

**Examples**

```
fml <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
          correlation = corAR1(form = ~ 1 | Mare))
residuals(fml)
```

---

residuals.glsStruct

*Calculate glsStruct Residuals*

---

**Description**

The residuals for the linear model represented by `object` are extracted.

**Usage**

```
## S3 method for class 'glsStruct':
residuals(object, glsFit, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>glsStruct</code> , representing a list of linear model components, such as <code>corStruct</code> and <code>varFunc</code> objects.
<code>glsFit</code>	an optional list with components <code>logLik</code> (log-likelihood), <code>beta</code> (coefficients), <code>sigma</code> (standard deviation for error term), <code>varBeta</code> (coefficients' covariance matrix), <code>fitted</code> (fitted values), and <code>residuals</code> (residuals). Defaults to <code>attr(object, "glsFit")</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a vector with the residuals for the linear model represented by `object`.

**Note**

This method function is primarily used inside `gls` and `residuals.gls`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[gls](#), [glsStruct](#), [residuals.gls](#), [fitted.glsStruct](#)

---

`residuals.gnlsStruct`

*Calculate gnlsStruct Residuals*

---

**Description**

The residuals for the nonlinear model represented by `object` are extracted.

**Usage**

```
## S3 method for class 'gnlsStruct':
residuals(object, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>gnlsStruct</code> , representing a list of model components, such as <code>corStruct</code> and <code>varFunc</code> objects, and attributes specifying the underlying nonlinear model and the response variable.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a vector with the residuals for the nonlinear model represented by `object`.

**Note**

This method function is primarily used inside `gnls` and `residuals.gnls`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[gnls](#), [residuals.gnls](#), [fitted.gnlsStruct](#)

---

residuals.lme      *Extract lme Residuals*

---

**Description**

The residuals at level  $i$  are obtained by subtracting the fitted levels at that level from the response vector (and dividing by the estimated within-group standard error, if `type="pearson"`). The fitted values at level  $i$  are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels less or equal to  $i$ .

**Usage**

```
## S3 method for class 'lme':
residuals(object, level, type, asList, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>lme</code> , representing a fitted linear mixed-effects model.
<code>level</code>	an optional integer vector giving the level(s) of grouping to be used in extracting the residuals from <code>object</code> . Level values increase from outermost to innermost grouping, with level zero corresponding to the population residuals. Defaults to the highest or innermost level of grouping.
<code>type</code>	an optional character string specifying the type of residuals to be used. If <code>"response"</code> , the <code>"raw"</code> residuals (observed - fitted) are used; else, if <code>"pearson"</code> , the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if <code>"normalized"</code> , the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to <code>"pearson"</code> .
<code>asList</code>	an optional logical value. If <code>TRUE</code> and a single value is given in <code>level</code> , the returned object is a list with the residuals split by groups; else the returned value is either a vector or a data frame, according to the length of <code>level</code> . Defaults to <code>FALSE</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

if a single level of grouping is specified in `level`, the returned value is either a list with the residuals split by groups (`asList = TRUE`) or a vector with the residuals (`asList = FALSE`); else, when multiple grouping levels are specified in `level`, the returned object is a data frame with columns given by the residuals at different levels and the grouping factors. For a vector or data frame result the `naresid` method is applied.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[lme](#), [fitted.lme](#)

**Examples**

```
fml <- lme(distance ~ age + Sex, data = Orthodont, random = ~ 1)
residuals(fml, level = 0:1)
```

---

```
residuals.lmeStruct
```

*Calculate lmeStruct Residuals*

---

**Description**

The residuals at level  $i$  are obtained by subtracting the fitted values at that level from the response vector. The fitted values at level  $i$  are obtained by adding together the population fitted values (based only on the fixed effects estimates) and the estimated contributions of the random effects to the fitted values at grouping levels less or equal to  $i$ .

**Usage**

```
## S3 method for class 'lmeStruct':
residuals(object, level, conLin, lmeFit, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>lmeStruct</code> , representing a list of linear mixed-effects model components, such as <code>reStruct</code> , <code>corStruct</code> , and <code>varFunc</code> objects.
<code>level</code>	an optional integer vector giving the level(s) of grouping to be used in extracting the residuals from <code>object</code> . Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.
<code>conLin</code>	an optional condensed linear model object, consisting of a list with components <code>"Xy"</code> , corresponding to a regression matrix ( $X$ ) combined with a response vector ( $y$ ), and <code>"logLik"</code> , corresponding to the log-likelihood of the underlying <code>lme</code> model. Defaults to <code>attr(object, "conLin")</code> .

`lmeFit` an optional list with components `beta` and `b` containing respectively the fixed effects estimates and the random effects estimates to be used to calculate the residuals. Defaults to `attr(object, "lmeFit")`.

`...` some methods for this generic accept optional arguments.

**Value**

if a single level of grouping is specified in `level`, the returned value is a vector with the residuals at the desired level; else, when multiple grouping levels are specified in `level`, the returned object is a matrix with columns given by the residuals at different levels.

**Note**

This method function is primarily used within the `lme` function.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[lme](#), [residuals.lme](#), [fitted.lmeStruct](#)

---

`residuals.lmList` *Extract lmList Residuals*

---

**Description**

The residuals are extracted from each `lm` component of `object` and arranged into a list with as many components as `object`, or combined into a single vector.

**Usage**

```
## S3 method for class 'lmList':
residuals(object, type, subset, asList, ...)
```

**Arguments**

`object` an object inheriting from class `lmList`, representing a list of `lm` objects with a common model.

`subset` an optional character or integer vector naming the `lm` components of `object` from which the residuals are to be extracted. Default is `NULL`, in which case all components are used.

`type` an optional character string specifying the type of residuals to be extracted. Options include `"response"` for the "raw" residuals (observed - fitted), `"pearson"` for the standardized residuals (raw residuals divided by the estimated residual standard error) using different standard errors for each `lm` fit, and `"pooled.pearson"` for the standardized residuals using a pooled estimate of the residual standard error. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to `"response"`.



`asList` an optional logical value. If `TRUE`, the returned object is a list with the residuals split by groups; else the returned value is a vector. Defaults to `FALSE`.

`...` some methods for this generic require additional arguments. None are used in this method.

### Value

a list with components given by the residuals of each `lm` component of `object`, or a vector with the residuals for all `lm` components of `object`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[lmList](#), [fitted.lmList](#)

### Examples

```
fm1 <- lmList(distance ~ age | Subject, Orthodont)
residuals(fm1)
```

---

residuals.nlmeStruct

*Calculate nlmeStruct Residuals*

---

### Description

The residuals at level  $i$  are obtained by subtracting the fitted values at that level from the response vector. The fitted values at level  $i$  are obtained by adding together the contributions from the estimated fixed effects and the estimated random effects at levels less or equal to  $i$  and evaluating the model function at the resulting estimated parameters.

### Usage

```
## S3 method for class 'nlmeStruct':
residuals(object, level, conLin, ...)
```

### Arguments

`object` an object inheriting from class `nlmeStruct`, representing a list of mixed-effects model components, such as `reStruct`, `corStruct`, and `varFunc` objects.

`level` an optional integer vector giving the level(s) of grouping to be used in extracting the residuals from `object`. Level values increase from outermost to innermost grouping, with level zero corresponding to the population fitted values. Defaults to the highest or innermost level of grouping.

conLin an optional condensed linear model object, consisting of a list with components "Xy", corresponding to a regression matrix (X) combined with a response vector (y), and "logLik", corresponding to the log-likelihood of the underlying nlme model. Defaults to `attr(object, "conLin")`.

... optional arguments to the residuals generic. Not used.

### Value

if a single level of grouping is specified in `level`, the returned value is a vector with the residuals at the desired level; else, when multiple grouping levels are specified in `level`, the returned object is a matrix with columns given by the residuals at different levels.

### Note

This method function is primarily used within the `nlme` function.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Bates, D.M. and Pinheiro, J.C. (1998) "Computational methods for multilevel models" available in PostScript or PDF formats at <http://nlme.stat.wisc.edu>

### See Also

[nlme](#), [fitted.nlmeStruct](#)

---

reStruct

*Random Effects Structure*

---

### Description

This function is a constructor for the `reStruct` class, representing a random effects structure and consisting of a list of `pdMat` objects, plus a `settings` attribute containing information for the optimization algorithm used to fit the associated mixed-effects model.

### Usage

```
reStruct(object, pdClass, REML, data)
## S3 method for class 'reStruct':
print(x, sigma, reEstimates, verbose, ...)
```

**Arguments**

<code>object</code>	any of the following: (i) a one-sided formula of the form $\sim x_1 + \dots + x_n \mid g_1 / \dots / g_m$ , with $x_1 + \dots + x_n$ specifying the model for the random effects and $g_1 / \dots / g_m$ the grouping structure ( $m$ may be equal to 1, in which case no $/$ is required). The random effects formula will be repeated for all levels of grouping, in the case of multiple levels of grouping; (ii) a list of one-sided formulas of the form $\sim x_1 + \dots + x_n \mid g$ , with possibly different random effects models for each grouping level. The order of nesting will be assumed the same as the order of the elements in the list; (iii) a one-sided formula of the form $\sim x_1 + \dots + x_n$ , or a <code>pdMat</code> object with a formula (i.e. a non-NULL value for <code>formula(object)</code> ), or a list of such formulas or <code>pdMat</code> objects. In this case, the grouping structure formula will be derived from the data used to fit the mixed-effects model, which should inherit from class <code>groupedData</code> ; (iv) a named list of formulas or <code>pdMat</code> objects as in (iii), with the grouping factors as names. The order of nesting will be assumed the same as the order of the elements in the list; (v) an <code>reStruct</code> object.
<code>pdClass</code>	an optional character string with the name of the <code>pdMat</code> class to be used for the formulas in <code>object</code> . Defaults to <code>"pdSymm"</code> which corresponds to a general positive-definite matrix.
<code>REML</code>	an optional logical value. If <code>TRUE</code> , the associated mixed-effects model will be fitted using restricted maximum likelihood; else, if <code>FALSE</code> , maximum likelihood will be used. Defaults to <code>FALSE</code> .
<code>data</code>	an optional data frame in which to evaluate the variables used in the random effects formulas in <code>object</code> . It is used to obtain the levels for <code>factors</code> , which affect the dimensions and the row/column names of the underlying <code>pdMat</code> objects. If <code>NULL</code> , no attempt is made to obtain information on <code>factors</code> appearing in the formulas. Defaults to the parent frame from which the function was called.
<code>x</code>	an object inheriting from class <code>reStruct</code> to be printed.
<code>sigma</code>	an optional numeric value used as a multiplier for the square-root factors of the <code>pdMat</code> components (usually the estimated within-group standard deviation from a mixed-effects model). Defaults to 1.
<code>reEstimates</code>	an optional list with the random effects estimates for each level of grouping. Only used when <code>verbose = TRUE</code> .
<code>verbose</code>	an optional logical value determining if the random effects estimates should be printed. Defaults to <code>FALSE</code> .
<code>...</code>	Optional arguments can be given to other methods for this generic. None are used in this method.

**Value**

an object inheriting from class `reStruct`, representing a random effects structure.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

groupedData, lme, pdMat, solve.reStruct, summary.reStruct, update.reStruct

**Examples**

```
rs1 <- reStruct(list(Dog = ~day, Side = ~1), data = Pixel)
rs1
```

---

simulate.lme

*Simulate results from lme models*

---

**Description**

The model object is fit to the data. Using the fitted values of the parameters, `nsim` new data vectors from this model are simulated. Both `m1` and `m2` are fit by maximum likelihood (ML) and/or by restricted maximum likelihood (REML) to each of the simulated data vectors.

**Usage**

```
simulate.lme(object, nsim, seed, m2, method, niterEM, useGen, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>lme</code> , representing a fitted linear mixed-effects model, or a list containing an <code>lme</code> model specification. If given as a list, it should contain components <code>fixed</code> , <code>data</code> , and <code>random</code> with values suitable for a call to <code>lme</code> . This argument defines the null model.
<code>m2</code>	an <code>lme</code> object, or a list, like <code>m1</code> containing a second <code>lme</code> model specification. This argument defines the alternative model. If given as a list, only those parts of the specification that change between model <code>m1</code> and <code>m2</code> need to be specified.
<code>seed</code>	an optional integer that is passed to <code>set.seed</code> . Defaults to a random integer.
<code>method</code>	an optional character array. If it includes "REML" the models are fit by maximizing the restricted log-likelihood. If it includes "ML" the log-likelihood is maximized. Defaults to <code>c("REML", "ML")</code> , in which case both methods are used.
<code>nsim</code>	an optional positive integer specifying the number of simulations to perform. Defaults to <b>1</b> . <b>This has changed. Previously the default was 1000.</b>
<code>niterEM</code>	an optional integer vector of length 2 giving the number of iterations of the EM algorithm to apply when fitting the <code>m1</code> and <code>m2</code> to each simulated set of data. Defaults to <code>c(40, 200)</code> .
<code>useGen</code>	an optional logical value. If <code>TRUE</code> , numerical derivatives are used to obtain the gradient and the Hessian of the log-likelihood in the optimization algorithm in the <code>ms</code> function. If <code>FALSE</code> , the default algorithm in <code>ms</code> for functions that do not incorporate gradient and Hessian attributes is used. Default depends on the <code>pdMat</code> classes used in <code>m1</code> and <code>m2</code> : if both are standard classes (see <a href="#">pdClasses</a> ) then defaults to <code>TRUE</code> , otherwise defaults to <code>FALSE</code> .
<code>...</code>	optional additional arguments. None are used.

**Value**

an object of class `simulate.lme` with components `null` and `alt`. Each of these has components `ML` and/or `REML` which are matrices. An attribute called `Random.seed` contains the seed that was used for the random number generator.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[lme](#), [set.seed](#)

**Examples**

```
## Not run:
orthSim <-
  simulate.lme(list(fixed = distance ~ age, data = Orthodont,
                  random = ~ 1 | Subject), nsim = 1000,
              m2 = list(random = ~ age | Subject))

## End(Not run)
```

---

solve.pdMat

*Calculate Inverse of a Positive-Definite Matrix*

---

**Description**

The positive-definite matrix represented by `a` is inverted and assigned to `a`.

**Usage**

```
## S3 method for class 'pdMat':
solve(a, b, ...)
```

**Arguments**

`a` an object inheriting from class `pdMat`, representing a positive definite matrix.

`b` this argument is only included for consistency with the generic function and is not used in this method function.

`...` some methods for this generic require additional arguments. None are used in this method.

**Value**

a `pdMat` object similar to `a`, but with coefficients corresponding to the inverse of the positive-definite matrix represented by `a`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[pdMat](#)

**Examples**

```
pd1 <- pdCompSymm(3 * diag(3) + 1)
solve(pd1)
```

---

solve.reStruct      *Apply Solve to an reStruct Object*

---

**Description**

Solve is applied to each `pdMat` component of `a`, which results in inverting the positive-definite matrices they represent.

**Usage**

```
## S3 method for class 'reStruct':
solve(a, b, ...)
```

**Arguments**

<code>a</code>	an object inheriting from class <code>reStruct</code> , representing a random effects structure and consisting of a list of <code>pdMat</code> objects.
<code>b</code>	this argument is only included for consistency with the generic function and is not used in this method function.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

an `reStruct` object similar to `a`, but with the `pdMat` components representing the inverses of the matrices represented by the components of `a`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[solve.pdMat](#), [reStruct](#)

**Examples**

```
rs1 <- reStruct(list(A = pdSymm(diag(1:3), form = ~Score),
  B = pdDiag(2 * diag(4), form = ~Educ)))
solve(rs1)
```

Soybean

*Growth of soybean plants***Description**

The Soybean data frame has 412 rows and 5 columns.

**Format**

This data frame contains the following columns:

**Plot** a factor giving a unique identifier for each plot.

**Variety** a factor indicating the variety; Forrest (F) or Plant Introduction \#416937 (P).

**Year** a factor indicating the year the plot was planted.

**Time** a numeric vector giving the time the sample was taken (days after planting).

**weight** a numeric vector giving the average leaf weight per plant (g).

**Details**

These data are described in Davidian and Giltinan (1995, 1.1.3, p.7) as “Data from an experiment to compare growth patterns of two genotypes of soybeans: Plant Introduction \#416937 (P), an experimental strain, and Forrest (F), a commercial variety.”

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.27)

Davidian, M. and Giltinan, D. M. (1995), *Nonlinear Models for Repeated Measurement Data*, Chapman and Hall, London.

**Examples**

```
summary(fm1 <- nlsList(SSlogis, data = Soybean))
```

---

splitFormula                      *Split a Formula*

---

### Description

Splits the right hand side of `form` into a list of subformulas according to the presence of `sep`. The left hand side of `form`, if present, will be ignored. The length of the returned list will be equal to the number of occurrences of `sep` in `form` plus one.

### Usage

```
splitFormula(form, sep)
```

### Arguments

`form`                      a formula object.  
`sep`                        an optional character string specifying the separator to be used for splitting the formula. Defaults to `" / "`.

### Value

a list of formulas, corresponding to the split of `form` according to `sep`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

### See Also

[formula](#)

### Examples

```
splitFormula(~ g1/g2/g3)
```

---

Spruce                              *Growth of Spruce Trees*

---

### Description

The `Spruce` data frame has 1027 rows and 4 columns.

### Format

This data frame contains the following columns:

**Tree** a factor giving a unique identifier for each tree.

**days** a numeric vector giving the number of days since the beginning of the experiment.

**logSize** a numeric vector giving the logarithm of an estimate of the volume of the tree trunk.

**plot** a factor identifying the plot in which the tree was grown.



**Details**

Diggle, Liang, and Zeger (1994, Example 1.3, page 5) describe data on the growth of spruce trees that have been exposed to an ozone-rich atmosphere or to a normal atmosphere.

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York. (Appendix A.28)

Diggle, Peter J., Liang, Kung-Yee and Zeger, Scott L. (1994), *Analysis of longitudinal data*, Oxford University Press, Oxford.

---

summary.corStruct *Summarize a corStruct Object*

---

**Description**

This method function prepares `object` to be printed using the `print.summary` method, by changing its class and adding a `structName` attribute to it.

**Usage**

```
## S3 method for class 'corStruct':
summary(object, structName, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>corStruct</code> , representing a correlation structure.
<code>structName</code>	an optional character string defining the type of correlation structure associated with <code>object</code> , to be used in the <code>print.summary</code> method. Defaults to <code>class(object)[1]</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

an object identical to `object`, but with its class changed to `summary.corStruct` and an additional attribute `structName`. The returned value inherits from the same classes as `object`.

**Author(s)**

Jose Pinheiro and Douglas Bates

**See Also**

[corClasses](#), [corNatural](#), [Initialize.corStruct](#), [summary](#)

**Examples**

```
cs1 <- corAR1(0.2)
summary(cs1)
```

---

`summary.gls`*Summarize a gls Object*

---

**Description**

Additional information about the linear model fit represented by `object` is extracted and included as components of `object`.

**Usage**

```
## S3 method for class 'gls':  
summary(object, verbose, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>gls</code> , representing a generalized least squares fitted linear model.
<code>verbose</code>	an optional logical value used to control the amount of output when the object is printed. Defaults to <code>FALSE</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

an object inheriting from class `summary.gls` with all components included in `object` (see [glsObject](#) for a full description of the components) plus the following components:

<code>corBeta</code>	approximate correlation matrix for the coefficients estimates
<code>tTable</code>	a data frame with columns <code>Value</code> , <code>Std. Error</code> , <code>t-value</code> , and <code>p-value</code> representing respectively the coefficients estimates, their approximate standard errors, the ratios between the estimates and their standard errors, and the associated p-value under a <i>t</i> approximation. Rows correspond to the different coefficients.
<code>residuals</code>	if more than five observations are used in the <code>gls</code> fit, a vector with the minimum, first quartile, median, third quartile, and maximum of the residuals distribution; else the residuals.
<code>AIC</code>	the Akaike Information Criterion corresponding to <code>object</code> .
<code>BIC</code>	the Bayesian Information Criterion corresponding to <code>object</code> .

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[AIC](#), [BIC](#), [gls](#), [summary](#)

**Examples**

```
fm1 <- gls(follicles ~ sin(2*pi*Time) + cos(2*pi*Time), Ovary,
           correlation = corAR1(form = ~ 1 | Mare))
summary(fm1)
```

summary.lme

*Summarize an lme Object***Description**

Additional information about the linear mixed-effects fit represented by `object` is extracted and included as components of `object`. The returned object is suitable for printing with the `print.summary.lme` method.

**Usage**

```
## S3 method for class 'lme':
summary(object, adjustSigma, verbose, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>lme</code> , representing a fitted linear mixed-effects model.
<code>adjustSigma</code>	an optional logical value. If <code>TRUE</code> and the estimation method used to obtain <code>object</code> was maximum likelihood, the residual standard error is multiplied by $\sqrt{n_{obs}/(n_{obs} - n_{par})}$ , converting it to a REML-like estimate. This argument is only used when a single fitted object is passed to the function. Default is <code>TRUE</code> .
<code>verbose</code>	an optional logical value used to control the amount of output in the <code>print.summary.lme</code> method. Defaults to <code>FALSE</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

an object inheriting from class `summary.lme` with all components included in `object` (see [lmeObject](#) for a full description of the components) plus the following components:

<code>corFixed</code>	approximate correlation matrix for the fixed effects estimates
<code>tTable</code>	a data frame with columns <code>Value</code> , <code>Std. Error</code> , <code>DF</code> , <code>t-value</code> , and <code>p-value</code> representing respectively the fixed effects estimates, their approximate standard errors, the denominator degrees of freedom, the ratios between the estimates and their standard errors, and the associated p-value from a t distribution. Rows correspond to the different fixed effects.
<code>residuals</code>	if more than five observations are used in the <code>lme</code> fit, a vector with the minimum, first quartile, median, third quartile, and maximum of the innermost grouping level residuals distribution; else the innermost grouping level residuals.
<code>AIC</code>	the Akaike Information Criterion corresponding to <code>object</code> .
<code>BIC</code>	the Bayesian Information Criterion corresponding to <code>object</code> .

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[AIC](#), [BIC](#), [lme](#), [print.summary.lme](#)

**Examples**

```
fm1 <- lme(distance ~ age, Orthodont, random = ~ age | Subject)
summary(fm1)
```

---

summary.lmList      *Summarize an lmList Object*

---

**Description**

The `summary.lm` method is applied to each `lm` component of `object` to produce summary information on the individual fits, which is organized into a list of summary statistics. The returned object is suitable for printing with the `print.summary.lmList` method.

**Usage**

```
## S3 method for class 'lmList':
summary(object, pool, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>lmList</code> , representing a list of <code>lm</code> fitted objects.
<code>pool</code>	an optional logical value indicating whether a pooled estimate of the residual standard error should be used. Default is <code>attr(object, "pool")</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a list with summary statistics obtained by applying `summary.lm` to the elements of `object`, inheriting from class `summary.lmList`. The components of `value` are:

<code>call</code>	a list containing an image of the <code>lmList</code> call that produced <code>object</code> .
<code>coefficients</code>	a three dimensional array with summary information on the <code>lm</code> coefficients. The first dimension corresponds to the names of the <code>object</code> components, the second dimension is given by "Value", "Std. Error", "t value", and "Pr(> t )", corresponding, respectively, to the coefficient estimates and their associated standard errors, t-values, and p-values. The third dimension is given by the coefficients names.
<code>correlation</code>	a three dimensional array with the correlations between the individual <code>lm</code> coefficient estimates. The first dimension corresponds to the names of the <code>object</code> components. The third dimension is given by the coefficients names. For each coefficient, the rows of the associated array give the correlations between that coefficient and the remaining coefficients, by <code>lm</code> component.

<code>cov.unscaled</code>	a three dimensional array with the unscaled variances/covariances for the individual <code>lm</code> coefficient estimates (giving the estimated variance/covariance for the coefficients, when multiplied by the estimated residual errors). The first dimension corresponds to the names of the <code>object</code> components. The third dimension is given by the coefficients names. For each coefficient, the rows of the associated array give the unscaled covariances between that coefficient and the remaining coefficients, by <code>lm</code> component.
<code>df</code>	an array with the number of degrees of freedom for the model and for residuals, for each <code>lm</code> component.
<code>df.residual</code>	the total number of degrees of freedom for residuals, corresponding to the sum of residuals <code>df</code> of all <code>lm</code> components.
<code>fstatistics</code>	an array with the F test statistics and corresponding degrees of freedom, for each <code>lm</code> component.
<code>pool</code>	the value of the <code>pool</code> argument to the function.
<code>r.squared</code>	a vector with the multiple R-squared statistics for each <code>lm</code> component.
<code>residuals</code>	a list with components given by the residuals from individual <code>lm</code> fits.
<code>RSE</code>	the pooled estimate of the residual standard error.
<code>sigma</code>	a vector with the residual standard error estimates for the individual <code>lm</code> fits.
<code>terms</code>	the terms object used in fitting the individual <code>lm</code> components.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[lmList](#), [summary](#)

**Examples**

```
fml <- lmList(distance ~ age | Subject, Orthodont)
summary(fml)
```

---

summary.modelStruct

*Summarize a modelStruct Object*

---

**Description**

This method function applies `summary` to each element of `object`.

**Usage**

```
## S3 method for class 'modelStruct':
summary(object, ...)
```

**Arguments**

- `object` an object inheriting from class `modelStruct`, representing a list of model components, such as `reStruct`, `corStruct` and `varFunc` objects.
- `...` some methods for this generic require additional arguments. None are used in this method.

**Value**

a list with elements given by the summarized components of `object`. The returned value is of class `summary.modelStruct`, also inheriting from the same classes as `object`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[reStruct](#), [summary](#)

**Examples**

```
lms1 <- lmeStruct(reStruct = reStruct(pdDiag(diag(2), ~age)),
  corStruct = corAR1(0.3))
summary(lms1)
```

---

summary.nlsList      *Summarize an nlsList Object*

---

**Description**

The `summary` function is applied to each `nls` component of `object` to produce summary information on the individual fits, which is organized into a list of summary statistics. The returned object is suitable for printing with the `print.summary.nlsList` method.

**Usage**

```
## S3 method for class 'nlsList':
summary(object, ...)
```

**Arguments**

- `object` an object inheriting from class `nlsList`, representing a list of `nls` fitted objects.
- `...` optional arguments to the `summary.lmList` method. One such optional argument is `pool`, a logical value indicating whether a pooled estimate of the residual standard error should be used. Default is `attr(object, "pool")`.

**Value**

a list with summary statistics obtained by applying `summary` to the elements of `object`, inheriting from class `summary.nlsList`. The components of `value` are:

<code>call</code>	a list containing an image of the <code>nlsList</code> call that produced <code>object</code> .
<code>parameters</code>	a three dimensional array with summary information on the <code>nls</code> coefficients. The first dimension corresponds to the names of the <code>object</code> components, the second dimension is given by "Value", "Std. Error", "t value", and "Pr(> t )", corresponding, respectively, to the coefficient estimates and their associated standard errors, t-values, and p-values. The third dimension is given by the coefficients names.
<code>correlation</code>	a three dimensional array with the correlations between the individual <code>nls</code> coefficient estimates. The first dimension corresponds to the names of the <code>object</code> components. The third dimension is given by the coefficients names. For each coefficient, the rows of the associated array give the correlations between that coefficient and the remaining coefficients, by <code>nls</code> component.
<code>cov.unscaled</code>	a three dimensional array with the unscaled variances/covariances for the individual <code>lm</code> coefficient estimates (giving the estimated variance/covariance for the coefficients, when multiplied by the estimated residual errors). The first dimension corresponds to the names of the <code>object</code> components. The third dimension is given by the coefficients names. For each coefficient, the rows of the associated array give the unscaled covariances between that coefficient and the remaining coefficients, by <code>nls</code> component.
<code>df</code>	an array with the number of degrees of freedom for the model and for residuals, for each <code>nls</code> component.
<code>df.residual</code>	the total number of degrees of freedom for residuals, corresponding to the sum of residuals <code>df</code> of all <code>nls</code> components.
<code>pool</code>	the value of the <code>pool</code> argument to the function.
<code>RSE</code>	the pooled estimate of the residual standard error.
<code>sigma</code>	a vector with the residual standard error estimates for the individual <code>lm</code> fits.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[nlsList](#), [summary](#)

**Examples**

```
fml <- nlsList(SSasymp, Loblolly)
summary(fml)
```

---

`summary.pdMat`*Summarize a pdMat Object*

---

## Description

Attributes `structName` and `noCorrelation`, with the values of the corresponding arguments to the method function, are appended to `object` and its class is changed to `summary.pdMat`.

## Usage

```
## S3 method for class 'pdMat':
summary(object, structName, noCorrelation, ...)
```

## Arguments

<code>object</code>	an object inheriting from class <code>pdMat</code> , representing a positive definite matrix.
<code>structName</code>	an optional character string with a description of the <code>pdMat</code> class. Default depends on the method function: "Blocked" for <code>pdBlocked</code> , "Compound Symmetry" for <code>pdCompSymm</code> , "Diagonal" for <code>pdDiag</code> , "Multiple of an Identity" for <code>pdIdent</code> , "General Positive-Definite, Natural Parametrization" for <code>pdNatural</code> , "General Positive-Definite" for <code>pdSymm</code> , and <code>data.class(object)</code> for <code>pdMat</code> .
<code>noCorrelation</code>	an optional logical value indicating whether correlations are to be printed in <code>print.summary.pdMat</code> . Default depends on the method function: FALSE for <code>pdDiag</code> and <code>pdIdent</code> , and TRUE for all other classes.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

## Value

an object similar to `object`, with additional attributes `structName` and `noCorrelation`, inheriting from class `summary.pdMat`.

## Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

## See Also

[print.summary.pdMat](#), [pdMat](#)

## Examples

```
summary(pdSymm(diag(4)))
```



---

summary.varFunc      *Summarize varFunc Object*

---

### Description

A `structName` attribute, with the value of corresponding argument, is appended to `object` and its class is changed to `summary.varFunc`.

### Usage

```
## S3 method for class 'varFunc':  
summary(object, structName, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>varFunc</code> , representing a variance function structure.
<code>structName</code>	an optional character string with a description of the <code>varFunc</code> class. Default depends on the method function: "Combination of variance functions" for <code>varComb</code> , "Constant plus power of covariate" for <code>varConstPower</code> , "Exponential of variance covariate" for <code>varExp</code> , "Different standard deviations per stratum" for <code>varIdent</code> , "Power of variance covariate" for <code>varPower</code> , and <code>data.class(object)</code> for <code>varFunc</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

an object similar to `object`, with an additional attribute `structName`, inheriting from class `summary.varFunc`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[varClasses](#), [varFunc](#)

### Examples

```
vf1 <- varPower(0.3, form = ~age)  
vf1 <- Initialize(vf1, Orthodont)  
summary(vf1)
```

---

Tetracycline1

*Pharmacokinetics of tetracycline*

---

### Description

The Tetracycline1 data frame has 40 rows and 4 columns.

### Format

This data frame contains the following columns:

**conc** a numeric vector

**Time** a numeric vector

**Subject** an ordered factor with levels 5 < 3 < 2 < 4 < 1

**Formulation** a factor with levels tetrachel tetracyn

### Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

---

Tetracycline2

*Pharmacokinetics of tetracycline*

---

### Description

The Tetracycline2 data frame has 40 rows and 4 columns.

### Format

This data frame contains the following columns:

**conc** a numeric vector

**Time** a numeric vector

**Subject** an ordered factor with levels 4 < 5 < 2 < 1 < 3

**Formulation** a factor with levels Berkmycin tetramycin

### Source

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

---

update.modelStruct *Update a modelStruct Object*

---

### Description

This method function updates each element of `object`, allowing the access to `data`.

### Usage

```
## S3 method for class 'modelStruct':
update(object, data, ...)
```

### Arguments

<code>object</code>	an object inheriting from class <code>modelStruct</code> , representing a list of model components, such as <code>corStruct</code> and <code>varFunc</code> objects.
<code>data</code>	a data frame in which to evaluate the variables needed for updating the elements of <code>object</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

an object similar to `object` (same class, length, and names), but with updated elements.

### Note

This method function is primarily used within model fitting functions, such as `lme` and `gls`, that allow model components such as variance functions.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### See Also

[reStruct](#)

---

update.varFunc *Update varFunc Object*

---

### Description

If the `formula(object)` includes a `"."` term, representing a fitted object, the variance covariate needs to be updated upon completion of an optimization cycle (in which the variance function weights are kept fixed). This method function allows a reevaluation of the variance covariate using the current fitted object and, optionally, other variables in the original data.

**Usage**

```
## S3 method for class 'varFunc':
update(object, data, ...)
```

**Arguments**

`object` an object inheriting from class `varFunc`, representing a variance function structure.

`data` a list with a component named "." with the current version of the fitted object (from which fitted values, coefficients, and residuals can be extracted) and, if necessary, other variables used to evaluate the variance covariate(s).

... some methods for this generic require additional arguments. None are used in this method.

**Value**

if `formula(object)` includes a "." term, an `varFunc` object similar to `object`, but with the variance covariate reevaluated at the current fitted object value; else `object` is returned unchanged.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[needUpdate](#), [covariate<-varFunc](#)

---

varClasses	<i>Variance Function Classes</i>
------------	----------------------------------

---

**Description**

Standard classes of variance function structures (`varFunc`) available in the `nlme` library. Covariates included in the variance function, denoted by variance covariates, may involve functions of the fitted model object, such as the fitted values and the residuals. Different coefficients may be assigned to the levels of a classification factor.

**Value**

Available standard classes ():

<code>varExp</code>	exponential of a variance covariate.
<code>varPower</code>	power of a variance covariate.
<code>varConstPower</code>	constant plus power of a variance covariate.
<code>varIdent</code>	constant variance(s), generally used to allow different variances according to the levels of a classification factor.
<code>varFixed</code>	fixed weights, determined by a variance covariate.
<code>varComb</code>	combination of variance functions.

**Note**

Users may define their own `varFunc` classes by specifying a constructor function and, at a minimum, methods for the functions `coef`, `coef<-`, and `initialize`. For examples of these functions, see the methods for class `varPower`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

`varComb`, `varConstPower`, `varExp`, `varFixed`, `varIdent`, `varPower`, `summary.varFunc`

---

varComb

*Combination of Variance Functions*

---

**Description**

This function is a constructor for the `varComb` class, representing a combination of variance functions. The corresponding variance function is equal to the product of the variance functions of the `varFunc` objects listed in . . . .

**Usage**

```
varComb(...)
```

**Arguments**

. . . objects inheriting from class `varFunc` representing variance function structures.

**Value**

a `varComb` object representing a combination of variance functions, also inheriting from class `varFunc`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[varClasses](#), [varWeights.varComb](#), [coef.varComb](#)

**Examples**

```
vfl <- varComb(varIdent(form = ~1|Sex), varPower())
```

---

varConstPower                      *Constant Plus Power Variance Function*

---

**Description**

This function is a constructor for the `varConstPower` class, representing a constant plus power variance function structure. Letting  $v$  denote the variance covariate and  $\sigma^2(v)$  denote the variance function evaluated at  $v$ , the constant plus power variance function is defined as  $\sigma^2(v) = (\theta_1 + |v|_2^{\theta_2})^2$ , where  $\theta_1, \theta_2$  are the variance function coefficients. When a grouping factor is present, different  $\theta_1, \theta_2$  are used for each factor level.

**Usage**

```
varConstPower(const, power, form, fixed)
```

**Arguments**

- `const`, `power` optional numeric vectors, or lists of numeric values, with, respectively, the coefficients for the constant and the power terms. Both arguments must have length one, unless a grouping factor is specified in `form`. If either argument has length greater than one, it must have names which identify its elements to the levels of the grouping factor defined in `form`. If a grouping factor is present in `form` and the argument has length one, its value will be assigned to all grouping levels. Only positive values are allowed for `const`. Default is `numeric(0)`, which results in a vector of zeros of appropriate length being assigned to the coefficients when `object` is initialized (corresponding to constant variance equal to one).
- `form` an optional one-sided formula of the form `~ v`, or `~ v | g`, specifying a variance covariate `v` and, optionally, a grouping factor `g` for the coefficients. The variance covariate must evaluate to a numeric vector and may involve expressions using `"."`, representing a fitted model object from which fitted values (`fitted(.)`) and residuals (`resid(.)`) can be extracted (this allows the variance covariate to be updated during the optimization of an object function). When a grouping factor is present in `form`, a different coefficient value is used for each of its levels. Several grouping variables may be simultaneously specified, separated by the `*` operator, as in `~ v | g1 * g2 * g3`. In this case, the levels of each grouping variable are pasted together and the resulting factor is used to group the observations. Defaults to `~ fitted(.)` representing a variance covariate given by the fitted values of a fitted model object and no grouping factor.
- `fixed` an optional list with components `const` and/or `power`, consisting of numeric vectors, or lists of numeric values, specifying the values at which some or all

of the coefficients in the variance function should be fixed. If a grouping factor is specified in `form`, the components of `fixed` must have names identifying which coefficients are to be fixed. Coefficients included in `fixed` are not allowed to vary during the optimization of an objective function. Defaults to `NULL`, corresponding to no fixed coefficients.

### Value

a `varConstPower` object representing a constant plus power variance function structure, also inheriting from class `varFunc`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

### See Also

[varClasses](#), [varWeights.varFunc](#), [coef.varConstPower](#)

### Examples

```
vf1 <- varConstPower(1.2, 0.2, form = ~age|Sex)
```

---

VarCorr

*Extract variance and correlation components*

---

### Description

This function calculates the estimated variances, standard deviations, and correlations between the random-effects terms in a linear mixed-effects model, of class `lme`, or a nonlinear mixed-effects model, of class `nlme`. The within-group error variance and standard deviation are also calculated.

### Usage

```
VarCorr(x, sigma, rdig)
```

### Arguments

<code>x</code>	a fitted model object, usually an object inheriting from class <code>lme</code> .
<code>sigma</code>	an optional numeric value used as a multiplier for the standard deviations. Default is 1.
<code>rdig</code>	an optional integer value specifying the number of digits used to represent correlation estimates. Default is 3.

**Value**

a matrix with the estimated variances, standard deviations, and correlations for the random effects. The first two columns, named `Variance` and `StdDev`, give, respectively, the variance and the standard deviations. If there are correlation components in the random effects model, the third column, named `Corr`, and the remaining unnamed columns give the estimated correlations among random effects within the same level of grouping. The within-group error variance and standard deviation are included as the last row in the matrix.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer, esp. pp. 100, 461.

**See Also**

[lme](#), [nlme](#)

**Examples**

```
fml <- lme(distance ~ age, data = Orthodont, random = ~age)
VarCorr(fml)
```

---

varExp

*Exponential Variance Function*


---

**Description**

This function is a constructor for the `varExp` class, representing an exponential variance function structure. Letting  $v$  denote the variance covariate and  $\sigma^2(v)$  denote the variance function evaluated at  $v$ , the exponential variance function is defined as  $\sigma^2(v) = \exp(2\theta v)$ , where  $\theta$  is the variance function coefficient. When a grouping factor is present, a different  $\theta$  is used for each factor level.

**Usage**

```
varExp(value, form, fixed)
```

**Arguments**

`value` an optional numeric vector, or list of numeric values, with the variance function coefficients. `Value` must have length one, unless a grouping factor is specified in `form`. If `value` has length greater than one, it must have names which identify its elements to the levels of the grouping factor defined in `form`. If a grouping factor is present in `form` and `value` has length one, its value will be assigned to all grouping levels. Default is `numeric(0)`, which results in a vector of zeros of appropriate length being assigned to the coefficients when `object` is initialized (corresponding to constant variance equal to one).



form	an optional one-sided formula of the form $\sim v$ , or $\sim v \mid g$ , specifying a variance covariate $v$ and, optionally, a grouping factor $g$ for the coefficients. The variance covariate must evaluate to a numeric vector and may involve expressions using <code>"."</code> , representing a fitted model object from which fitted values ( <code>fitted(.)</code> ) and residuals ( <code>resid(.)</code> ) can be extracted (this allows the variance covariate to be updated during the optimization of an object function). When a grouping factor is present in <code>form</code> , a different coefficient value is used for each of its levels. Several grouping variables may be simultaneously specified, separated by the <code>*</code> operator, like in $\sim v \mid g1 * g2 * g3$ . In this case, the levels of each grouping variable are pasted together and the resulting factor is used to group the observations. Defaults to $\sim fitted(.)$ representing a variance covariate given by the fitted values of a fitted model object and no grouping factor.
fixed	an optional numeric vector, or list of numeric values, specifying the values at which some or all of the coefficients in the variance function should be fixed. If a grouping factor is specified in <code>form</code> , <code>fixed</code> must have names identifying which coefficients are to be fixed. Coefficients included in <code>fixed</code> are not allowed to vary during the optimization of an objective function. Defaults to <code>NULL</code> , corresponding to no fixed coefficients.

**Value**

a `varExp` object representing an exponential variance function structure, also inheriting from class `varFunc`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[varClasses](#), [varWeights.varFunc](#), [coef.varExp](#)

**Examples**

```
vf1 <- varExp(0.2, form = ~age|Sex)
```

---

varFixed

*Fixed Variance Function*

---

**Description**

This function is a constructor for the `varFixed` class, representing a variance function with fixed variances. Letting  $v$  denote the variance covariate defined in `value`, the variance function  $\sigma^2(v)$  for this class is  $\sigma^2(v) = |v|$ . The variance covariate  $v$  is evaluated once at initialization and remains fixed thereafter. No coefficients are required to represent this variance function.

**Usage**

```
varFixed(value)
```

**Arguments**

value a one-sided formula of the form  $\sim v$  specifying a variance covariate  $v$ . Grouping factors are ignored.

**Value**

a `varFixed` object representing a fixed variance function structure, also inheriting from class `varFunc`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[varClasses](#), [varWeights.varFunc](#), [varFunc](#)

**Examples**

```
vf1 <- varFixed(~age)
```

---

varFunc

*Variance Function Structure*

---

**Description**

If `object` is a one-sided formula, it is used as the argument to `varFixed` and the resulting object is returned. Else, if `object` inherits from class `varFunc`, it is returned unchanged.

**Usage**

```
varFunc(object)
```

**Arguments**

object either an one-sided formula specifying a variance covariate, or an object inheriting from class `varFunc`, representing a variance function structure.

**Value**

an object from class `varFunc`, representing a variance function structure.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**See Also**

[summary.varFunc](#), [varFixed](#), [varWeights.varFunc](#), [coef.varFunc](#)

**Examples**

```
vf1 <- varFunc(~age)
```

---

varIdent

*Constant Variance Function*


---

**Description**

This function is a constructor for the `varIdent` class, representing a constant variance function structure. If no grouping factor is present in `form`, the variance function is constant and equal to one, and no coefficients required to represent it. When `form` includes a grouping factor with  $M > 1$  levels, the variance function allows  $M$  different variances, one for each level of the factor. For identifiability reasons, the coefficients of the variance function represent the ratios between the variances and a reference variance (corresponding to a reference group level). Therefore, only  $M - 1$  coefficients are needed to represent the variance function. By default, if the elements in `value` are unnamed, the first group level is taken as the reference level.

**Usage**

```
varIdent(value, form, fixed)
```

**Arguments**

<code>value</code>	an optional numeric vector, or list of numeric values, with the variance function coefficients. If no grouping factor is present in <code>form</code> , this argument is ignored, as the resulting variance function contains no coefficients. If <code>value</code> has length one, its value is repeated for all coefficients in the variance function. If <code>value</code> has length greater than one, it must have length equal to the number of grouping levels minus one and names which identify its elements to the levels of the grouping factor. Only positive values are allowed for this argument. Default is <code>numeric(0)</code> , which results in a vector of zeros of appropriate length being assigned to the coefficients when <code>object</code> is initialized (corresponding to constant variance equal to one).
<code>form</code>	an optional one-sided formula of the form <code>~ v</code> , or <code>~ v   g</code> , specifying a variance covariate <code>v</code> and, optionally, a grouping factor <code>g</code> for the coefficients. The variance covariate is ignored in this variance function. When a grouping factor is present in <code>form</code> , a different coefficient value is used for each of its levels less one reference level (see description section below). Several grouping variables may be simultaneously specified, separated by the <code>*</code> operator, like in <code>~ v   g1 * g2 * g3</code> . In this case, the levels of each grouping variable are pasted together and the resulting factor is used to group the observations. Defaults to <code>~ 1</code> .

`fixed` an optional numeric vector, or list of numeric values, specifying the values at which some or all of the coefficients in the variance function should be fixed. It must have names identifying which coefficients are to be fixed. Coefficients included in `fixed` are not allowed to vary during the optimization of an objective function. Defaults to `NULL`, corresponding to no fixed coefficients.

### Value

a `varIdent` object representing a constant variance function structure, also inheriting from class `varFunc`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

### See Also

[varClasses](#), [varWeights.varFunc](#), [coef.varIdent](#)

### Examples

```
vfl <- varIdent(c(Female = 0.5), form = ~ 1 | Sex)
```

---

Variogram

*Calculate Semi-variogram*

---

### Description

This function is generic; method functions can be written to handle specific classes of objects. Classes which already have methods for this function include `default`, `gls` and `lme`. See the appropriate method documentation for a description of the arguments.

### Usage

```
Variogram(object, distance, ...)
```

### Arguments

`object` a numeric vector with the values to be used for calculating the semi-variogram, usually a residual vector from a fitted model.

`distance` a numeric vector with the pairwise distances corresponding to the elements of `object`. The order of the elements in `distance` must correspond to the pairs  $(1, 2)$ ,  $(1, 3)$ ,  $\dots$ ,  $(n-1, n)$ , with  $n$  representing the length of `object`, and must have length  $n(n-1)/2$ .

`...` some methods for this generic function require additional arguments.

**Value**

will depend on the method function used; see the appropriate documentation.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[Variogram.corExp](#), [Variogram.corGaus](#), [Variogram.corLin](#),  
[Variogram.corRatio](#), [Variogram.corSpatial](#), [Variogram.corSpher](#),  
[Variogram.default](#), [Variogram.gls](#), [Variogram.lme](#), [plot.Variogram](#)

**Examples**

```
## see the method function documentation
```

---

`Variogram.corExp` *Calculate Semi-variogram for a corExp Object*

---

**Description**

This method function calculates the semi-variogram values corresponding to the Exponential correlation model, using the estimated coefficients corresponding to `object`, at the distances defined by `distance`.

**Usage**

```
## S3 method for class 'corExp':
Variogram(object, distance, sig2, length.out, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>corExp</code> , representing an exponential spatial correlation structure.
<code>distance</code>	an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to <code>NULL</code> , in which case a sequence of length <code>length.out</code> between the minimum and maximum values of <code>getCovariate(object)</code> is used.
<code>sig2</code>	an optional numeric value representing the process variance. Defaults to 1.
<code>length.out</code>	an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when <code>distance = NULL</code> . Defaults to 50.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

**See Also**

`corExp`, `plot.Variogram`, `Variogram`

**Examples**

```
stopifnot(require("stats", quietly = TRUE))
cs1 <- corExp(3, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
```

---

`Variogram.corGaus` *Calculate Semi-variogram for a corGaus Object*

---

**Description**

This method function calculates the semi-variogram values corresponding to the Gaussian correlation model, using the estimated coefficients corresponding to `object`, at the distances defined by `distance`.

**Usage**

```
## S3 method for class 'corGaus':
Variogram(object, distance, sig2, length.out, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>corGaus</code> , representing an Gaussian spatial correlation structure.
<code>distance</code>	an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to <code>NULL</code> , in which case a sequence of length <code>length.out</code> between the minimum and maximum values of <code>getCovariate(object)</code> is used.
<code>sig2</code>	an optional numeric value representing the process variance. Defaults to 1.
<code>length.out</code>	an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when <code>distance = NULL</code> . Defaults to 50.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

**See Also**

[corGaus](#), [plot.Variogram](#), [Variogram](#)

**Examples**

```
cs1 <- corGaus(3, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
```

---

Variogram.corLin     *Calculate Semi-variogram for a corLin Object*

---

**Description**

This method function calculates the semi-variogram values corresponding to the Linear correlation model, using the estimated coefficients corresponding to `object`, at the distances defined by `distance`.

**Usage**

```
## S3 method for class 'corLin':
Variogram(object, distance, sig2, length.out, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>corLin</code> , representing an Linear spatial correlation structure.
<code>distance</code>	an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to <code>NULL</code> , in which case a sequence of length <code>length.out</code> between the minimum and maximum values of <code>getCovariate(object)</code> is used.
<code>sig2</code>	an optional numeric value representing the process variance. Defaults to 1.
<code>length.out</code>	an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when <code>distance = NULL</code> . Defaults to 50.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

**See Also**

`corLin`, `plot.Variogram`, `Variogram`

**Examples**

```
cs1 <- corLin(15, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
```

---

`Variogram.corRatio` *Calculate Semi-variogram for a corRatio Object*

---

**Description**

This method function calculates the semi-variogram values corresponding to the Rational Quadratic correlation model, using the estimated coefficients corresponding to `object`, at the distances defined by `distance`.

**Usage**

```
## S3 method for class 'corRatio':
Variogram(object, distance, sig2, length.out, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>corRatio</code> , representing an Rational Quadratic spatial correlation structure.
<code>distance</code>	an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to <code>NULL</code> , in which case a sequence of length <code>length.out</code> between the minimum and maximum values of <code>getCovariate(object)</code> is used.
<code>sig2</code>	an optional numeric value representing the process variance. Defaults to 1.
<code>length.out</code>	an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when <code>distance = NULL</code> . Defaults to 50.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.



**Value**

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

**See Also**

[corRatio](#), [plot.Variogram](#) `Variogram`

**Examples**

```
cs1 <- corRatio(7, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
```

---

Variogram.corSpatial

*Calculate Semi-variogram for a corSpatial Object*

---

**Description**

This method function calculates the semi-variogram values corresponding to the model defined in `FUN`, using the estimated coefficients corresponding to `object`, at the distances defined by `distance`.

**Usage**

```
## S3 method for class 'corSpatial':
Variogram(object, distance, sig2, length.out, FUN, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>corSpatial</code> , representing spatial correlation structure.
<code>distance</code>	an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to <code>NULL</code> , in which case a sequence of length <code>length.out</code> between the minimum and maximum values of <code>getCovariate(object)</code> is used.
<code>sig2</code>	an optional numeric value representing the process variance. Defaults to 1.
<code>length.out</code>	an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when <code>distance = NULL</code> . Defaults to 50.

FUN a function of two arguments, the distance and the range corresponding to object, specifying the semi-variogram model.

... some methods for this generic require additional arguments. None are used in this method.

### Value

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

### See Also

[corSpatial](#), [Variogram](#), [Variogram.default](#), [Variogram.corExp](#),  
[Variogram.corGaus](#), [Variogram.corLin](#), [Variogram.corRatio](#),  
[Variogram.corSpher](#), [plot.Variogram](#)

### Examples

```
cs1 <- corExp(3, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1, FUN = function(x, y) (1 - exp(-x/y))[1:10,])
```

---

Variogram.corSpher *Calculate Semi-variogram for a corSpher Object*

---

### Description

This method function calculates the semi-variogram values corresponding to the Spherical correlation model, using the estimated coefficients corresponding to `object`, at the distances defined by `distance`.

### Usage

```
## S3 method for class 'corSpher':
Variogram(object, distance, sig2, length.out, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>corSpher</code> , representing an Spherical spatial correlation structure.
<code>distance</code>	an optional numeric vector with the distances at which the semi-variogram is to be calculated. Defaults to <code>NULL</code> , in which case a sequence of length <code>length.out</code> between the minimum and maximum values of <code>getCovariate(object)</code> is used.
<code>sig2</code>	an optional numeric value representing the process variance. Defaults to 1.
<code>length.out</code>	an optional integer specifying the length of the sequence of distances to be used for calculating the semi-variogram, when <code>distance = NULL</code> . Defaults to 50.
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

**See Also**

[corSpher](#), [plot.Variogram](#), [Variogram](#)

**Examples**

```
cs1 <- corSpher(15, form = ~ Time | Rat)
cs1 <- Initialize(cs1, BodyWeight)
Variogram(cs1)[1:10,]
```

---

Variogram.default *Calculate Semi-variogram*

---

**Description**

This method function calculates the semi-variogram for an arbitrary vector `object`, according to the distances in `distance`. For each pair of elements  $x, y$  in `object`, the corresponding semi-variogram is  $(x - y)^2/2$ . The semi-variogram is useful for identifying and modeling spatial correlation structures in observations with constant expectation and constant variance.

**Usage**

```
## Default S3 method:
Variogram(object, distance, ...)
```

**Arguments**

<code>object</code>	a numeric vector with the values to be used for calculating the semi-variogram, usually a residual vector from a fitted model.
<code>distance</code>	a numeric vector with the pairwise distances corresponding to the elements of <code>object</code> . The order of the elements in <code>distance</code> must correspond to the pairs $(1, 2)$ , $(1, 3)$ , ..., $(n-1, n)$ , with $n$ representing the length of <code>object</code> , and must have length $n(n-1)/2$ .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

**Value**

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. The returned value inherits from class `Variogram`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

**References**

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

**See Also**

[Variogram](#), [Variogram.gls](#), [Variogram.lme](#), [plot.Variogram](#)

**Examples**

```
## Not run:
fm1 <- lm(follicles ~ sin(2 * pi * Time) + cos(2 * pi * Time), Ovary,
         subset = Mare == 1)
Variogram(resid(fm1), dist(1:29))[1:10,]

## End(Not run)
```

---

Variogram.gls

*Calculate Semi-variogram for Residuals from a gls Object*

---

**Description**

This method function calculates the semi-variogram for the residuals from a `gls` fit. The semi-variogram values are calculated for pairs of residuals within the same group level, if a grouping factor is present. If `collapse` is different from "none", the individual semi-variogram values are collapsed using either a robust estimator (`robust = TRUE`) defined in Cressie (1993), or the average of the values within the same distance interval. The semi-variogram is useful for modeling the error term correlation structure.

**Usage**

```
## S3 method for class 'gls':
Variogram(object, distance, form, resType, data,
          na.action, maxDist, length.out, collapse, nint, breaks,
          robust, metric, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>gls</code> , representing a generalized least squares fitted model.
<code>distance</code>	an optional numeric vector with the distances between residual pairs. If a grouping variable is present, only the distances between residual pairs within the same group should be given. If missing, the distances are calculated based on the values of the arguments <code>form</code> , <code>data</code> , and <code>metric</code> , unless <code>object</code> includes a <code>corSpatial</code> element, in which case the associated covariate (obtained with the <code>getCovariate</code> method) is used.
<code>form</code>	an optional one-sided formula specifying the covariate(s) to be used for calculating the distances between residual pairs and, optionally, a grouping factor for partitioning the residuals (which must appear to the right of a <code> </code> operator in <code>form</code> ). Default is <code>~1</code> , implying that the observation order within the groups is used to obtain the distances.
<code>resType</code>	an optional character string specifying the type of residuals to be used. If <code>"response"</code> , the <code>"raw"</code> residuals (observed - fitted) are used; else, if <code>"pearson"</code> , the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if <code>"normalized"</code> , the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to <code>"pearson"</code> .
<code>data</code>	an optional data frame in which to interpret the variables in <code>form</code> . By default, the same data used to fit <code>object</code> is used.
<code>na.action</code>	a function that indicates what should happen when the data contain NAs. The default action ( <code>na.fail</code> ) causes an error message to be printed and the function to terminate, if there are any incomplete observations.
<code>maxDist</code>	an optional numeric value for the maximum distance used for calculating the semi-variogram between two residuals. By default all residual pairs are included.
<code>length.out</code>	an optional integer value. When <code>object</code> includes a <code>corSpatial</code> element, its semi-variogram values are calculated and this argument is used as the <code>length.out</code> argument to the corresponding <code>Variogram</code> method. Defaults to 50.
<code>collapse</code>	an optional character string specifying the type of collapsing to be applied to the individual semi-variogram values. If equal to <code>"quantiles"</code> , the semi-variogram values are split according to quantiles of the distance distribution, with equal number of observations per group, with possibly varying distance interval lengths. Else, if <code>"fixed"</code> , the semi-variogram values are divided according to distance intervals of equal lengths, with possibly different number of observations per interval. Else, if <code>"none"</code> , no collapsing is used and the individual semi-variogram values are returned. Defaults to <code>"quantiles"</code> .

nint	an optional integer with the number of intervals to be used when collapsing the semi-variogram values. Defaults to 20.
robust	an optional logical value specifying if a robust semi-variogram estimator should be used when collapsing the individual values. If TRUE the robust estimator is used. Defaults to FALSE.
breaks	an optional numeric vector with the breakpoints for the distance intervals to be used in collapsing the semi-variogram values. If not missing, the option specified in collapse is ignored.
metric	an optional character string specifying the distance metric to be used. The currently available options are "euclidean" for the root sum-of-squares of distances; "maximum" for the maximum difference; and "manhattan" for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to "euclidean".
...	some methods for this generic require additional arguments. None are used in this method.

### Value

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. If the semi-variogram values are collapsed, an extra column, `n.pairs`, with the number of residual pairs used in each semi-variogram calculation, is included in the returned data frame. If `object` includes a `corSpatial` element, a data frame with its corresponding semi-variogram is included in the returned value, as an attribute "modelVariog". The returned value inherits from class `Variogram`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

### See Also

[gls](#), [Variogram](#), [Variogram.default](#), [Variogram.lme](#), [plot.Variogram](#)

### Examples

```
## Not run:
fml <- gls(weight ~ Time * Diet, BodyWeight)
Variogram(fml, form = ~ Time | Rat)[1:10,]

## End(Not run)
```

Variogram.lme

*Calculate Semi-variogram for Residuals from an lme Object***Description**

This method function calculates the semi-variogram for the within-group residuals from an `lme` fit. The semi-variogram values are calculated for pairs of residuals within the same group. If `collapse` is different from "none", the individual semi-variogram values are collapsed using either a robust estimator (`robust = TRUE`) defined in Cressie (1993), or the average of the values within the same distance interval. The semi-variogram is useful for modeling the error term correlation structure.

**Usage**

```
## S3 method for class 'lme':
Variogram(object, distance, form, resType, data,
          na.action, maxDist, length.out, collapse, nint, breaks,
          robust, metric, ...)
```

**Arguments**

<code>object</code>	an object inheriting from class <code>lme</code> , representing a fitted linear mixed-effects model.
<code>distance</code>	an optional numeric vector with the distances between residual pairs. If a grouping variable is present, only the distances between residual pairs within the same group should be given. If missing, the distances are calculated based on the values of the arguments <code>form</code> , <code>data</code> , and <code>metric</code> , unless <code>object</code> includes a <code>corSpatial</code> element, in which case the associated covariate (obtained with the <code>getCovariate</code> method) is used.
<code>form</code>	an optional one-sided formula specifying the covariate(s) to be used for calculating the distances between residual pairs and, optionally, a grouping factor for partitioning the residuals (which must appear to the right of a <code> </code> operator in <code>form</code> ). Default is <code>~1</code> , implying that the observation order within the groups is used to obtain the distances.
<code>resType</code>	an optional character string specifying the type of residuals to be used. If "response", the "raw" residuals (observed - fitted) are used; else, if "pearson", the standardized residuals (raw residuals divided by the corresponding standard errors) are used; else, if "normalized", the normalized residuals (standardized residuals pre-multiplied by the inverse square-root factor of the estimated error correlation matrix) are used. Partial matching of arguments is used, so only the first character needs to be provided. Defaults to "pearson".
<code>data</code>	an optional data frame in which to interpret the variables in <code>form</code> . By default, the same data used to fit <code>object</code> is used.
<code>na.action</code>	a function that indicates what should happen when the data contain NAs. The default action ( <code>na.fail</code> ) causes an error message to be printed and the function to terminate, if there are any incomplete observations.
<code>maxDist</code>	an optional numeric value for the maximum distance used for calculating the semi-variogram between two residuals. By default all residual pairs are included.

<code>length.out</code>	an optional integer value. When <code>object</code> includes a <code>corSpatial</code> element, its semi-variogram values are calculated and this argument is used as the <code>length.out</code> argument to the corresponding <code>Variogram</code> method. Defaults to 50.
<code>collapse</code>	an optional character string specifying the type of collapsing to be applied to the individual semi-variogram values. If equal to <code>"quantiles"</code> , the semi-variogram values are split according to quantiles of the distance distribution, with equal number of observations per group, with possibly varying distance interval lengths. Else, if <code>"fixed"</code> , the semi-variogram values are divided according to distance intervals of equal lengths, with possibly different number of observations per interval. Else, if <code>"none"</code> , no collapsing is used and the individual semi-variogram values are returned. Defaults to <code>"quantiles"</code> .
<code>nint</code>	an optional integer with the number of intervals to be used when collapsing the semi-variogram values. Defaults to 20.
<code>robust</code>	an optional logical value specifying if a robust semi-variogram estimator should be used when collapsing the individual values. If <code>TRUE</code> the robust estimator is used. Defaults to <code>FALSE</code> .
<code>breaks</code>	an optional numeric vector with the breakpoints for the distance intervals to be used in collapsing the semi-variogram values. If not missing, the option specified in <code>collapse</code> is ignored.
<code>metric</code>	an optional character string specifying the distance metric to be used. The currently available options are <code>"euclidean"</code> for the root sum-of-squares of distances; <code>"maximum"</code> for the maximum difference; and <code>"manhattan"</code> for the sum of the absolute differences. Partial matching of arguments is used, so only the first three characters need to be provided. Defaults to <code>"euclidean"</code> .
<code>...</code>	some methods for this generic require additional arguments. None are used in this method.

### Value

a data frame with columns `variog` and `dist` representing, respectively, the semi-variogram values and the corresponding distances. If the semi-variogram values are collapsed, an extra column, `n.pairs`, with the number of residual pairs used in each semi-variogram calculation, is included in the returned data frame. If `object` includes a `corSpatial` element, a data frame with its corresponding semi-variogram is included in the returned value, as an attribute `"modelVariog"`. The returned value inherits from class `Variogram`.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Cressie, N.A.C. (1993), "Statistics for Spatial Data", J. Wiley & Sons.

### See Also

[lme](#), [Variogram](#), [Variogram.default](#), [Variogram.gls](#), [plot.Variogram](#)



**Examples**

```
fml <- lme(weight ~ Time * Diet, data=BodyWeight, ~ Time | Rat)
Variogram(fml, form = ~ Time | Rat, nint = 10, robust = TRUE)
```

varPower

*Power Variance Function***Description**

This function is a constructor for the `varPower` class, representing a power variance function structure. Letting  $v$  denote the variance covariate and  $\sigma^2(v)$  denote the variance function evaluated at  $v$ , the power variance function is defined as  $\sigma^2(v) = |v|^{2\theta}$ , where  $\theta$  is the variance function coefficient. When a grouping factor is present, a different  $\theta$  is used for each factor level.

**Usage**

```
varPower(value, form, fixed)
```

**Arguments**

value	an optional numeric vector, or list of numeric values, with the variance function coefficients. Value must have length one, unless a grouping factor is specified in <code>form</code> . If <code>value</code> has length greater than one, it must have names which identify its elements to the levels of the grouping factor defined in <code>form</code> . If a grouping factor is present in <code>form</code> and <code>value</code> has length one, its value will be assigned to all grouping levels. Default is <code>numeric(0)</code> , which results in a vector of zeros of appropriate length being assigned to the coefficients when object is initialized (corresponding to constant variance equal to one).
form	an optional one-sided formula of the form <code>~ v</code> , or <code>~ v   g</code> , specifying a variance covariate <code>v</code> and, optionally, a grouping factor <code>g</code> for the coefficients. The variance covariate must evaluate to a numeric vector and may involve expressions using <code>"."</code> , representing a fitted model object from which fitted values ( <code>fitted(.)</code> ) and residuals ( <code>resid(.)</code> ) can be extracted (this allows the variance covariate to be updated during the optimization of an object function). When a grouping factor is present in <code>form</code> , a different coefficient value is used for each of its levels. Several grouping variables may be simultaneously specified, separated by the <code>*</code> operator, like in <code>~ v   g1 * g2 * g3</code> . In this case, the levels of each grouping variable are pasted together and the resulting factor is used to group the observations. Defaults to <code>~ fitted(.)</code> representing a variance covariate given by the fitted values of a fitted model object and no grouping factor.
fixed	an optional numeric vector, or list of numeric values, specifying the values at which some or all of the coefficients in the variance function should be fixed. If a grouping factor is specified in <code>form</code> , <code>fixed</code> must have names identifying which coefficients are to be fixed. Coefficients included in <code>fixed</code> are not allowed to vary during the optimization of an objective function. Defaults to <code>NULL</code> , corresponding to no fixed coefficients.

**Value**

a `varPower` object representing a power variance function structure, also inheriting from class `varFunc`.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[varWeights.varFunc](#), [coef.varPower](#)

**Examples**

```
vf1 <- varPower(0.2, form = ~age|Sex)
```

---

varWeights

*Extract Variance Function Weights*

---

**Description**

The inverse of the standard deviations corresponding to the variance function structure represented by `object` are returned.

**Usage**

```
varWeights(object)
```

**Arguments**

`object` an object inheriting from class `varFunc`, representing a variance function structure.

**Value**

if `object` has a `weights` attribute, its value is returned; else `NULL` is returned.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**References**

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

**See Also**

[logLik.varFunc](#), [varWeights](#)

## Examples

```
vf1 <- varPower(form=~age)
vf1 <- Initialize(vf1, Orthodont)
coef(vf1) <- 0.3
varWeights(vf1)[1:10]
```

---

varWeights.glsStruct

*Variance Weights for glsStruct Object*

---

## Description

If `object` includes a `varStruct` component, the inverse of the standard deviations of the variance function structure represented by the corresponding `varFunc` object are returned; else, a vector of ones of length equal to the number of observations in the data frame used to fit the associated linear model is returned.

## Usage

```
## S3 method for class 'glsStruct':
varWeights(object)
```

## Arguments

`object` an object inheriting from class `glsStruct`, representing a list of linear model components, such as `corStruct` and `varFunc` objects.

## Value

if `object` includes a `varStruct` component, a vector with the corresponding variance weights; else, or a vector of ones.

## Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

## References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

## See Also

[varWeights](#)

---

`varWeights.lmeStruct`*Variance Weights for lmeStruct Object*

---

### Description

If `object` includes a `varStruct` component, the inverse of the standard deviations of the variance function structure represented by the corresponding `varFunc` object are returned; else, a vector of ones of length equal to the number of observations in the data frame used to fit the associated linear mixed-effects model is returned.

### Usage

```
## S3 method for class 'lmeStruct':  
varWeights(object)
```

### Arguments

`object` an object inheriting from class `lmeStruct`, representing a list of linear mixed-effects model components, such as `reStruct`, `corStruct`, and `varFunc` objects.

### Value

if `object` includes a `varStruct` component, a vector with the corresponding variance weights; else, or a vector of ones.

### Author(s)

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates <bates@stat.wisc.edu>

### References

Pinheiro, J.C., and Bates, D.M. (2000) "Mixed-Effects Models in S and S-PLUS", Springer.

### See Also

[varWeights](#)

---

`Wafer`*Modeling of Analog MOS Circuits*

---

### Description

The `Wafer` data frame has 400 rows and 4 columns.

**Format**

This data frame contains the following columns:

**Wafer** a factor with levels 1 2 3 4 5 6 7 8 9 10

**Site** a factor with levels 1 2 3 4 5 6 7 8

**voltage** a numeric vector

**current** a numeric vector

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

---

Wheat	<i>Yields by growing conditions</i>
-------	-------------------------------------

---

**Description**

The Wheat data frame has 48 rows and 4 columns.

**Format**

This data frame contains the following columns:

**Tray** an ordered factor with levels 3 < 1 < 2 < 4 < 5 < 6 < 8 < 9 < 7 < 12 < 11 < 10

**Moisture** a numeric vector

**fertilizer** a numeric vector

**DryMatter** a numeric vector

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

---

Wheat2	<i>Wheat Yield Trials</i>
--------	---------------------------

---

**Description**

The Wheat2 data frame has 224 rows and 5 columns.

**Format**

This data frame contains the following columns:

**Block** an ordered factor with levels 4 < 2 < 3 < 1

**variety** a factor with levels ARAPAHOE BRULE BUCKSKIN CENTURA CENTURK78 CHEYENNE  
 CODY COLT GAGE HOMESTEAD KS831374 LANCER LANCOTA NE83404 NE83406  
 NE83407 NE83432 NE83498 NE83T12 NE84557 NE85556 NE85623 NE86482  
 NE86501 NE86503 NE86507 NE86509 NE86527 NE86582 NE86606 NE86607  
 NE86T666 NE87403 NE87408 NE87409 NE87446 NE87451 NE87457 NE87463  
 NE87499 NE87512 NE87513 NE87522 NE87612 NE87613 NE87615 NE87619  
 NE87627 NORKAN REDLAND ROUGHRIDER SCOUT66 SIOUXLAND TAM107 TAM200  
 VONA

**yield** a numeric vector

**latitude** a numeric vector

**longitude** a numeric vector

**Source**

Pinheiro, J. C. and Bates, D. M. (2000), *Mixed-Effects Models in S and S-PLUS*, Springer, New York.

[.pdMat

*Subscript a pdMat Object***Description**

This method function extracts sub-matrices from the positive-definite matrix represented by `x`.

**Usage**

```
## S3 method for class 'pdMat':
x[i, j, drop = TRUE]
## S3 replacement method for class 'pdMat':
x[i, j] <- value
```

**Arguments**

<code>x</code>	an object inheriting from class <code>pdMat</code> representing a positive-definite matrix.
<code>i, j</code>	optional subscripts applying respectively to the rows and columns of the positive-definite matrix represented by <code>object</code> . When <code>i</code> ( <code>j</code> ) is omitted, all rows (columns) are extracted.
<code>drop</code>	a logical value. If <code>TRUE</code> , single rows or columns are converted to vectors. If <code>FALSE</code> the returned value retains its matrix representation.
<code>value</code>	a vector, or matrix, with the replacement values for the relevant piece of the matrix represented by <code>x</code> .

**Value**

if `i` and `j` are identical, the returned value will be `pdMat` object with the same class as `x`. Otherwise, the returned value will be a matrix. In the case a single row (or column) is selected, the returned value may be converted to a vector, according to the rules above.

**Author(s)**

Jose Pinheiro <Jose.Pinheiro@pharma.novartis.com> and Douglas Bates  
<bates@stat.wisc.edu>

**See Also**

[\[,pdMat\]](#)

**Examples**

```
pd1 <- pdSymm(diag(3))
pd1[1, , drop = FALSE]
pd1[1:2, 1:2] <- 3 * diag(2)
```

## Chapter 20

# The `nnet` package

---

`class.ind`

*Generates Class Indicator Matrix from a Factor*

---

### Description

Generates a class indicator function from a given factor.

### Usage

```
class.ind(cl)
```

### Arguments

`cl` factor or vector of classes for cases.

### Value

a matrix which is zero except for the column corresponding to the class.

### References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### Examples

```
# The function is currently defined as
class.ind <- function(cl)
{
  n <- length(cl)
  cl <- as.factor(cl)
  x <- matrix(0, n, length(levels(cl)) )
  x[(1:n) + n*(unclass(cl)-1)] <- 1
  dimnames(x) <- list(names(cl), levels(cl))
  x
}
```



---

multinom

*Fit Multinomial Log-linear Models*


---

### Description

Fits multinomial log-linear models via neural networks.

### Usage

```
multinom(formula, data, weights, subset, na.action,
         contrasts = NULL, Hess = FALSE, summ = 0, censored = FALSE,
         model = FALSE, ...)
```

### Arguments

<code>formula</code>	a formula expression as for regression models, of the form <code>response ~ predictors</code> . The response should be a factor or a matrix with <code>K</code> columns, which will be interpreted as counts for each of <code>K</code> classes. A log-linear model is fitted, with coefficients zero for the first class. An offset can be included: it should be a numeric matrix with <code>K</code> columns if the response is either a matrix with <code>K</code> columns or a factor with <code>K &gt; 2</code> classes, or a numeric vector for a response factor with 2 levels. See the documentation of <code>formula()</code> for other details.
<code>data</code>	an optional data frame in which to interpret the variables occurring in <code>formula</code> .
<code>weights</code>	optional case weights in fitting.
<code>subset</code>	expression saying which subset of the rows of the data should be used in the fit. All observations are included by default.
<code>na.action</code>	a function to filter missing data.
<code>contrasts</code>	a list of contrasts to be used for some or all of the factors appearing as variables in the model formula.
<code>Hess</code>	logical for whether the Hessian (the observed/expected information matrix) should be returned.
<code>summ</code>	integer; if non-zero summarize by deleting duplicate rows and adjust weights. Methods 1 and 2 differ in speed (2 uses C); method 3 also combines rows with the same X and different Y, which changes the baseline for the deviance.
<code>censored</code>	If Y is a matrix with <code>K &gt; 2</code> columns, interpret the entries as one for possible classes, zero for impossible classes, rather than as counts.
<code>model</code>	logical. If true, the model frame is saved as component <code>model</code> of the returned object.
<code>...</code>	additional arguments for <code>nnet</code>

### Details

`multinom` calls `nnet`. The variables on the rhs of the formula should be roughly scaled to [0,1] or the fit will be slow or may not converge at all.

**Value**

A `nnet` object with additional components:

deviance	the residual deviance, compared to the full saturated model (that explains individual observations exactly). Also, minus twice log-likelihood.
edf	the (effective) number of degrees of freedom used by the model
AIC	the AIC for this fit.
Hessian	(if <code>Hess</code> is true).
model	(if <code>model</code> is true).

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[nnet](#)

**Examples**

```
options(contrasts = c("contr.treatment", "contr.poly"))
library(MASS)
example(birthwt)
(bwt.mu <- multinom(low ~ ., bwt))
## Not run: Call:
multinom(formula = low ~ ., data = bwt)

Coefficients:
(Intercept)      age      lwt raceblack raceother
  0.823477 -0.03724311 -0.01565475  1.192371  0.7406606
  smoke      ptd      ht      ui      ftv1      ftv2+
  0.7555234  1.343648  1.913213  0.6802007 -0.4363238  0.1789888

Residual Deviance: 195.4755
AIC: 217.4755

## End(Not run)
```

---

nnet

*Fit Neural Networks*


---

**Description**

Fit single-hidden-layer neural network, possibly with skip-layer connections.

**Usage**

```
nnet(x, ...)

## S3 method for class 'formula':
nnet(formula, data, weights, ...,
      subset, na.action, contrasts = NULL)

## Default S3 method:
nnet(x, y, weights, size, Wts, mask,
      linout = FALSE, entropy = FALSE, softmax = FALSE,
      censored = FALSE, skip = FALSE, rang = 0.7, decay = 0,
      maxit = 100, Hess = FALSE, trace = TRUE, MaxNWts = 1000,
      abstol = 1.0e-4, reltol = 1.0e-8, ...)
```

**Arguments**

<code>formula</code>	A formula of the form <code>class ~ x1 + x2 + ...</code>
<code>x</code>	matrix or data frame of <code>x</code> values for examples.
<code>y</code>	matrix or data frame of target values for examples.
<code>weights</code>	(case) weights for each example – if missing defaults to 1.
<code>size</code>	number of units in the hidden layer. Can be zero if there are skip-layer units.
<code>data</code>	Data frame from which variables specified in <code>formula</code> are preferentially to be taken.
<code>subset</code>	An index vector specifying the cases to be used in the training sample. (NOTE: If given, this argument must be named.)
<code>na.action</code>	A function to specify the action to be taken if NAs are found. The default action is for the procedure to fail. An alternative is <code>na.omit</code> , which leads to rejection of cases with missing values on any required variable. (NOTE: If given, this argument must be named.)
<code>contrasts</code>	a list of contrasts to be used for some or all of the factors appearing as variables in the model formula.
<code>Wts</code>	initial parameter vector. If missing chosen at random.
<code>mask</code>	logical vector indicating which parameters should be optimized (default all).
<code>linout</code>	switch for linear output units. Default logistic output units.
<code>entropy</code>	switch for entropy (= maximum conditional likelihood) fitting. Default by least-squares.
<code>softmax</code>	switch for softmax (log-linear model) and maximum conditional likelihood fitting. <code>linout</code> , <code>entropy</code> , <code>softmax</code> and <code>censored</code> are mutually exclusive.
<code>censored</code>	A variant on <code>softmax</code> , in which non-zero targets mean possible classes. Thus for <code>softmax</code> a row of (0, 1, 1) means one example each of classes 2 and 3, but for <code>censored</code> it means one example whose class is only known to be 2 or 3.
<code>skip</code>	switch to add skip-layer connections from input to output.
<code>rang</code>	Initial random weights on <code>[-rang, rang]</code> . Value about 0.5 unless the inputs are large, in which case it should be chosen so that <code>rang * max( x )</code> is about 1.
<code>decay</code>	parameter for weight decay. Default 0.
<code>maxit</code>	maximum number of iterations. Default 100.

Hess	If true, the Hessian of the measure of fit at the best set of weights found is returned as component <code>Hessian</code> .
trace	switch for tracing optimization. Default TRUE.
MaxNWts	The maximum allowable number of weights. There is no intrinsic limit in the code, but increasing <code>MaxNWts</code> will probably allow fits that are very slow and time-consuming.
abstol	Stop if the fit criterion falls below <code>abstol</code> , indicating an essentially perfect fit.
reltol	Stop if the optimizer is unable to reduce the fit criterion by a factor of at least <code>1 - reltol</code> .
...	arguments passed to or from other methods.

### Details

If the response in `formula` is a factor, an appropriate classification network is constructed; this has one output and entropy fit if the number of levels is two, and a number of outputs equal to the number of classes and a softmax output stage for more levels. If the response is not a factor, it is passed on unchanged to `nnet.default`.

Optimization is done via the BFGS method of `optim`.

### Value

object of class "nnet" or "nnet.formula". Mostly internal structure, but has components

<code>wts</code>	the best set of weights found
<code>value</code>	value of fitting criterion plus weight decay term.
<code>fitted.values</code>	the fitted values for the training data.
<code>residuals</code>	the residuals for the training data.
<code>convergence</code>	1 if the maximum number of iterations was reached, otherwise 0.

### References

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### See Also

[predict.nnet](#), [nnetHess](#)

### Examples

```
# use half the iris data
ir <- rbind(iris3[, , 1], iris3[, , 2], iris3[, , 3])
targets <- class.ind( c(rep("s", 50), rep("c", 50), rep("v", 50)) )
samp <- c(sample(1:50, 25), sample(51:100, 25), sample(101:150, 25))
irl <- nnet(ir[samp,], targets[samp,], size = 2, rang = 0.1,
           decay = 5e-4, maxit = 200)
test.cl <- function(true, pred) {
  true.col <- max.col(true)
  cres <- max.col(pred)
  table(true, cres)
```

```

}
test.cl(targets[-samp,], predict(ir1, ir[-samp,]))

# or
ird <- data.frame(rbind(iris3[,1], iris3[,2], iris3[,3]),
  species = factor(c(rep("s",50), rep("c", 50), rep("v", 50))))
ir.nn2 <- nnet(species ~ ., data = ird, subset = samp, size = 2, rang = 0.1,
  decay = 5e-4, maxit = 200)
table(ird$species[-samp], predict(ir.nn2, ird[-samp,], type = "class"))

```

---

nnetHess

*Evaluates Hessian for a Neural Network*


---

### Description

Evaluates the Hessian (matrix of second derivatives) of the specified neural network. Normally called via argument `Hess=TRUE` to `nnet` or via `vcov.multinom`.

### Usage

```
nnetHess(net, x, y, weights)
```

### Arguments

<code>net</code>	object of class <code>nnet</code> as returned by <code>nnet</code> .
<code>x</code>	training data.
<code>y</code>	classes for training data.
<code>weights</code>	the (case) weights used in the <code>nnet</code> fit.

### Value

square symmetric matrix of the Hessian evaluated at the weights stored in the net.

### References

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.  
 Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### See Also

[nnet](#), [predict.nnet](#)

### Examples

```

# use half the iris data
ir <- rbind(iris3[,1], iris3[,2], iris3[,3])
targets <- matrix(c(rep(c(1,0,0),50), rep(c(0,1,0),50), rep(c(0,0,1),50)),
  150, 3, byrow=TRUE)
samp <- c(sample(1:50,25), sample(51:100,25), sample(101:150,25))
ir1 <- nnet(ir[samp,], targets[samp,], size=2, rang=0.1, decay=5e-4, maxit=200)
eigen(nnetHess(ir1, ir[samp,], targets[samp,]), TRUE)$values

```

---

predict.nnet                      *Predict New Examples by a Trained Neural Net*

---

## Description

Predict new examples by a trained neural net.

## Usage

```
## S3 method for class 'nnet':
predict(object, newdata, type = c("raw", "class"), ...)
```

## Arguments

object	an object of class nnet as returned by nnet.
newdata	matrix or data frame of test examples. A vector is considered to be a row vector comprising a single case.
type	Type of output
...	arguments passed to or from other methods.

## Details

This function is a method for the generic function `predict()` for class "nnet". It can be invoked by calling `predict(x)` for an object `x` of the appropriate class, or directly by calling `predict.nnet(x)` regardless of the class of the object.

## Value

If `type = "raw"`, the matrix of values returned by the trained network; if `type = "class"`, the corresponding class (which is probably only useful if the net was generated by `nnet.formula`).

## References

Ripley, B. D. (1996) *Pattern Recognition and Neural Networks*. Cambridge.  
 Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

## See Also

[nnet, which.is.max](#)

## Examples

```
# use half the iris data
ir <- rbind(iris3[,1], iris3[,2], iris3[,3])
targets <- class.ind( c(rep("s", 50), rep("c", 50), rep("v", 50)) )
samp <- c(sample(1:50,25), sample(51:100,25), sample(101:150,25))
irl <- nnet(ir[samp,], targets[samp,], size = 2, rang = 0.1,
           decay = 5e-4, maxit = 200)
test.cl <- function(true, pred){
  true <- max.col(true)
```

```

      cres <- max.col(pred)
      table(true, cres)
    }
test.cl(targets[-samp,], predict(ir1, ir[-samp,]))

# or
ird <- data.frame(rbind(iris3[,1], iris3[,2], iris3[,3]),
  species=factor(c(rep("s",50), rep("c", 50), rep("v", 50))))
ir.nn2 <- nnet(species ~ ., data = ird, subset = samp, size = 2, rang = 0.1,
  decay = 5e-4, maxit = 200)
table(ird$species[-samp], predict(ir.nn2, ird[-samp,], type = "class"))

```

---

which.is.max

*Find Maximum Position in Vector*


---

### Description

Find the maximum position in a vector, breaking ties at random.

### Usage

```
which.is.max(x)
```

### Arguments

x                    a vector

### Details

Ties are broken at random.

### Value

index of a maximal value.

### References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### See Also

[max.col](#), [which.max](#) which takes the first of ties.

### Examples

```

## Not run:
pred <- predict(nnet, test)
table(true, apply(pred,1,which.is.max))

## End(Not run)

```

## Chapter 21

# The rpart package

---

`car.test.frame`      *Automobile Data from 'Consumer Reports' 1990*

---

### Description

The `car.test.frame` data frame has 60 rows and 8 columns, giving data on makes of cars taken from the April, 1990 issue of *Consumer Reports*. This is part of a larger dataset, some columns of which are given in [cu.summary](#).

### Usage

```
car.test.frame
```

### Format

This data frame contains the following columns:

`Price` a numeric vector giving the list price in US dollars of a standard model

`Country of origin`, a factor with levels France Germany Japan Japan/USA Korea Mexico Sweden USA

`Reliability` a numeric vector coded 1 to 5.

`Mileage` fuel consumption miles per US gallon, as tested.

`Type` a factor with levels Compact Large Medium Small Sporty Van

`Weight` kerb weight in pounds.

`Disp.` the engine capacity (displacement) in litres.

`HP` the net horsepower of the vehicle.

### Source

*Consumer Reports*, April, 1990, pp. 235–288 quoted in

John M. Chambers and Trevor J. Hastie eds. (1992) *Statistical Models in S*, Wadsworth and Brooks/Cole, Pacific Grove, CA 1992, pp. 46–47.



**See Also**

[cu.summary](#)

**Examples**

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
summary(z.auto)
```

---

cu.summary

*Automobile Data from 'Consumer Reports' 1990*

---

**Description**

The `cu.summary` data frame has 117 rows and 5 columns, giving data on makes of cars taken from the April, 1990 issue of *Consumer Reports*.

**Usage**

```
cu.summary
```

**Format**

This data frame contains the following columns:

`Price` a numeric vector giving the list price in US dollars of a standard model

`Country of origin`, a factor with levels Brazil England France Germany Japan  
Japan/USA Korea Mexico Sweden USA

`Reliability` an ordered factor with levels Much worse < worse < average < better <  
Much better

`Mileage` fuel consumption miles per US gallon, as tested.

`Type` a factor with levels Compact Large Medium Small Sporty Van

**Source**

*Consumer Reports*, April, 1990, pp. 235–288 quoted in

John M. Chambers and Trevor J. Hastie eds. (1992) *Statistical Models in S*, Wadsworth and Brooks/Cole, Pacific Grove, CA 1992, pp. 46–47.

**See Also**

[car.test.frame](#)

**Examples**

```
fit <- rpart(Price ~ Mileage + Type + Country, cu.summary)
plot(fit, compress=TRUE)
text(fit, use.n=TRUE)
```

kyphosis

*Data on Children who have had Corrective Spinal Surgery***Description**

The `kyphosis` data frame has 81 rows and 4 columns. representing data on children who have had corrective spinal surgery

**Usage**

```
kyphosis
```

**Format**

This data frame contains the following columns:

`Kyphosis` a factor with levels `absent` `present` indicating if a kyphosis (a type of deformation) was present after the operation.

`Age` in months

`Number` the number of vertebrae involved

`Start` the number of the first (topmost) vertebra operated on.

**Source**

John M. Chambers and Trevor J. Hastie eds. (1992) *Statistical Models in S*, Wadsworth and Brooks/Cole, Pacific Grove, CA 1992.

**Examples**

```
fit <- rpart(Kyphosis ~ Age + Number + Start, data=kyphosis)
fit2 <- rpart(Kyphosis ~ Age + Number + Start, data=kyphosis,
             parms=list(prior=c(.65,.35), split='information'))
fit3 <- rpart(Kyphosis ~ Age + Number + Start, data=kyphosis,
             control=rpart.control(cp=.05))
par(mfrow=c(1,2))
plot(fit)
text(fit, use.n=TRUE)
plot(fit2)
text(fit2, use.n=TRUE)
```

labels.rpart

*Create Split Labels For an Rpart Object***Description**

This function provides labels for the branches of an `rpart` tree.

**Usage**

```
## S3 method for class 'rpart':
labels(object, digits=4, minlength=1L, pretty, collapse=TRUE, ...)
```

**Arguments**

object	fitted model object of class <code>rpart</code> . This is assumed to be the result of some function that produces an object with the same named components as that returned by the <code>rpart</code> function.
digits	the number of digits to be used for numeric values. All of the <code>rpart</code> functions that call labels explicitly set this value, with <code>options("digits")</code> as the default.
minlength	the minimum length for abbreviation of character or factor variables. If 0 no abbreviation is done; if 1 then single letters are used with "a" for the first level, "b" for the second and so on. If the value is greater than 1, the <code>abbreviate</code> function is used.
pretty	an argument included for backwards compatibility: <code>pretty=0</code> implies <code>minlength=0</code> , <code>pretty=NULL</code> implies <code>minlength=1</code> , and <code>pretty=TRUE</code> implies <code>minlength=4</code> .
collapse	logical. The returned set of labels is always of the same length as the number of nodes in the tree. If <code>collapse=TRUE</code> (default), the returned value is a vector of labels for the branch leading into each node, with "root" as the label for the top node. If <code>FALSE</code> , the returned value is a two column matrix of labels for the left and right branches leading out from each node, with "leaf" as the branch labels for terminal nodes.
...	optional arguments to <code>abbreviate</code> .

**Value**

Vector of split labels (`collapse=TRUE`) or matrix of left and right splits (`collapse=FALSE`) for the supplied `rpart` object. This function is called by printing methods for `rpart` and is not intended to be called directly by the users.

**See Also**

[abbreviate](#)

---

`meanvar.rpart`

*Mean-Variance Plot for an Rpart Object*

---

**Description**

Creates a plot on the current graphics device of the deviance of the node divided by the number of observations at the node. Also returns the node number.

**Usage**

```
meanvar(tree, ...)
```

```
## S3 method for class 'rpart':
meanvar(tree, xlab="ave(y)", ylab="ave(deviance)", ...)
```

**Arguments**

tree	fitted model object of class <code>rpart</code> . This is assumed to be the result of some function that produces an object with the same named components as that returned by the <code>rpart</code> function.
xlab	x-axis label for the plot.
ylab	y-axis label for the plot.
...	additional graphical parameters may be supplied as arguments to this function.

**Value**

an invisible list containing the following vectors is returned.

x	fitted value at terminal nodes ( <code>yval</code> ).
y	deviance of node divided by number of observations at node.
label	node number.

**Side Effects**

a plot is put on the current graphics device.

**See Also**

[plot.rpart](#).

**Examples**

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
meanvar(z.auto, log='xy')
```

---

na.rpart

*Handles Missing Values in an Rpart Object*

---

**Description**

Handles missing values in an `rpart` object.

**Usage**

```
na.rpart(x)
```

**Arguments**

x	a model frame.
---	----------------

**Details**

Internal function that handles missing values when calling the function `rpart`.

---

path.rpart                      *Follow Paths to Selected Nodes of an Rpart Object*

---

### Description

Returns a names list where each element contains the splits on the path from the root to the selected nodes.

### Usage

```
path.rpart(tree, nodes, pretty=0, print.it=TRUE)
```

### Arguments

tree	fitted model object of class <code>rpart</code> . This is assumed to be the result of some function that produces an object with the same named components as that returned by the <code>rpart</code> function.
nodes	an integer vector containing indices (node numbers) of all nodes for which paths are desired. If missing, user selects nodes as described below.
pretty	an integer denoting the extent to which factor levels in split labels will be abbreviated. A value of (0) signifies no abbreviation. A <code>NULL</code> , the default, signifies using elements of letters to represent the different factor levels.
print.it	Logical. Denotes whether paths will be printed out as nodes are interactively selected. Irrelevant if <code>nodes</code> argument is supplied.

### Details

The function has a required argument as an `rpart` object and a list of nodes as optional arguments. Omitting a list of nodes will cause the function to wait for the user to select nodes from the dendrogram. It will return a list, with one component for each node specified or selected. The component contains the sequence of splits leading to that node. In the graphical interaction, the individual paths are printed out as nodes are selected.

### Value

A named (by node) list, each element of which contains all the splits on the path from the root to the specified or selected nodes.

### Graphical Interaction

A dendrogram of the `rpart` object is expected to be visible on the graphics device, and a graphics input device (e.g. a mouse) is required. Clicking (the selection button) on a node selects that node. This process may be repeated any number of times. Clicking the exit button will stop the selection process and return the list of paths.

### References

This function was modified from `path.tree` in `S`.

### See Also

[rpart](#)

**Examples**

```
fit <- rpart(Kyphosis ~ Age + Number + Start, data=kyphosis)
summary(fit)
path.rpart(fit, node=c(11, 22))
```

---

plot.rpart	<i>Plot an Rpart Object</i>
------------	-----------------------------

---

**Description**

Plots an rpart object on the current graphics device.

**Usage**

```
## S3 method for class 'rpart':
plot(x, uniform=FALSE, branch=1, compress=FALSE, nspace,
      margin=0, minbranch=.3, ...)
```

**Arguments**

x	a fitted object of class <code>rpart</code> , containing a classification, regression, or rate tree.
uniform	if <code>TRUE</code> , uniform vertical spacing of the nodes is used; this may be less cluttered when fitting a large plot onto a page. The default is to use a non-uniform spacing proportional to the error in the fit.
branch	controls the shape of the branches from parent to child node. Any number from 0 to 1 is allowed. A value of 1 gives square shouldered branches, a value of 0 give V shaped branches, with other values being intermediate.
compress	if <code>FALSE</code> , the leaf nodes will be at the horizontal plot coordinates of <code>1:nleaves</code> . If <code>TRUE</code> , the routine attempts a more compact arrangement of the tree. The compaction algorithm assumes <code>uniform=TRUE</code> ; surprisingly, the result is usually an improvement even when that is not the case.
nspace	the amount of extra space between a node with children and a leaf, as compared to the minimal space between leaves. Applies to compressed trees only. The default is the value of <code>branch</code> .
margin	an extra percentage of white space to leave around the borders of the tree. (Long labels sometimes get cut off by the default computation).
minbranch	set the minimum length for a branch to <code>minbranch</code> times the average branch length. This parameter is ignored if <code>uniform=TRUE</code> . Sometimes a split will give very little improvement, or even (in the classification case) no improvement at all. A tree with branch lengths strictly proportional to improvement leaves no room to squeeze in node labels.
...	arguments to be passed to or from other methods.

**Details**

This function is a method for the generic function `plot`, for objects of class `rpart`. The y-coordinate of the top node of the tree will always be 1.

**Value**

The coordinates of the nodes are returned as a list, with components `x` and `y`.

**Side Effects**

An unlabeled plot is produced on the current graphics device.

**See Also**

`rpart`, `text.rpart`

**Examples**

```
fit <- rpart(Price ~ Mileage + Type + Country, cu.summary)
plot(fit, compress=TRUE)
text(fit, use.n=TRUE)
```

---

plotcp

*Plot a Complexity Parameter Table for an Rpart Fit*

---

**Description**

Gives a visual representation of the cross-validation results in an `rpart` object.

**Usage**

```
plotcp(x, minline = TRUE, lty = 3, col = 1,
       upper = c("size", "splits", "none"), ...)
```

**Arguments**

<code>x</code>	an object of class <code>rpart</code>
<code>minline</code>	whether a horizontal line is drawn 1SE above the minimum of the curve.
<code>lty</code>	line type for this line
<code>col</code>	colour for this line
<code>upper</code>	what is plotted on the top axis: the size of the tree (the number of leaves), the number of splits or nothing.
<code>...</code>	additional plotting parameters

**Details**

The set of possible cost-complexity prunings of a tree from a nested set. For the geometric means of the intervals of values of `cp` for which a pruning is optimal, a cross-validation has (usually) been done in the initial construction by `rpart`. The `cpstable` in the fit contains the mean and standard deviation of the errors in the cross-validated prediction against each of the geometric means, and these are plotted by this function. A good choice of `cp` for pruning is often the leftmost value for which the mean lies below the horizontal line.

**Value**

None.

**Side Effects**

A plot is produced on the current graphical device.

**See Also**

[rpart](#), [printcp](#), [rpart.object](#)

---

post.rpart

*PostScript Presentation Plot of an Rpart Object*

---

**Description**

Generates a PostScript presentation plot of an `rpart` object.

**Usage**

```
post(tree, ...)

## S3 method for class 'rpart':
post(tree, title.,
      filename = paste(deparse(substitute(tree)), ".ps", sep = ""),
      digits = getOption("digits") - 3, pretty = TRUE,
      use.n = TRUE, horizontal = TRUE, ...)
```

**Arguments**

<code>tree</code>	fitted model object of class <code>rpart</code> . This is assumed to be the result of some function that produces an object with the same named components as that returned by the <code>rpart</code> function.
<code>title.</code>	a title which appears at the top of the plot. By default, the name of the <code>rpart</code> endpoint is printed out.
<code>filename</code>	ASCII file to contain the output. By default, the name of the file is the name of the object given by <code>rpart</code> (with the suffix <code>.ps</code> added). If <code>filename = ""</code> , the plot appears on the current graphical device.
<code>digits</code>	number of significant digits to include in numerical data.
<code>pretty</code>	an integer denoting the extent to which factor levels will be abbreviated in the character strings defining the splits; (0) signifies no abbreviation of levels. A <code>NULL</code> signifies using elements of letters to represent the different factor levels. The default ( <code>TRUE</code> ) indicates the maximum possible abbreviation.
<code>use.n</code>	Logical. If <code>TRUE</code> (default), adds to label ( <code>\#events level1/\#events level2/etc.</code> for method <code>class</code> , <code>n</code> for method <code>anova</code> , and <code>\#events/n</code> for methods <code>poisson</code> and <code>exp</code> ).
<code>horizontal</code>	Logical. If <code>TRUE</code> (default), plot is horizontal. If <code>FALSE</code> , plot appears as landscape.
<code>...</code>	other arguments to the <code>postscript</code> function.



**Details**

The plot created uses the functions `plot.rpart` and `text.rpart` (with the `fancy` option). The settings were chosen because they looked good to us, but other options may be better, depending on the `rpart` object. Users are encouraged to write their own function containing favorite options.

**Side Effects**

a plot of `rpart` is created using the `postscript` driver, or the current device if `filename = ""`.

**See Also**

[plot.rpart](#), [rpart](#), [text.rpart](#), [abbreviate](#)

**Examples**

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
post(z.auto, file = "") # display tree on active device
# now construct postscript version on file "pretty.ps"
# with no title
post(z.auto, file = "pretty.ps", title = " ")
z.hp <- rpart(Mileage ~ Weight + HP, car.test.frame)
post(z.hp)
```

---

`predict.rpart`

*Predictions from a Fitted Rpart Object*

---

**Description**

Returns a vector of predicted responses from a fitted `rpart` object.

**Usage**

```
## S3 method for class 'rpart':
predict(object, newdata = list(),
        type = c("vector", "prob", "class", "matrix"),
        na.action = na.pass, ...)
```

**Arguments**

<code>object</code>	fitted model object of class <code>rpart</code> . This is assumed to be the result of some function that produces an object with the same named components as that returned by the <code>rpart</code> function.
<code>newdata</code>	data frame containing the values at which predictions are required. The predictors referred to in the right side of <code>formula(object)</code> must be present by name in <code>newdata</code> . If missing, the fitted values are returned.
<code>type</code>	character string denoting the type of predicted value returned. If the <code>rpart</code> object is a classification tree, then the default is to return <code>prob</code> predictions, a matrix whose columns are the probability of the first, second, etc. class. (This agrees with the default behavior of <code>tree</code> ). Otherwise, a vector result is returned.

`na.action` a function to determine what should be done with missing values in `newdata`. The default is to pass them down the tree using surrogates in the way selected when the model was built. Other possibilities are `na.omit` and `na.fail`.

`...` further arguments passed to or from other methods.

## Details

This function is a method for the generic function `predict` for class `rpart`. It can be invoked by calling `predict` for an object of the appropriate class, or directly by calling `predict.rpart` regardless of the class of the object.

## Value

A new object is obtained by dropping `newdata` down the object. For factor predictors, if an observation contains a level not used to grow the tree, it is left at the deepest possible node and `frame$yval` at the node is the prediction.

If `type="vector"`:

vector of predicted responses. For regression trees this is the mean response at the node, for Poisson trees it is the estimated response rate, and for classification trees it is the predicted class (as a number).

If `type="prob"`:

(for a classification tree) a matrix of class probabilities.

If `type="matrix"`:

a matrix of the full responses (`frame$yval2` if this exists, otherwise `frame$yval`). For regression trees, this is the mean response, for Poisson trees it is the response rate and the number of events at that node in the fitted tree, and for classification trees it is the concatenation of the predicted class, the class counts at that node in the fitted tree, and the class probabilities.

If `type="class"`:

(for a classification tree) a factor of classifications based on the responses.

## See Also

[predict, rpart.object](#)

## Examples

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
predict(z.auto)

fit <- rpart(Kyphosis ~ Age + Number + Start, data=kyphosis)
predict(fit, type="prob") # class probabilities (default)
predict(fit, type="vector") # level numbers
predict(fit, type="class") # factor
predict(fit, type="matrix") # level number, class frequencies, probabilities

sub <- c(sample(1:50, 25), sample(51:100, 25), sample(101:150, 25))
fit <- rpart(Species ~ ., data=iris, subset=sub)
fit
table(predict(fit, iris[-sub,], type="class"), iris[-sub, "Species"])
```

---

```
print.rpart
```

*Print an Rpart Object*

---

### Description

This function prints an `rpart` object. It is a method for the generic function `print` of class `rpart`.

### Usage

```
## S3 method for class 'rpart':
print(x, minlength=0, spaces=2, cp, digits= getOption("digits"), ...)
```

### Arguments

<code>x</code>	fitted model object of class <code>rpart</code> . This is assumed to be the result of some function that produces an object with the same named components as that returned by the <code>rpart</code> function.
<code>minlength</code>	Controls the abbreviation of labels: see <a href="#">labels.rpart</a> .
<code>spaces</code>	the number of spaces to indent nodes of increasing depth.
<code>digits</code>	the number of digits of numbers to print.
<code>cp</code>	prune all nodes with a complexity less than <code>cp</code> from the printout. Ignored if unspecified.
<code>...</code>	arguments to be passed to or from other methods.

### Details

This function is a method for the generic function `print` for class `"rpart"`. It can be invoked by calling `print` for an object of the appropriate class, or directly by calling `print.rpart` regardless of the class of the object.

### Side Effects

A semi-graphical layout of the contents of `x$frame` is printed. Indentation is used to convey the tree topology. Information for each node includes the node number, split, size, deviance, and fitted value. For the `"class"` method, the class probabilities are also printed.

### See Also

[print](#), [rpart.object](#), [summary.rpart](#), [printcp](#)

### Examples

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
z.auto
## Not run: node), split, n, deviance, yval
      * denotes terminal node

1) root 60 1354.58300 24.58333
  2) Weight>=2567.5 45 361.20000 22.46667
    4) Weight>=3087.5 22 61.31818 20.40909 *
```

```

5) Weight<3087.5 23 117.65220 24.43478
10) Weight>=2747.5 15 60.40000 23.80000 *
11) Weight<2747.5 8 39.87500 25.62500 *
3) Weight<2567.5 15 186.93330 30.93333 *

## End(Not run)

```

---

printcp

*Displays CP table for Fitted Rpart Object*


---

## Description

Displays the cp table for fitted rpart object.

## Usage

```
printcp(x, digits=getOption("digits") - 2)
```

## Arguments

**x** fitted model object of class `rpart`. This is assumed to be the result of some function that produces an object with the same named components as that returned by the `rpart` function.

**digits** the number of digits of numbers to print.

## Details

Prints a table of optimal prunings based on a complexity parameter.

## See Also

[summary.rpart](#), [rpart.object](#)

## Examples

```

z.auto <- rpart(Mileage ~ Weight, car.test.frame)
printcp(z.auto)
## Not run:
Regression tree:
rpart(formula = Mileage ~ Weight, data = car.test.frame)

Variables actually used in tree construction:
[1] Weight

Root node error: 1354.6/60 = 22.576

      CP nsplit rel error  xerror   xstd
1 0.595349     0  1.00000 1.03436 0.178526
2 0.134528     1  0.40465 0.60508 0.105217
3 0.012828     2  0.27012 0.45153 0.083330
4 0.010000     3  0.25729 0.44826 0.076998

## End(Not run)

```

---

prune.rpart	<i>Cost-complexity Pruning of an Rpart Object</i>
-------------	---

---

**Description**

Determines a nested sequence of subtrees of the supplied `rpart` object by recursively snipping off the least important splits, based on the complexity parameter (`cp`).

**Usage**

```
prune(tree, ...)
```

```
## S3 method for class 'rpart':
```

```
prune(tree, cp, ...)
```

**Arguments**

<code>tree</code>	fitted model object of class <code>rpart</code> . This is assumed to be the result of some function that produces an object with the same named components as that returned by the <code>rpart</code> function.
<code>cp</code>	Complexity parameter to which the <code>rpart</code> object will be trimmed.
<code>...</code>	further arguments passed to or from other methods.

**Value**

A new `rpart` object that is trimmed to the value `cp`.

**See Also**

[rpart](#)

**Examples**

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
```

```
zp <- prune(z.auto, cp=0.1)
```

```
plot(zp) #plot smaller rpart object
```

---

residuals.rpart	<i>Residuals From a Fitted Rpart Object</i>
-----------------	---

---

**Description**

Method for residuals for an `rpart` object.

**Usage**

```
## S3 method for class 'rpart':
```

```
residuals(object, type = c("usual", "pearson", "deviance"), ...)
```

**Arguments**

object	fitted model object of class "rpart".
type	Indicates the type of residual desired. For regression or anova trees all three residual definitions reduce to $y - \text{fitted}$ . This is the residual returned for user method trees as well. For classification trees the usual residuals are the misclassification losses $L(\text{actual}, \text{predicted})$ where $L$ is the loss matrix. With default losses this residual is 0/1 for correct/incorrect classification. The pearson residual is $(1 - \text{fitted})/\sqrt{\text{fitted}(1 - \text{fitted})}$ and the deviance residual is $\sqrt{\text{minus twice log-arithm of fitted}}$ . For poisson and exp (or survival) trees, the usual residual is the observed - expected number of events. The pearson and deviance residuals are as defined in McCullagh and Nelder.
...	further arguments passed to or from other methods.

**Value**

Vector of residuals of type type from a fitted rpart object.

**References**

McCullagh P. and Nelder, J. A. (1989) *Generalized Linear Models*. London: Chapman and Hall.

**Examples**

```
fit <- rpart(skips ~ Opening + Solder + Mask + PadType + Panel,
            data=solder, method='anova')
summary(residuals(fit))
plot(predict(fit), residuals(fit))
```

---

rpart

*Recursive Partitioning and Regression Trees*


---

**Description**

Fit a rpart model

**Usage**

```
rpart(formula, data, weights, subset, na.action = na.rpart, method,
      model = FALSE, x = FALSE, y = TRUE, parms, control, cost, ...)
```

**Arguments**

formula	a formula, as in the lm function.
data	an optional data frame in which to interpret the variables named in the formula
weights	optional case weights.
subset	optional expression saying that only a subset of the rows of the data should be used in the fit.

<code>na.action</code>	The default action deletes all observations for which <code>y</code> is missing, but keeps those in which one or more predictors are missing.
<code>method</code>	one of "anova", "poisson", "class" or "exp". If <code>method</code> is missing then the routine tries to make an intelligent guess. If <code>y</code> is a survival object, then <code>method="exp"</code> is assumed, if <code>y</code> has 2 columns then <code>method="poisson"</code> is assumed, if <code>y</code> is a factor then <code>method="class"</code> is assumed, otherwise <code>method="anova"</code> is assumed. It is wisest to specify the method directly, especially as more criteria are added to the function.  Alternatively, <code>method</code> can be a list of functions named <code>init</code> , <code>split</code> and <code>eval</code> . Examples are given in the file 'tests/usersplits.R' in the sources.
<code>model</code>	if logical: keep a copy of the model frame in the result? If the input value for <code>model</code> is a model frame (likely from an earlier call to the <code>rpart</code> function), then this frame is used rather than constructing new data.
<code>x</code>	keep a copy of the <code>x</code> matrix in the result.
<code>y</code>	keep a copy of the dependent variable in the result. If missing and <code>model</code> is supplied this defaults to <code>FALSE</code> .
<code>parms</code>	optional parameters for the splitting function. Anova splitting has no parameters. Poisson splitting has a single parameter, the coefficient of variation of the prior distribution on the rates. The default value is 1. Exponential splitting has the same parameter as Poisson. For classification splitting, the list can contain any of: the vector of prior probabilities (component <code>prior</code> ), the loss matrix (component <code>loss</code> ) or the splitting index (component <code>split</code> ). The priors must be positive and sum to 1. The loss matrix must have zeros on the diagonal and positive off-diagonal elements. The splitting index can be <code>gini</code> or <code>information</code> . The default priors are proportional to the data counts, the losses default to 1, and the split defaults to <code>gini</code> .
<code>control</code>	options that control details of the <code>rpart</code> algorithm.
<code>cost</code>	a vector of non-negative costs, one for each variable in the model. Defaults to one for all variables. These are scalings to be applied when considering splits, so the improvement on splitting on a variable is divided by its cost in deciding which split to choose.
<code>...</code>	arguments to <code>rpart.control</code> may also be specified in the call to <code>rpart</code> . They are checked against the list of valid arguments.

### Details

This differs from the `tree` function mainly in its handling of surrogate variables. In most details it follows Breiman et. al. quite closely.

### Value

An object of class `rpart`, a superset of class `tree`.

### References

Breiman, Friedman, Olshen, and Stone. (1984) *Classification and Regression Trees*. Wadsworth.

### See Also

[rpart.control](#), [rpart.object](#), [summary.rpart](#), [print.rpart](#)

**Examples**

```
fit <- rpart(Kyphosis ~ Age + Number + Start, data=kyphosis)
fit2 <- rpart(Kyphosis ~ Age + Number + Start, data=kyphosis,
             parms=list(prior=c(.65,.35), split='information'))
fit3 <- rpart(Kyphosis ~ Age + Number + Start, data=kyphosis,
             control=rpart.control(cp=.05))
par(mfrow=c(1,2), xpd=NA) # otherwise on some devices the text is clipped
plot(fit)
text(fit, use.n=TRUE)
plot(fit2)
text(fit2, use.n=TRUE)
```

---

rpart.control                      *Control for Rpart Models*

---

**Description**

Various parameters that control aspects of the rpart fit.

**Usage**

```
rpart.control(minsplit=20, minbucket=round(minsplit/3), cp=0.01,
             maxcompete=4, maxsurrogate=5, usesurrogate=2, xval=10,
             surrogatestyle=0, maxdepth=30, ...)
```

**Arguments**

minsplit	the minimum number of observations that must exist in a node, in order for a split to be attempted.
minbucket	the minimum number of observations in any terminal <code>&lt;leaf&gt;</code> node. If only one of <code>minbucket</code> or <code>minsplit</code> is specified, the code either sets <code>minsplit</code> to <code>minbucket*3</code> or <code>minbucket</code> to <code>minsplit/3</code> , as appropriate.
cp	complexity parameter. Any split that does not decrease the overall lack of fit by a factor of <code>cp</code> is not attempted. For instance, with <code>anova</code> splitting, this means that the overall <code>Rsquare</code> must increase by <code>cp</code> at each step. The main role of this parameter is to save computing time by pruning off splits that are obviously not worthwhile. Essentially, the user informs the program that any split which does not improve the fit by <code>cp</code> will likely be pruned off by cross-validation, and that hence the program need not pursue it.
maxcompete	the number of competitor splits retained in the output. It is useful to know not just which split was chosen, but which variable came in second, third, etc.
maxsurrogate	the number of surrogate splits retained in the output. If this is set to zero the compute time will be shortened, since approximately half of the computational time (other than setup) is used in the search for surrogate splits.
usesurrogate	how to use surrogates in the splitting process. 0= display only; an observation with a missing value for the primary split rule is not sent further down the tree. 1= use surrogates, in order, to split subjects missing the primary variable; if all surrogates are missing the observation is not split. 2= if all surrogates are missing, then send the observation in the majority direction. A value of 0 corresponds to the action of <code>tree</code> , and 2 to the recommendations of Breiman, et.al.



xval	number of cross-validations
surrogatestyle	controls the selection of a best surrogate. If set to 0 (default) the program uses the total number of correct classification for a potential surrogate variable, if set to 1 it uses the percent correct, calculated over the non-missing values of the surrogate. The first option more severely penalizes covariates with a large number of missing values.
maxdepth	Set the maximum depth of any node of the final tree, with the root node counted as depth 0 (past 30 rpart will give nonsense results on 32-bit machines).
...	mop up other arguments.

**Value**

A list containing the options.

**See Also**

[rpart](#)

---

rpart.object

*Recursive Partitioning and Regression Trees Object*

---

**Description**

These are objects representing fitted rpart trees.

**Value**

frame	data frame with one row for each node in the tree. The row.names of frame contain the (unique) node numbers that follow a binary ordering indexed by node depth. Elements of frame include var, a factor giving the variable used in the split at each node (leaf nodes are denoted by the string <leaf>), n, the size of each node, wt, the sum of case weights for the node, dev, the deviance of each node, yval, the fitted value of the response at each node, and splits, a two column matrix of left and right split labels for each node. All of these are the same as for an rpart object. Extra response information is in yval2, which contains the number of events at the node (poisson), or a matrix containing the fitted class, the class counts for each node and the class probabilities (classification). Also included in the frame are complexity, the complexity parameter at which this split will collapse, ncompete, the number of competitor splits retained, and nsurrogate, the number of surrogate splits retained.
where	integer vector, the same length as the number of observations in the root node, containing the row number of frame corresponding to the leaf node that each observation falls into.
splits	a numeric matrix describing the splits. The row label is the name of the split variable, and columns are count, the number of observations sent left or right by the split (for competitor splits this is the number that would have been sent left or right had this split been used, for surrogate splits it is the number missing the primary split variable which were decided using this surrogate), ncat, the

	number of categories or levels for the variable (+/-1 for a continuous variable), <code>improve</code> , which is the improvement in deviance given by this split, or, for surrogates, the concordance of the surrogate with the primary, and <code>split</code> , the numeric split point. The last column <code>adj</code> gives the adjusted concordance for surrogate splits. For a factor, the <code>split</code> column contains the row number of the <code>csplit</code> matrix. For a continuous variable, the sign of <code>ncat</code> determines whether the subset <code>x &lt; cutpoint</code> or <code>x &gt; cutpoint</code> is sent to the left.
<code>csplit</code>	this will be present only if one of the split variables is a factor. There is one row for each such split, and column <code>i = 1</code> if this level of the factor goes to the left, 3 if it goes to the right, and 2 if that level is not present at this node of the tree. For an ordered categorical variable all levels are marked as R/L, including levels that are not present.
<code>method</code>	the method used to grow the tree.
<code>cptable</code>	the table of optimal prunings based on a complexity parameter.
<code>terms</code>	an object of mode <code>expression</code> and class <code>term</code> summarizing the formula. Used by various methods, but typically not of direct relevance to users.
<code>call</code>	an image of the call that produced the object, but with the arguments all named and with the actual formula included as the formula argument. To re-evaluate the call, say <code>update(tree)</code> . Optional components include the matrix of predictors ( <code>x</code> ) and the response variable ( <code>y</code> ) used to construct the <code>rpart</code> object.

### Structure

The following components must be included in a legitimate `rpart` object. Of these, only the `where` component has the same length as the data used to fit the `rpart` object.

### See Also

[rpart](#).

---

`rpconvert`

*Update an rpart object*

---

### Description

`Rpart` objects changed (slightly) in their internal format in order to accommodate the changes for user-written split functions. This routine updates an old object to the new format.

### Usage

```
rpconvert(x)
```

### Arguments

`x` an `rpart` object

### Value

An updated object

**See Also**

rpart

---

rsq.rpart

*Plots the Approximate R-Square for the Different Splits*

---

**Description**

Produces 2 plots. The first plots the r-square (apparent and apparent - from cross-validation) versus the number of splits. The second plots the Relative Error(cross-validation) +/- 1-SE from cross-validation versus the number of splits.

**Usage**

```
rsq.rpart(x)
```

**Arguments**

`x` fitted model object of class `rpart`. This is assumed to be the result of some function that produces an object with the same named components as that returned by the `rpart` function.

**Side Effects**

Two plots are produced.

**Note**

The labels are only appropriate for the "anova" method.

**Examples**

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
rsq.rpart(z.auto)
```

---

snip.rpart

*Snip Subtrees of an Rpart Object*

---

**Description**

Creates a "snipped" `rpart` object, containing the nodes that remain after selected subtrees have been snipped off. The user can snip nodes using the `toss` argument, or interactively by clicking the mouse button on specified nodes within the graphics window.

**Usage**

```
snip.rpart(x, toss)
```

**Arguments**

x	fitted model object of class <code>rpart</code> . This is assumed to be the result of some function that produces an object with the same named components as that returned by the <code>rpart</code> function.
toss	an integer vector containing indices (node numbers) of all subtrees to be snipped off. If missing, user selects branches to snip off as described below.

**Details**

A dendrogram of `rpart` is expected to be visible on the graphics device, and a graphics input device (e.g., a mouse) is required. Clicking (the selection button) on a node displays the node number, sample size, response *y*-value, and Error (dev). Clicking a second time on the same node snips that subtree off and visually erases the subtree. This process may be repeated an number of times. Warnings result from selecting the root or leaf nodes. Clicking the exit button will stop the snipping process and return the resulting `rpart` object.

See the documentation for the specific graphics device for details on graphical input techniques.

**Value**

A `rpart` object containing the nodes that remain after specified or selected subtrees have been snipped off.

**Warning**

Visually erasing the plot is done by over-plotting with the background colour. This will do nothing if the background is transparent (often true for screen devices).

**See Also**

[plot.rpart](#)

**Examples**

```
## dataset not in R
## Not run:
z.survey <- rpart(market.survey) #grow the rpart object
plot(z.survey) #plot the tree
z.survey2 <- snip.rpart(z.survey,toss=2) #trim subtree at node 2
plot(z.survey2) #plot new tree

# can also interactively select the node using the mouse in the
# graphics window

## End(Not run)
```

---

solder

*Soldering of Components on Printed-Circuit Boards*


---

### Description

The `solder` data frame has 720 rows and 6 columns, representing a balanced subset of a designed experiment varying 5 factors on the soldering of components on printed-circuit boards.

### Usage

```
solder
```

### Format

This data frame contains the following columns:

`Opening` a factor with levels `L M S` indicating the amount of clearance around the mounting pad.

`Solder` a factor with levels `Thick Thin` giving the thickness of the solder used.

`Mask` a factor with levels `A1 .5 A3 B3 B6` indicating the type and thickness of mask used.

`PadType` a factor with levels `D4 D6 D7 L4 L6 L7 L8 L9 W4 W9` giving the size and geometry of the mounting pad.

`Panel` `1:3` indicating the panel on a board being tested.

`skips` a numeric vector giving the number of visible solder skips.

### Source

John M. Chambers and Trevor J. Hastie eds. (1992) *Statistical Models in S*, Wadsworth and Brooks/Cole, Pacific Grove, CA 1992.

### Examples

```
fit <- rpart(skips ~ Opening + Solder + Mask + PadType + Panel,
            data=solder, method='anova')
summary(residuals(fit))
plot(predict(fit), residuals(fit))
```

---

summary.rpart

*Summarize a Fitted Rpart Object*


---

### Description

Returns a detailed listing of a fitted `rpart` object.

### Usage

```
## S3 method for class 'rpart':
summary(object, cp=0, digits=getOption("digits"), file, ...)
```

**Arguments**

object	fitted model object of class <code>rpart</code> . This is assumed to be the result of some function that produces an object with the same named components as that returned by the <code>rpart</code> function.
digits	Number of significant digits to be used in the result.
cp	trim nodes with a complexity of less than <code>cp</code> from the listing.
file	write the output to a given file name. (Full listings of a tree are often quite long).
...	arguments to be passed to or from other methods.

**Details**

This function is a method for the generic function `summary` for class `"rpart"`. It can be invoked by calling `summary` for an object of the appropriate class, or directly by calling `summary.rpart` regardless of the class of the object.

**See Also**

`summary`, `rpart.object`, `printcp`.

**Examples**

```
z.auto <- rpart(Mileage ~ Weight, car.test.frame)
summary(z.auto)
```

---

text.rpart

*Place Text on a Dendrogram*

---

**Description**

Labels the current plot of the tree dendrogram with text.

**Usage**

```
## S3 method for class 'rpart':
text(x, splits=TRUE, label, FUN=text, all=FALSE,
     pretty=NULL, digits=getOption("digits") - 3, use.n=FALSE,
     fancy=FALSE, fwidth=0.8, fheight=0.8, ...)
```

**Arguments**

x	fitted model object of class <code>rpart</code> . This is assumed to be the result of some function that produces an object with the same named components as that returned by the <code>rpart</code> function.
splits	logical flag. If <code>TRUE</code> (default), then the splits in the tree are labeled with the criterion for the split.
label	For compatibility with <code>rpart2</code> , ignored in this version (with a warning).
FUN	the name of a labeling function, e.g. <code>text</code> .
all	Logical. If <code>TRUE</code> , all nodes are labeled, otherwise just terminal nodes.

<code>pretty</code>	an integer denoting the extent to which factor levels in split labels will be abbreviated. A value of (0) signifies no abbreviation. A <code>NULL</code> , the default, signifies using elements of letters to represent the different factor levels.
<code>digits</code>	number of significant digits to include in numerical labels.
<code>use.n</code>	Logical. If <code>TRUE</code> , adds to label ( <code>\#events level1/\#events level2/etc.</code> for <code>class</code> , <code>n</code> for <code>anova</code> , and <code>\#events/n</code> for <code>poisson</code> and <code>exp</code> ).
<code>fancy</code>	Logical. If <code>TRUE</code> , nodes are represented by ellipses (interior nodes) and rectangles (leaves) and labeled by <code>yval</code> . The edges connecting the nodes are labeled by left and right splits.
<code>fwidth</code>	Relates to option <code>fancy</code> and the width of the ellipses and rectangles. If <code>fwidth &lt; 1</code> then it is a scaling factor (default = 0.8). If <code>fwidth &gt; 1</code> then it represents the number of character widths (for current graphical device) to use.
<code>fheight</code>	Relates to option <code>fancy</code> and the height of the ellipses and rectangles. If <code>fheight &lt; 1</code> then it is a scaling factor (default = 0.8). If <code>fheight &gt; 1</code> then it represents the number of character heights (for current graphical device) to use.
<code>...</code>	Graphical parameters may also be supplied as arguments to this function (see <code>par</code> ). As labels often extend outside the plot region it can be helpful to specify <code>xpd = TRUE</code> .

### Side Effects

the current plot of a tree dendrogram is labeled.

### See Also

[text](#), [plot.rpart](#), [rpart](#), [post.rpart](#), [abbreviate](#)

### Examples

```
freen.tr <- rpart(y ~ ., freeny)
plot(freen.tr)
text(freen.tr, use.n=TRUE, all=TRUE)
```

---

xpred.rpart

*Return Cross-Validated Predictions*

---

### Description

Gives the predicted values for an `rpart` fit, under cross validation, for a set of complexity parameter values.

### Usage

```
xpred.rpart(fit, xval=10, cp)
```

**Arguments**

<code>fit</code>	a <code>rpart</code> object.
<code>xval</code>	number of cross-validation groups. This may also be an explicit list of integers that define the cross-validation groups.
<code>cp</code>	the desired list of complexity values. By default it is taken from the <code>cptable</code> component of the fit.

**Details**

Complexity penalties are actually ranges, not values. If the `cp` values found in the table were .36, .28, and .13, for instance, this means that the first row of the table holds for all complexity penalties in the range  $[\text{.36}, 1]$ , the second row for `cp` in the range  $[\text{.28}, \text{.36})$  and the third row for  $[\text{.13}, \text{.28})$ . By default, the geometric mean of each interval is used for cross validation.

**Value**

A matrix with one row for each observation and one column for each complexity value.

**See Also**

[rpart](#)

**Examples**

```
fit <- rpart(Mileage ~ Weight, car.test.frame)
xmat <- xpred.rpart(fit)
xerr <- (xmat - car.test.frame$Mileage)^2
apply(xerr, 2, sum) # cross-validated error estimate

# approx same result as rel. error from printcp(fit)
apply(xerr, 2, sum)/var(car.test.frame$Mileage)
printcp(fit)
```





## Chapter 22

# The `spatial` package

---

`anova.trls`

*Anova tables for fitted trend surface objects*

---

### Description

Compute analysis of variance tables for one or more fitted trend surface model objects; where `anova.trls` is called with multiple objects, it passes on the arguments to `anovalist.trls`.

### Usage

```
## S3 method for class 'trls':  
anova(object, ...)  
anovalist.trls(object, ...)
```

### Arguments

<code>object</code>	A fitted trend surface model object from <code>surf.ls</code>
<code>...</code>	Further objects of the same kind

### Value

`anova.trls` and `anovalist.trls` return objects corresponding to their printed tabular output.

### References

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### See Also

[surf.ls](#)

**Examples**

```
library(stats)
data(topo, package="MASS")
topo0 <- surf.ls(0, topo)
topo1 <- surf.ls(1, topo)
topo2 <- surf.ls(2, topo)
topo3 <- surf.ls(3, topo)
topo4 <- surf.ls(4, topo)
anova(topo0, topo1, topo2, topo3, topo4)
summary(topo4)
```

---

correlogram                      *Compute Spatial Correlograms*

---

**Description**

Compute spatial correlograms of spatial data or residuals.

**Usage**

```
correlogram(krig, nint, plotit = TRUE, ...)
```

**Arguments**

krig	trend-surface or kriging object with columns <i>x</i> , <i>y</i> , and <i>z</i>
nint	number of bins used
plotit	logical for plotting
...	parameters for the plot

**Details**

Divides range of data into `nint` bins, and computes the covariance for pairs with separation in each bin, then divides by the variance. Returns results for bins with 6 or more pairs.

**Value**

*x* and *y* coordinates of the correlogram, and *cnt*, the number of pairs averaged per bin.

**Side Effects**

Plots the correlogram if `plotit = TRUE`.

**References**

Ripley, B. D. (1981) *Spatial Statistics*. Wiley.  
Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[variogram](#)

**Examples**

```
data(topo, package="MASS")
topo.kr <- surf.ls(2, topo)
correlogram(topo.kr, 25)
d <- seq(0, 7, 0.1)
lines(d, expcov(d, 0.7))
```

---

expcov

*Spatial Covariance Functions*

---

**Description**

Spatial covariance functions for use with `surf.gls`.

**Usage**

```
expcov(r, d, alpha = 0, se = 1)
gaucov(r, d, alpha = 0, se = 1)
sphercov(r, d, alpha = 0, se = 1, D = 2)
```

**Arguments**

<code>r</code>	vector of distances at which to evaluate the covariance
<code>d</code>	range parameter
<code>alpha</code>	proportion of nugget effect
<code>se</code>	standard deviation at distance zero
<code>D</code>	dimension of spheres.

**Value**

vector of covariance values.

**References**

Ripley, B. D. (1981) *Spatial Statistics*. Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[surf.gls](#)

**Examples**

```
data(topo, package="MASS")
topo.kr <- surf.ls(2, topo)
correlogram(topo.kr, 25)
d <- seq(0, 7, 0.1)
lines(d, expcov(d, 0.7))
```

---

 Kaver

*Average K-functions from Simulations*


---

**Description**

Forms the average of a series of (usually simulated) K-functions.

**Usage**

```
Kaver(fs, nsim, ...)
```

**Arguments**

<code>fs</code>	full scale for K-fn
<code>nsim</code>	number of simulations
<code>...</code>	arguments to simulate one point process object

**Value**

list with components `x` and `y` of the average K-fn on L-scale.

**References**

Ripley, B. D. (1981) *Spatial Statistics*. Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[Kfn](#), [Kenvl](#)

**Examples**

```
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 40), type="b")
plot(Kfn(towns, 10), type="b", xlab="distance", ylab="L(t)")
for(i in 1:10) lines(Kfn(Psim(69), 10))
lims <- Kenvl(10,100,Psim(69))
lines(lims$x,lims$lower, lty=2, col="green")
lines(lims$x,lims$upper, lty=2, col="green")
lines(Kaver(10,25,Strauss(69,0.5,3.5)), col="red")
```

Kenvl

*Compute Envelope and Average of Simulations of K-fns***Description**

Computes envelope (upper and lower limits) and average of simulations of K-fns

**Usage**

```
Kenvl(fs, nsim, ...)
```

**Arguments**

fs	full scale for K-fn
nsim	number of simulations
...	arguments to produce one simulation

**Value**

list with components

x	distances
lower	min of K-fns
upper	max of K-fns
aver	average of K-fns

**References**

Ripley, B. D. (1981) *Spatial Statistics*. Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[Kfn](#), [Kaver](#)

**Examples**

```
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 40), type="b")
plot(Kfn(towns, 10), type="b", xlab="distance", ylab="L(t)")
for(i in 1:10) lines(Kfn(Psim(69), 10))
lims <- Kenvl(10,100,Psim(69))
lines(lims$x,lims$lower, lty=2, col="green")
lines(lims$x,lims$upper, lty=2, col="green")
lines(Kaver(10,25,Strauss(69,0.5,3.5)), col="red")
```

Kfn

*Compute K-fn of a Point Pattern***Description**

Actually computes  $L = \sqrt{K/\pi}$ .

**Usage**

```
Kfn(pp, fs, k=100)
```

**Arguments**

pp	a list such as a pp object, including components <code>x</code> and <code>y</code>
fs	full scale of the plot
k	number of regularly spaced distances in (0, fs)

**Details**

relies on the domain `D` having been set by `ppinit` or `ppregion`.

**Value**

A list with components

<code>x</code>	vector of distances
<code>y</code>	vector of L-fn values
<code>k</code>	number of distances returned – may be less than <code>k</code> if <code>fs</code> is too large
<code>dmin</code>	minimum distance between pair of points
<code>lm</code>	maximum deviation from $L(t) = t$

**References**

Ripley, B. D. (1981) *Spatial Statistics*. Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[ppinit](#), [ppregion](#), [Kaver](#), [Kenvl](#)

**Examples**

```
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 10), type="s", xlab="distance", ylab="L(t)")
```

---

`ppgetregion`*Get Domain for Spatial Point Pattern Analyses*

---

**Description**

Retrieves the rectangular domain  $(x_l, x_u) \times (y_l, y_u)$  from the underlying C code.

**Usage**

```
ppgetregion()
```

**Value**

A vector of length four with names `c("xl", "xu", "yl", "yu")`.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[ppregion](#)

---

`ppinit`*Read a Point Process Object from a File*

---

**Description**

Read a file in standard format and create a point process object.

**Usage**

```
ppinit(file)
```

**Arguments**

`file`                      string giving file name

**Details**

The file should contain  
the number of points  
a header (ignored)  
`xl xu yl yu scale`  
`x y` (repeated `n` times)

**Value**

class "pp" object with components `x, y, xl, xu, yl, yu`



**Side Effects**

Calls `ppregion` to set the domain.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[ppregion](#)

**Examples**

```
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 10), type="b", xlab="distance", ylab="L(t)")
```

---

pplik

*Pseudo-likelihood Estimation of a Strauss Spatial Point Process*

---

**Description**

Pseudo-likelihood estimation of a Strauss spatial point process.

**Usage**

```
pplik(pp, R, ng=50, trace=FALSE)
```

**Arguments**

<code>pp</code>	a <code>pp</code> object
<code>R</code>	the fixed parameter <code>R</code>
<code>ng</code>	use a <code>ng</code> x <code>ng</code> grid with border <code>R</code> in the domain for numerical integration.
<code>trace</code>	logical? Should function evaluations be printed?

**Value**

estimate for  $c$  in the interval  $[0, 1]$ .

**References**

Ripley, B. D. (1988) *Statistical Inference for Spatial Processes*. Cambridge.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[Strauss](#)

**Examples**

```
pinetrees <- ppinit("pinetrees.dat")
pplik(pinetrees, 0.7)
```

---

`ppregion`*Set Domain for Spatial Point Pattern Analyses*

---

**Description**

Sets the rectangular domain  $(x_l, x_u) \times (y_l, y_u)$ .

**Usage**

```
ppregion(xl = 0, xu = 1, yl = 0, yu = 1)
```

**Arguments**

`xl` Either `xl` or a list containing components `xl`, `xu`, `yl`, `yu` (such as a point-process object)

`xu`

`yl`

`yu`

**Value**

none

**Side Effects**

initializes variables in the C subroutines.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[ppinit](#), [ppgetregion](#)

---

`predict.trls`*Predict method for trend surface fits*

---

**Description**

Predicted values based on trend surface model object

**Usage**

```
## S3 method for class 'trls':  
predict(object, x, y, ...)
```

**Arguments**

<code>object</code>	Fitted trend surface model object returned by <code>surf.ls</code>
<code>x</code>	Vector of prediction location eastings (x coordinates)
<code>y</code>	Vector of prediction location northings (y coordinates)
<code>...</code>	further arguments passed to or from other methods.

**Value**

`predict.trls` produces a vector of predictions corresponding to the prediction locations. To display the output with `image` or `contour`, use `trmat` or convert the returned vector to matrix form.

**References**

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[surf.ls](#), [trmat](#)

**Examples**

```
data(topo, package="MASS")
topo2 <- surf.ls(2, topo)
topo4 <- surf.ls(4, topo)
x <- c(1.78, 2.21)
y <- c(6.15, 6.15)
z2 <- predict(topo2, x, y)
z4 <- predict(topo4, x, y)
cat("2nd order predictions:", z2, "\n4th order predictions:", z4, "\n")
```

---

prmat

*Evaluate Kriging Surface over a Grid*

---

**Description**

Evaluate Kriging surface over a grid.

**Usage**

```
prmat(obj, xl, xu, yl, yu, n)
```

**Arguments**

<code>obj</code>	object returned by <code>surf.gls</code>
<code>xl</code>	limits of the rectangle for grid
<code>xu</code>	
<code>yl</code>	
<code>yu</code>	
<code>n</code>	use $n \times n$ grid within the rectangle

**Value**

list with components `x`, `y` and `z` suitable for `contour` and `image`.

**References**

Ripley, B. D. (1981) *Spatial Statistics*. Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[surf.gls](#), [trmat](#), [semat](#)

**Examples**

```
data(topo, package="MASS")
topo.kr <- surf.gls(2, expcov, topo, d=0.7)
prsurf <- prmat(topo.kr, 0, 6.5, 0, 6.5, 50)
contour(prsurf, levels=seq(700, 925, 25))
```

---

Psim

*Simulate Binomial Spatial Point Process*

---

**Description**

Simulate Binomial spatial point process.

**Usage**

```
Psim(n)
```

**Arguments**

`n`                    number of points

**Details**

relies on the region being set by `ppinit` or `ppregion`.

**Value**

list of vectors of `x` and `y` coordinates.

**Side Effects**

uses the random number generator.

**References**

Ripley, B. D. (1981) *Spatial Statistics*. Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[SSI](#), [Strauss](#)

**Examples**

```
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 10), type="s", xlab="distance", ylab="L(t)")
for(i in 1:10) lines(Kfn(Psim(69), 10))
```

---

semat

*Evaluate Kriging Standard Error of Prediction over a Grid*

---

**Description**

Evaluate Kriging standard error of prediction over a grid.

**Usage**

```
semat(obj, xl, xu, yl, yu, n, se)
```

**Arguments**

obj	object returned by <code>surf.gls</code>
xl	limits of the rectangle for grid
xu	
yl	
yu	
n	use $n \times n$ grid within the rectangle
se	standard error at distance zero as a multiple of the supplied covariance. Otherwise estimated, and it assumed that a correlation function was supplied.

**Value**

list with components x, y and z suitable for `contour` and `image`.

**References**

Ripley, B. D. (1981) *Spatial Statistics*. Wiley.  
Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[surf.gls](#), [trmat](#), [prmat](#)

**Examples**

```
data(topo, package="MASS")
topo.kr <- surf.gls(2, expcov, topo, d=0.7)
prsurf <- prmat(topo.kr, 0, 6.5, 0, 6.5, 50)
contour(prsurf, levels=seq(700, 925, 25))
sesurf <- semat(topo.kr, 0, 6.5, 0, 6.5, 30)
contour(sesurf, levels=c(22,25))
```

---

SSI

*Simulates Sequential Spatial Inhibition Point Process*

---

**Description**

Simulates SSI (sequential spatial inhibition) point process.

**Usage**

```
SSI(n, r)
```

**Arguments**

n	number of points
r	inhibition distance

**Details**

uses the region set by `ppinit` or `ppregion`.

**Value**

list of vectors of  $x$  and  $y$  coordinates

**Side Effects**

uses the random number generator.

**Warnings**

will never return if  $r$  is too large and it cannot place  $n$  points.

**References**

Ripley, B. D. (1981) *Spatial Statistics*. Wiley.  
Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[Psim](#), [Strauss](#)

**Examples**

```
towns <- ppinit("towns.dat")
par(pty = "s")
plot(Kfn(towns, 10), type = "b", xlab = "distance", ylab = "L(t)")
lines(Kaver(10, 25, SSI(69, 1.2)))
```

Strauss

*Simulates Strauss Spatial Point Process***Description**

Simulates Strauss spatial point process.

**Usage**

```
Strauss(n, c=0, r)
```

**Arguments**

n	number of points
c	parameter $c$ in $[0, 1]$ . $c = 0$ corresponds to complete inhibition at distances up to $r$ .
r	inhibition distance

**Details**

Uses spatial birth-and-death process for  $4n$  steps, or for  $40n$  steps starting from a binomial pattern on the first call from an other function. Uses the region set by `ppinit` or `ppregion`.

**Value**

list of vectors of  $x$  and  $y$  coordinates

**Side Effects**

uses the random number generator

**References**

Ripley, B. D. (1981) *Spatial Statistics*. Wiley.  
 Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[Psim](#), [SSI](#)

**Examples**

```
towns <- ppinit("towns.dat")
par(pty="s")
plot(Kfn(towns, 10), type="b", xlab="distance", ylab="L(t)")
lines(Kaver(10, 25, Strauss(69, 0.5, 3.5)))
```

surf.gls

*Fits a Trend Surface by Generalized Least-squares***Description**

Fits a trend surface by generalized least-squares.

**Usage**

```
surf.gls(np, covmod, x, y, z, nx = 1000, ...)
```

**Arguments**

np	degree of polynomial surface
covmod	function to evaluate covariance or correlation function
x	x coordinates or a data frame with columns x, y, z
y	y coordinates
z	z coordinates. Will supersede x\$z
nx	Number of bins for table of the covariance. Increasing adds accuracy, and increases size of the object.
...	parameters for covmod

**Value**

list with components

beta	the coefficients
x	
y	
z	and others for internal use only.

**References**

Ripley, B. D. (1981) *Spatial Statistics*. Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[trmat](#), [surf.ls](#), [prmat](#), [semat](#), [expcov](#), [gaucov](#), [sphercov](#)

**Examples**

```
library(MASS) # for eqscplot
data(topo, package="MASS")
topo.kr <- surf.gls(2, expcov, topo, d=0.7)
trsurf <- trmat(topo.kr, 0, 6.5, 0, 6.5, 50)
eqscplot(trsurf, type = "n")
contour(trsurf, add = TRUE)

prsurf <- prmat(topo.kr, 0, 6.5, 0, 6.5, 50)
```



```
contour(prsurf, levels=seq(700, 925, 25))
sesurf <- semat(topo.kr, 0, 6.5, 0, 6.5, 30)
eqscplot(sesurf, type = "n")
contour(sesurf, levels = c(22, 25), add = TRUE)
```

---

`surf.ls`*Fits a Trend Surface by Least-squares*

---

### Description

Fits a trend surface by least-squares.

### Usage

```
surf.ls(np, x, y, z)
```

### Arguments

<code>np</code>	degree of polynomial surface
<code>x</code>	x coordinates or a data frame with columns x, y, z
<code>y</code>	y coordinates
<code>z</code>	z coordinates. Will supersede <code>x\$z</code>

### Value

list with components

<code>beta</code>	the coefficients
<code>x</code>	
<code>y</code>	
<code>z</code>	and others for internal use only.

### References

Ripley, B. D. (1981) *Spatial Statistics*. Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

### See Also

[tmat](#), [surf.gls](#)

**Examples**

```

library(MASS) # for eqscplot
data(topo, package="MASS")
topo.kr <- surf.ls(2, topo)
trsurf <- trmat(topo.kr, 0, 6.5, 0, 6.5, 50)
eqscplot(trsurf, type = "n")
contour(trsurf, add = TRUE)
points(topo)

eqscplot(trsurf, type = "n")
contour(trsurf, add = TRUE)
plot(topo.kr, add = TRUE)
title(xlab= "Circle radius proportional to Cook's influence statistic")

```

---

trls.influence      *Regression diagnostics for trend surfaces*


---

**Description**

This function provides the basic quantities which are used in forming a variety of diagnostics for checking the quality of regression fits for trend surfaces calculated by `surf.ls`.

**Usage**

```

trls.influence(object)
## S3 method for class 'trls':
plot(x, border = "red", col = NA, pch = 4, cex = 0.6,
     add = FALSE, div = 8, ...)

```

**Arguments**

<code>object, x</code>	Fitted trend surface model from <code>surf.ls</code>
<code>div</code>	scaling factor for influence circle radii in <code>plot.trls</code>
<code>add</code>	add influence plot to existing graphics if TRUE
<code>border, col, pch, cex, ...</code>	additional graphical parameters

**Value**

`trls.influence` returns a list with components:

<code>r</code>	raw residuals as given by <code>residuals.trls</code>
<code>hii</code>	diagonal elements of the Hat matrix
<code>stresid</code>	standardised residuals
<code>Di</code>	Cook's statistic

**References**

Unwin, D. J., Wrigley, N. (1987) Towards a general-theory of control point distribution effects in trend surface models. *Computers and Geosciences*, **13**, 351–355.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[surf.ls](#), [influence.measures](#), [plot.lm](#)

**Examples**

```
library(MASS) # for eqscplot
data(topo, package = "MASS")
topo2 <- surf.ls(2, topo)
infl.topo2 <- trls.influence(topo2)
(cand <- as.data.frame(infl.topo2)[abs(infl.topo2$stresid) > 1.5, ])
cand.xy <- topo[as.integer(rownames(cand)), c("x", "y")]
trsurf <- trmat(topo2, 0, 6.5, 0, 6.5, 50)
eqscplot(trsurf, type = "n")
contour(trsurf, add = TRUE, col = "grey")
plot(topo2, add = TRUE, div = 3)
points(cand.xy, pch = 16, col = "orange")
text(cand.xy, labels = rownames(cand.xy), pos = 4, offset = 0.5)
```

---

trmat

*Evaluate Trend Surface over a Grid*


---

**Description**

Evaluate trend surface over a grid.

**Usage**

```
trmat(obj, xl, xu, yl, yu, n)
```

**Arguments**

obj	object returned by <code>surf.ls</code> or <code>surf.gls</code>
xl	limits of the rectangle for grid
xu	
yl	
yu	
n	use $n \times n$ grid within the rectangle

**Value**

list with components `x`, `y` and `z` suitable for `contour` and `image`.

**References**

Ripley, B. D. (1981) *Spatial Statistics*. Wiley.  
 Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[surf.ls](#), [surf.gls](#)

**Examples**

```
data(topo, package="MASS")
topo.kr <- surf.ls(2, topo)
trsurf <- trmat(topo.kr, 0, 6.5, 0, 6.5, 50)
```

---

variogram

*Compute Spatial Variogram*

---

**Description**

Compute spatial (semi-)variogram of spatial data or residuals.

**Usage**

```
variogram(krig, nint, plotit = TRUE, ...)
```

**Arguments**

krig	trend-surface or kriging object with columns <i>x</i> , <i>y</i> , and <i>z</i>
nint	number of bins used
plotit	logical for plotting
...	parameters for the plot

**Details**

Divides range of data into *nint* bins, and computes the average squared difference for pairs with separation in each bin. Returns results for bins with 6 or more pairs.

**Value**

*x* and *y* coordinates of the variogram and *cnt*, the number of pairs averaged per bin.

**Side Effects**

Plots the variogram if *plotit* = TRUE

**References**

Ripley, B. D. (1981) *Spatial Statistics*. Wiley.

Venables, W. N. and Ripley, B. D. (2002) *Modern Applied Statistics with S*. Fourth edition. Springer.

**See Also**

[correlogram](#)

**Examples**

```
data(topo, package="MASS")
topo.kr <- surf.ls(2, topo)
variogram(topo.kr, 25)
```



## Chapter 23

# The `splines` package

---

`splines`-package      *Regression Spline Functions and Classes*

---

### Description

Regression spline functions and classes.

### Details

This package provides functions for working with regression splines using the B-spline basis, `bs`, and the natural cubic spline basis, `ns`.

For a complete list of functions, use `library(help="splines")`.

### Author(s)

Douglas M. Bates <bates@stat.wisc.edu>      and      William N. Venables  
<Bill.Venables@csiro.au>

Maintainer: R Core Team <R-core@r-project.org>

---

`asVector`      *Coerce an Object to a Vector*

---

### Description

This is a generic function. Methods for this function coerce objects of given classes to vectors.

### Usage

```
asVector(object)
```

### Arguments

`object`      An object.

**Details**

Methods for vector coercion in new classes must be created for the `asVector` generic instead of `as.vector`. The `as.vector` function is internal and not easily extended. Currently the only class with an `asVector` method is the `xyVector` class.

**Value**

a vector

**Author(s)**

Douglas Bates and Bill Venables

**See Also**

[xyVector](#)

**Examples**

```
require(stats)
ispl <- interpSpline( weight ~ height, women )
pred <- predict(ispl)
class(pred)
utils::str(pred)
asVector(pred)
```

---

backSpline

*Monotone Inverse Spline*


---

**Description**

Create a monotone inverse of a monotone natural spline.

**Usage**

```
backSpline(object)
```

**Arguments**

`object` an object that inherits from class `nbSpline` or `npolySpline`. That is, the object must represent a natural interpolation spline but it can be either in the B-spline representation or the piecewise polynomial one. The spline is checked to see if it represents a monotone function.

**Value**

An object of class `polySpline` that contains the piecewise polynomial representation of a function that has the appropriate values and derivatives at the knot positions to be an inverse of the spline represented by `object`. Technically this object is not a spline because the second derivative is not constrained to be continuous at the knot positions. However, it is often a much better approximation to the inverse than fitting an interpolation spline to the  $y/x$  pairs.

**Author(s)**

Douglas Bates and Bill Venables

**See Also**[interpSpline](#)**Examples**

```
require(graphics)
ispl <- interpSpline( women$height, women$weight )
bspl <- backSpline( ispl )
plot( bspl ) # plots over the range of the knots
points( women$weight, women$height )
```

bs

*B-Spline Basis for Polynomial Splines***Description**

Generate the B-spline basis matrix for a polynomial spline.

**Usage**

```
bs(x, df = NULL, knots = NULL, degree = 3, intercept = FALSE,
   Boundary.knots = range(x))
```

**Arguments**

<code>x</code>	the predictor variable. Missing values are allowed.
<code>df</code>	degrees of freedom; one can specify <code>df</code> rather than <code>knots</code> ; <code>bs()</code> then chooses <code>df-degree</code> (minus one if there is an intercept) knots at suitable quantiles of <code>x</code> (which will ignore missing values).
<code>knots</code>	the <i>internal</i> breakpoints that define the spline. The default is <code>NULL</code> , which results in a basis for ordinary polynomial regression. Typical values are the mean or median for one knot, quantiles for more knots. See also <code>Boundary.knots</code> .
<code>degree</code>	degree of the piecewise polynomial—default is 3 for cubic splines.
<code>intercept</code>	if <code>TRUE</code> , an intercept is included in the basis; default is <code>FALSE</code> .
<code>Boundary.knots</code>	boundary points at which to anchor the B-spline basis (default the range of the data). If both <code>knots</code> and <code>Boundary.knots</code> are supplied, the basis parameters do not depend on <code>x</code> . Data can extend beyond <code>Boundary.knots</code> .



**Value**

A matrix of dimension  $c(\text{length}(x), \text{df})$ , where either `df` was supplied or if `knots` were supplied,  $\text{df} = \text{length}(\text{knots}) + \text{degree} + 1$  if there is an intercept. Attributes are returned that correspond to the arguments to `bs`, and explicitly give the `knots`, `Boundary.knots` etc for use by `predict.bs()`.

`bs()` is based on the function `spline.des()`. It generates a basis matrix for representing the family of piecewise polynomials with the specified interior knots and degree, evaluated at the values of `x`. A primary use is in modeling formulas to directly specify a piecewise polynomial term in a model.

**References**

Hastie, T. J. (1992) Generalized additive models. Chapter 7 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

[ns](#), [poly](#), [smooth.spline](#), [predict.bs](#), [SafePrediction](#)

**Examples**

```
require(stats); require(graphics)
bs(women$height, df = 5)
summary(fml <- lm(weight ~ bs(height, df = 5), data = women))

## example of safe prediction
plot(women, xlab = "Height (in)", ylab = "Weight (lb)")
ht <- seq(57, 73, length.out = 200)
lines(ht, predict(fml, data.frame(height=ht)))
## Not run:
## Consistency:
x <- c(1:3, 5:6)
stopifnot(identical(bs(x), bs(x, df = 3)),
           !is.null(kk <- attr(bs(x), "knots")), # not true till 1.5.1
           length(kk) == 0)

## End(Not run)
```

---

 interpSpline

*Create an Interpolation Spline*


---

**Description**

Create an interpolation spline, either from `x` and `y` vectors, or from a formula/data.frame combination.

**Usage**

```
interpSpline(obj1, obj2, bSpline = FALSE, period = NULL,
             na.action = na.fail)
```

**Arguments**

<code>obj1</code>	Either a numeric vector of <code>x</code> values or a formula.
<code>obj2</code>	If <code>obj1</code> is numeric this should be a numeric vector of the same length. If <code>obj1</code> is a formula this can be an optional data frame in which to evaluate the names in the formula.
<code>bSpline</code>	If <code>TRUE</code> the b-spline representation is returned, otherwise the piecewise polynomial representation is returned. Defaults to <code>FALSE</code> .
<code>period</code>	An optional positive numeric value giving a period for a periodic interpolation spline.
<code>na.action</code>	a optional function which indicates what should happen when the data contain NAs. The default action ( <code>na.omit</code> ) is to omit any incomplete observations. The alternative action <code>na.fail</code> causes <code>interpSpline</code> to print an error message and terminate if there are any incomplete observations.

**Value**

An object that inherits from class `spline`. The object can be in the B-spline representation, in which case it will be of class `nbSpline` for natural B-spline, or in the piecewise polynomial representation, in which case it will be of class `npolySpline`.

**Author(s)**

Douglas Bates and Bill Venables

**See Also**

[splineKnots](#), [splineOrder](#), [periodicSpline](#).

**Examples**

```
require(graphics); require(stats)
ispl <- interpSpline( women$height, women$weight )
ispl2 <- interpSpline( weight ~ height, women )
# ispl and ispl2 should be the same
plot( predict( ispl, seq( 55, 75, length.out = 51 ) ), type = "l" )
points( women$height, women$weight )
plot( ispl ) # plots over the range of the knots
points( women$height, women$weight )
splineKnots( ispl )
```

---

 ns

*Generate a Basis Matrix for Natural Cubic Splines*

---

**Description**

Generate the B-spline basis matrix for a natural cubic spline.

**Usage**

```
ns(x, df = NULL, knots = NULL, intercept = FALSE,
   Boundary.knots = range(x))
```

**Arguments**

<code>x</code>	the predictor variable. Missing values are allowed.
<code>df</code>	degrees of freedom. One can supply <code>df</code> rather than <code>knots</code> ; <code>ns()</code> then chooses <code>df - 1 - intercept</code> knots at suitably chosen quantiles of <code>x</code> (which will ignore missing values).
<code>knots</code>	breakpoints that define the spline. The default is no knots; together with the natural boundary conditions this results in a basis for linear regression on <code>x</code> . Typical values are the mean or median for one knot, quantiles for more knots. See also <code>Boundary.knots</code> .
<code>intercept</code>	if <code>TRUE</code> , an intercept is included in the basis; default is <code>FALSE</code> .
<code>Boundary.knots</code>	boundary points at which to impose the natural boundary conditions and anchor the B-spline basis (default the range of the data). If both <code>knots</code> and <code>Boundary.knots</code> are supplied, the basis parameters do not depend on <code>x</code> . Data can extend beyond <code>Boundary.knots</code>

**Value**

A matrix of dimension `length(x) * df` where either `df` was supplied or if `knots` were supplied, `df = length(knots) + 1 + intercept`. Attributes are returned that correspond to the arguments to `ns`, and explicitly give the `knots`, `Boundary.knots` etc for use by `predict.ns()`.

`ns()` is based on the function `spline.des`. It generates a basis matrix for representing the family of piecewise-cubic splines with the specified sequence of interior knots, and the natural boundary conditions. These enforce the constraint that the function is linear beyond the boundary knots, which can either be supplied, else default to the extremes of the data. A primary use is in modeling formula to directly specify a natural spline term in a model.

**References**

Hastie, T. J. (1992) Generalized additive models. Chapter 7 of *Statistical Models in S* eds J. M. Chambers and T. J. Hastie, Wadsworth & Brooks/Cole.

**See Also**

[bs](#), [predict.ns](#), [SafePrediction](#)

**Examples**

```
require(stats); require(graphics)
ns(women$height, df = 5)
summary(fm1 <- lm(weight ~ ns(height, df = 5), data = women))

## example of safe prediction
plot(women, xlab = "Height (in)", ylab = "Weight (lb)")
ht <- seq(57, 73, length.out = 200)
lines(ht, predict(fm1, data.frame(height=ht)))
```

---

periodicSpline      *Create a Periodic Interpolation Spline*

---

### Description

Create a periodic interpolation spline, either from  $x$  and  $y$  vectors, or from a formula/data.frame combination.

### Usage

```
periodicSpline(obj1, obj2, knots, period = 2*pi, ord = 4)
```

### Arguments

obj1	either a numeric vector of $x$ values or a formula.
obj2	if obj1 is numeric this should be a numeric vector of the same length. If obj1 is a formula this can be an optional data frame in which to evaluate the names in the formula.
knots	optional numeric vector of knot positions.
period	positive numeric value giving the period for the periodic spline. Defaults to $2 * \pi$ .
ord	integer giving the order of the spline, at least 2. Defaults to 4. See <a href="#">splineOrder</a> for a definition of the order of a spline.

### Value

An object that inherits from class `spline`. The object can be in the B-spline representation, in which case it will be a `pbSpline` object, or in the piecewise polynomial representation (a `ppolySpline` object).

### Author(s)

Douglas Bates and Bill Venables

### See Also

[splineKnots](#), [interpSpline](#)

### Examples

```
require(graphics); require(stats)
xx <- seq(-pi, pi, length.out = 16)[-1]
yy <- sin( xx )
frm <- data.frame( xx, yy )
( pisp1 <- periodicSpline( xx, yy, period = 2 * pi ) )
pisp2 <- periodicSpline( yy ~ xx, frm, period = 2 * pi )
stopifnot(all.equal(pisp1, pisp2))# pisp1 and pisp2 are the same

plot( pisp1 )                    # displays over one period
points( yy ~ xx, col = "brown" )
plot( predict( pisp1, seq(-3*pi, 3*pi, length.out = 101) ), type = "l" )
```

---

polySpline	<i>Piecewise Polynomial Spline Representation</i>
------------	---

---

### Description

Create the piecewise polynomial representation of a spline object.

### Usage

```
polySpline(object, ...)  
as.polySpline(object, ...)
```

### Arguments

object	An object that inherits from class <code>spline</code> .
...	Optional additional arguments. At present no additional arguments are used.

### Value

An object that inherits from class `polySpline`. This is the piecewise polynomial representation of a univariate spline function. It is defined by a set of distinct numeric values called knots. The spline function is a polynomial function between each successive pair of knots. At each interior knot the polynomial segments on each side are constrained to have the same value of the function and some of its derivatives.

### Author(s)

Douglas Bates and Bill Venables

### See Also

[interpSpline](#), [periodicSpline](#), [splineKnots](#), [splineOrder](#)

### Examples

```
require(graphics)  
ispl <- polySpline( interpSpline( weight ~ height, women, bSpline = TRUE ) )  
print( ispl ) # print the piecewise polynomial representation  
plot( ispl ) # plots over the range of the knots  
points( women$height, women$weight )
```

---

`predict.bs`*Evaluate a Spline Basis*

---

### Description

Evaluate a predefined spline basis at given values.

### Usage

```
## S3 method for class 'bs':  
predict(object, newx, ...)  
  
## S3 method for class 'ns':  
predict(object, newx, ...)
```

### Arguments

<code>object</code>	the result of a call to <code>bs</code> or <code>ns</code> having attributes describing knots, degree, etc.
<code>newx</code>	the <code>x</code> values at which evaluations are required.
<code>...</code>	Optional additional arguments. At present no additional arguments are used.

### Value

An object just like `object`, except evaluated at the new values of `x`.

These are methods for the generic function `predict` for objects inheriting from classes "bs" or "ns". See `predict` for the general behavior of this function.

### See Also

`bs`, `ns`, `poly`.

### Examples

```
require(stats)  
basis <- ns(women$height, df = 5)  
newX <- seq(58, 72, length.out = 51)  
# evaluate the basis at the new data  
predict(basis, newX)
```

---

predict.bSpline      *Evaluate a Spline at New Values of x*

---

### Description

The `predict` methods for the classes that inherit from the virtual classes `bSpline` and `polySpline` are used to evaluate the spline or its derivatives. The `plot` method for a spline object first evaluates `predict` with the `x` argument missing, then plots the resulting `xyVector` with `type = "l"`.

### Usage

```
## S3 method for class 'bSpline':
predict(object, x, nseg=50, deriv=0, ...)
## S3 method for class 'nbSpline':
predict(object, x, nseg=50, deriv=0, ...)
## S3 method for class 'pbSpline':
predict(object, x, nseg=50, deriv=0, ...)
## S3 method for class 'npolySpline':
predict(object, x, nseg=50, deriv=0, ...)
## S3 method for class 'ppolySpline':
predict(object, x, nseg=50, deriv=0, ...)
```

### Arguments

<code>object</code>	An object that inherits from the <code>bSpline</code> or the <code>polySpline</code> class.
<code>x</code>	A numeric vector of <code>x</code> values at which to evaluate the spline. If this argument is missing a suitable set of <code>x</code> values is generated as a sequence of <code>nseg</code> segments spanning the range of the knots.
<code>nseg</code>	A positive integer giving the number of segments in a set of equally-spaced <code>x</code> values spanning the range of the knots in <code>object</code> . This value is only used if <code>x</code> is missing.
<code>deriv</code>	An integer between 0 and <code>splineOrder(object) - 1</code> specifying the derivative to evaluate.
<code>...</code>	further arguments passed to or from other methods.

### Value

	an <code>xyVector</code> with components
<code>x</code>	the supplied or inferred numeric vector of <code>x</code> values
<code>y</code>	the value of the spline (or its <code>deriv</code> 'th derivative) at the <code>x</code> vector

### Author(s)

Douglas Bates and Bill Venables

### See Also

[xyVector](#), [interpSpline](#), [periodicSpline](#)

**Examples**

```
require(graphics); require(stats)
ispl <- interpSpline( weight ~ height, women )
opar <- par(mfrow = c(2, 2), las = 1)
plot(predict(ispl, nseg = 201),      # plots over the range of the knots
      main = "Original data with interpolating spline", type = "l",
      xlab = "height", ylab = "weight")
points(women$height, women$weight, col = 4)
plot(predict(ispl, nseg = 201, deriv = 1),
      main = "First derivative of interpolating spline", type = "l",
      xlab = "height", ylab = "weight")
plot(predict(ispl, nseg = 201, deriv = 2),
      main = "Second derivative of interpolating spline", type = "l",
      xlab = "height", ylab = "weight")
plot(predict(ispl, nseg = 401, deriv = 3),
      main = "Third derivative of interpolating spline", type = "l",
      xlab = "height", ylab = "weight")
par(opar)
```

splineDesign

*Design Matrix for B-splines***Description**

Evaluate the design matrix for the B-splines defined by `knots` at the values in `x`.

**Usage**

```
splineDesign(knots, x, ord = 4, derivs, outer.ok = FALSE)
spline.des(knots, x, ord = 4, derivs, outer.ok = FALSE)
```

**Arguments**

<code>knots</code>	a numeric vector of knot positions with non-decreasing values.
<code>x</code>	a numeric vector of values at which to evaluate the B-spline functions or derivatives. Unless <code>outer.ok</code> is true, the values in <code>x</code> must be between <code>knots[ord]</code> and <code>knots[ length(knots) + 1 - ord ]</code> .
<code>ord</code>	a positive integer giving the order of the spline function. This is the number of coefficients in each piecewise polynomial segment, thus a cubic spline has order 4. Defaults to 4.
<code>derivs</code>	an integer vector of the same length as <code>x</code> and with values between 0 and <code>ord - 1</code> . The derivative of the given order is evaluated at the <code>x</code> positions. Defaults to a vector of zeroes of the same length as <code>x</code> .
<code>outer.ok</code>	logical indicating if <code>x</code> should be allowed outside the <i>inner</i> knots, see the <code>x</code> argument.

**Value**

A matrix with `length( x )` rows and `length( knots ) - ord` columns. The *i*'th row of the matrix contains the coefficients of the B-splines (or the indicated derivative of the B-splines) defined by the `knot` vector and evaluated at the *i*'th value of `x`. Each B-spline is defined by a set of `ord` successive knots so the total number of B-splines is `length(knots) - ord`.



**Note**

The older `spline.des` function takes the same arguments but returns a list with several components including `knots`, `ord`, `derivs`, and `design`. The `design` component is the same as the value of the `splineDesign` function.

**Author(s)**

Douglas Bates and Bill Venables

**Examples**

```
require(graphics)
splineDesign(knots = 1:10, x = 4:7)

knots <- c(1,1.8,3:5,6.5,7,8.1,9.2,10)# 10 => 10-4 = 6 Basis splines
x <- seq(min(knots)-1, max(knots)+1, length.out=501)
bb <- splineDesign(knots, x=x, outer.ok = TRUE)

plot(range(x), c(0,1), type="n", xlab="x", ylab="",
      main= "B-splines - sum to 1 inside inner knots")
mtext(expression(B[j](x) * and "*" sum(B[j](x), j==1, 6)), adj=0)
abline(v=knots, lty=3, col="light gray")
abline(v=knots[c(4,length(knots)-3)], lty=3, col="gray10")
lines(x, rowSums(bb), col="gray", lwd=2)
matlines(x, bb, ylim = c(0,1), lty=1)
```

---

splineKnots

*Knot Vector from a Spline*


---

**Description**

Return the knot vector corresponding to a spline object.

**Usage**

```
splineKnots(object)
```

**Arguments**

`object`            an object that inherits from class "spline".

**Value**

A non-decreasing numeric vector of knot positions.

**Author(s)**

Douglas Bates and Bill Venables

**Examples**

```
ispl <- interpSpline( weight ~ height, women )
splineKnots( ispl )
```

---

splineOrder	<i>Determine the Order of a Spline</i>
-------------	--

---

**Description**

Return the order of a spline object.

**Usage**

```
splineOrder(object)
```

**Arguments**

object      An object that inherits from class "spline".

**Details**

The order of a spline is the number of coefficients in each piece of the piecewise polynomial representation. Thus a cubic spline has order 4.

**Value**

A positive integer.

**Author(s)**

Douglas Bates and Bill Venables

**See Also**

[splineKnots](#), [interpSpline](#), [periodicSpline](#)

**Examples**

```
splineOrder( interpSpline( weight ~ height, women ) )
```

---

xyVector	<i>Construct an xyVector Object</i>
----------	-------------------------------------

---

**Description**

Create an object to represent a set of x-y pairs. The resulting object can be treated as a matrix or as a data frame or as a vector. When treated as a vector it reduces to the `y` component only.

The result of functions such as `predict.spline` is returned as an `xyVector` object so the x-values used to generate the y-positions are retained, say for purposes of generating plots.

**Usage**

```
xyVector(x, y)
```

**Arguments**

*x* a numeric vector  
*y* a numeric vector of the same length as *x*

**Value**

An object of class `xyVector` with components

*x* a numeric vector  
*y* a numeric vector of the same length as *x*

**Author(s)**

Douglas Bates and Bill Venables

**Examples**

```
require(stats); require(graphics)
ispl <- interpSpline( weight ~ height, women )
weights <- predict( ispl, seq( 55, 75, length.out = 51 ) )
class( weights )
plot( weights, type = "l", xlab = "height", ylab = "weight" )
points( women$height, women$weight )
weights
```

# Chapter 24

## The `stats4` package

---

`stats4-package`      *Statistical Functions using S4 Classes*

---

### Description

Statistical Functions using S4 classes.

### Details

This package contains functions and classes for statistics using the [S version 4](#) class system.

The methods currently support maximum likelihood (function `mle()` returning class `"mle"`), including methods for [AIC](#) and [BIC](#) for model selection.

### Author(s)

R Development Core Team and contributors worldwide

Maintainer: R Core Team <[R-core@r-project.org](mailto:R-core@r-project.org)>

---

`AIC-methods`      *Methods for Function 'AIC' in Package 'stats4'*

---

### Description

Calculate the Akaike information criterion for a fitted model object.

### Methods

`signature(object = "ANY")` Generic function: see [AIC](#).

---

**BIC***Bayesian Information Criterion*

---

**Description**

This generic function calculates the Bayesian information criterion, also known as Schwarz's Bayesian criterion (SBC), for one or several fitted model objects for which a log-likelihood value can be obtained, according to the formula  $-2\log\text{-likelihood} + n_{par} \log(n_{obs})$ , where  $n_{par}$  represents the number of parameters and  $n_{obs}$  the number of observations in the fitted model.

**Usage**

```
BIC(object, ...)
```

**Arguments**

<code>object</code>	An object of a suitable class for the BIC to be calculated - usually a "logLik" object or an object for which a <code>logLik</code> method exists.
<code>...</code>	optionally more fitted model objects.

**Value**

If just one object is provided, returns a numeric value with the corresponding BIC; if multiple objects are provided, returns a `data.frame` with rows corresponding to the objects and columns representing the number of parameters in the model (`df`) and the BIC.

**References**

Schwarz, G. (1978) "Estimating the Dimension of a Model", *Annals of Statistics*, **6**, 461–464.

**See Also**

[logLik-methods](#), [AIC-methods](#)

**Examples**

```
lm1 <- lm(Fertility ~ . , data = swiss)
AIC(lm1)
BIC(lm1)

## with two models:
lm1.< <- update(lm1, . ~ . -Examination)
AIC(lm1, lm1.)
BIC(lm1, lm1.)
```

---

`coef-methods`*Methods for Function 'coef' in Package 'stats4'*

---

**Description**

Extract the coefficient vector from "mle" objects.

**Methods**

`signature(object = "ANY")` Generic function: see [coef](#).

`signature(object = "mle")` Extract the full coefficient vector (including any fixed coefficients) from the fit.

`signature(object = "summary.mle")` Extract the coefficient vector and standard errors from the summary of the fit.

---

`confint-methods`*Methods for Function 'confint' in Package 'stats4'*

---

**Description**

Generate confidence intervals

**Methods**

`signature(object = "ANY")` Generic function: see [confint](#).

`signature(object = "mle")` First generate profile and then confidence intervals from the profile.

`signature(object = "profile.mle")` Generate confidence intervals based on likelihood profile.

---

`logLik-methods`*Methods for Function 'logLik' in Package 'stats4'*

---

**Description**

Extract the maximized log-likelihood from "mle" objects.

**Methods**

`signature(object = "ANY")` Generic function: see [logLik](#).

`signature(object = "mle")` Extract log-likelihood from the fit.

mle

*Maximum Likelihood Estimation***Description**

Estimate parameters by the method of maximum likelihood.

**Usage**

```
mle(minuslogl, start = formals(minuslogl), method = "BFGS",
    fixed = list(), ...)
```

**Arguments**

minuslogl	Function to calculate negative log-likelihood.
start	Named list. Initial values for optimizer.
method	Optimization method to use. See <a href="#">optim</a> .
fixed	Named list. Parameter values to keep fixed during optimization.
...	Further arguments to pass to <a href="#">optim</a> .

**Details**

The [optim](#) optimizer is used to find the minimum of the negative log-likelihood. An approximate covariance matrix for the parameters is obtained by inverting the Hessian matrix at the optimum.

**Value**

An object of class [mle-class](#).

**Note**

Be careful to note that the argument is  $-\log L$  (not  $-2 \log L$ ). It is for the user to ensure that the likelihood is correct, and that asymptotic likelihood inference is valid.

**See Also**

[mle-class](#)

**Examples**

```
x <- 0:10
y <- c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8)
## This needs a constrained parameter space: most methods will accept NA
ll <- function(ymax=15, xhalf=6)
  if(ymax > 0 && xhalf > 0) -sum(stats::dpois(y, lambda=ymax/(1+x/xhalf), log=TRUE)) else
  (fit <- mle(ll))
mle(ll, fixed=list(xhalf=6))
## alternative using bounds on optimization
ll2 <- function(ymax=15, xhalf=6)
  -sum(stats::dpois(y, lambda=ymax/(1+x/xhalf), log=TRUE))
mle(ll2, method="L-BFGS-B", lower=rep(0, 2))
```

```

summary(fit)
logLik(fit)
vcov(fit)
plot(profile(fit), absVal=FALSE)
confint(fit)

## use bounded optimization
## the lower bounds are really > 0, but we use >=0 to stress-test profiling
(fit1 <- mle(l1, method="L-BFGS-B", lower=c(0, 0)))
plot(profile(fit1), absVal=FALSE)

## a better parametrization:
l12 <- function(lymax=log(15), lxhalf=log(6))
  -sum(stats::dpois(y, lambda=exp(lymax)/(1+x/exp(lxhalf)), log=TRUE))
(fit2 <- mle(l12))
plot(profile(fit2), absVal=FALSE)
exp(confint(fit2))

```

---

mle-class

*Class "mle" for Results of Maximum Likelihood Estimation*


---

## Description

This class encapsulates results of a generic maximum likelihood procedure.

## Objects from the Class

Objects can be created by calls of the form `new("mle", ...)`, but most often as the result of a call to `mle`.

## Slots

**call**: Object of class "language". The call to `mle`.  
**coef**: Object of class "numeric". Estimated parameters.  
**fullcoef**: Object of class "numeric". Fixed and estimated parameters.  
**vcov**: Object of class "matrix". Approximate variance-covariance matrix.  
**min**: Object of class "numeric". Minimum value of objective function.  
**details**: Object of class "list". List returned from `optim`.  
**minuslogl**: Object of class "function". The negative loglikelihood function.  
**method**: Object of class "character". The optimization method used.

## Methods

**confint** signature(object = "mle"): Confidence intervals from likelihood profiles.  
**logLik** signature(object = "mle"): Extract maximized log-likelihood.  
**profile** signature(fitted = "mle"): Likelihood profile generation.  
**show** signature(object = "mle"): Display object briefly.  
**summary** signature(object = "mle"): Generate object summary.  
**update** signature(object = "mle"): Update fit.  
**vcov** signature(object = "mle"): Extract variance-covariance matrix.



---

 plot-methods

*Methods for Function 'plot' in Package 'stats4'*


---

**Description**

Plot profile likelihoods for "mle" objects.

**Usage**

```
## S4 method for signature 'profile.mle,missing':
plot(x, levels, conf = c(99, 95, 90, 80, 50)/100, nseg = 50,
     absVal = TRUE, ...)
```

**Arguments**

x	an object of class "profile.mle"
levels	levels, on the scale of the absolute value of a t statistic, at which to interpolate intervals. Usually conf is used instead of giving levels explicitly.
conf	a numeric vector of confidence levels for profile-based confidence intervals on the parameters.
nseg	an integer value giving the number of segments to use in the spline interpolation of the profile t curves.
absVal	a logical value indicating whether or not the plots should be on the scale of the absolute value of the profile t. Defaults to TRUE.
...	other arguments to the plot function can be passed here.

**Methods**

signature(x = "ANY", y = "ANY") Generic function: see [plot](#).

signature(x = "profile.mle", y = "missing") Plot likelihood profiles for x.

---

 profile-methods

*Methods for Function profile in Package 'stats4'*


---

**Description**

Profile likelihood for "mle" objects.

**Usage**

```
## S4 method for signature 'mle':
profile(fitted, which = 1:p, maxsteps = 100, alpha = 0.01,
       zmax = sqrt(qchisq(1 - alpha, 1L)), del = zmax/5,
       trace = FALSE, ...)
```

**Arguments**

fitted	Object to be profiled
which	Optionally select subset of parameters to profile.
maxsteps	Maximum number of steps to bracket <code>zmax</code> .
alpha	Significance level corresponding to <code>zmax</code> , based on a Scheffe-style multiple testing interval. Ignored if <code>zmax</code> is specified.
zmax	Cutoff for the profiled value of the signed root-likelihood.
del	Initial stepsize on root-likelihood scale.
trace	Logical. Print intermediate results.
...	Currently unused.

**Details**

The profiling algorithm tries to find an approximately evenly spaced set of at least five parameter values (in each direction from the optimum) to cover the root-likelihood function. Some care is taken to try and get sensible results in cases of high parameter curvature. Notice that it may not always be possible to obtain the cutoff value, since the likelihood might level off.

**Value**

An object of class "profile.mle", see "profile.mle-class".

**Methods**

`signature(fitted = "ANY")` Generic function: see [profile](#).  
`signature(fitted = "mle")` Profile the likelihood in the vicinity of the optimum of an "mle" object.

---

profile.mle-class    *Class "profile.mle"; Profiling information for "mle" object*

---

**Description**

Likelihood profiles along each parameter of likelihood function

**Objects from the Class**

Objects can be created by calls of the form `new("profile.mle", ...)`, but most often by invoking `profile` on an "mle" object.

**Slots**

`profile`: Object of class "list". List of profiles, one for each requested parameter. Each profile is a data frame with the first column called `z` being the signed square root of the  $-2 \log$  likelihood ratio, and the others being the parameters with names prefixed by `par.vals`.

`summary`: Object of class "summary.mle". Summary of object being profiled.

**Methods**

**confint** `signature(object = "profile.mle")`: Use `profile` to generate approximate confidence intervals for parameters.

**plot** `signature(x = "profile.mle", y = "missing")`: Plot profiles for each parameter.

**See Also**

[mle](#), [mle-class](#), [summary.mle-class](#)

---

show-methods

*Methods for Function show in Package 'stats4'*

---

**Description**

Show objects of classes `mle` and `summary.mle`

**Methods**

`signature(object = "mle")` Print simple summary of `mle` object. Just the coefficients and the call.

`signature(object = "summary.mle")` Shows call, table of coefficients and standard errors, and  $-2 \log L$ .

---

summary-methods

*Methods for Function summary in Package 'stats4'*

---

**Description**

Summarize objects

**Methods**

`signature(object = "ANY")` Generic function

`signature(object = "mle")` Generate a summary as an object of class `"summary.mle"`, containing estimates, asymptotic SE, and value of  $-2 \log L$ .

---

summary.mle-class *Class "summary.mle", summary of "mle" objects*

---

### Description

Extract of "mle" object

### Objects from the Class

Objects can be created by calls of the form `new("summary.mle", ...)`, but most often by invoking `summary` on an "mle" object. They contain values meant for printing by `show`.

### Slots

**call:** Object of class "language" The call that generated the "mle" object.

**coef:** Object of class "matrix". Estimated coefficients and standard errors

**m2logL:** Object of class "numeric". Minus twice the log likelihood.

### Methods

**show** signature(object = "summary.mle"): Pretty-prints object

**coef** signature(object = "summary.mle"): Extracts the contents of the `coef` slot

### See Also

[summary](#), [mle](#), [mle-class](#)

---

update-methods *Methods for Function 'update' in Package 'stats4'*

---

### Description

Update "mle" objects.

### Usage

```
## S4 method for signature 'mle':
update(object, ..., evaluate = TRUE)
```

### Arguments

`object` An existing fit.

`...` Additional arguments to the call, or arguments with changed values. Use `name=NULL` to remove the argument `name`.

`evaluate` If true evaluate the new call else return the call.

**Methods**

signature(object = "ANY") Generic function: see [update](#).

signature(object = "mle") Update a fit.

**Examples**

```
x <- 0:10
y <- c(26, 17, 13, 12, 20, 5, 9, 8, 5, 4, 8)
ll <- function(ymax=15, xhalf=6)
  -sum(stats::dpois(y, lambda=ymax/(1+x/xhalf), log=TRUE))
fit <- mle(ll)
## note the recorded call contains ..1, a problem with S4 dispatch
update(fit, fixed=list(xhalf=3))
```

---

vcov-methods

*Methods for Function 'vcov' in Package 'stats4'*

---

**Description**

Extract the approximate variance-covariance matrix from "mle" objects.

**Methods**

signature(object = "ANY") Generic function: see [vcov](#).

signature(object = "mle") Extract the estimated variance-covariance matrix for the estimated parameters (if any).

## Chapter 25

# The survival package

---

aareg	<i>Aalen's additive regression model for censored data</i>
-------	--

---

### Description

Returns an object of class "aareg" that represents an Aalen model.

### Usage

```
aareg(formula, data, weights, subset, na.action,  
      qrtol=1e-07, nmin, dfbeta=FALSE, taper=1,  
      test = c('aalen', 'variance', 'nrisk'),  
      model=FALSE, x=FALSE, y=FALSE)
```

### Arguments

formula	a formula object, with the response on the left of a '~' operator and the terms, separated by + operators, on the right. The response must be a <code>Surv</code> object. Due to a particular computational approach that is used, the model <b>MUST</b> include an intercept term. If "-1" is used in the model formula the program will ignore it.
data	data frame in which to interpret the variables named in the <code>formula</code> , <code>subset</code> , and <code>weights</code> arguments. This may also be a single number to handle some special cases – see below for details. If <code>data</code> is missing, the variables in the model formula should be in the search path.
weights	vector of observation weights. If supplied, the fitting algorithm minimizes the sum of the weights multiplied by the squared residuals (see below for additional technical details). The length of <code>weights</code> must be the same as the number of observations. The weights must be nonnegative and it is recommended that they be strictly positive, since zero weights are ambiguous. To exclude particular observations from the model, use the <code>subset</code> argument instead of zero weights.
subset	expression specifying which subset of observations should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), a numeric vector indicating the observation numbers to be included, or a character vector of the observation names that should be included. All observations are included by default.

<code>na.action</code>	a function to filter missing data. This is applied to the <code>model.frame</code> after any <code>subset</code> argument has been applied. The default is <code>na.fail</code> , which returns an error if any missing values are found. An alternative is <code>na.exclude</code> , which deletes observations that contain one or more missing values.
<code>qrtol</code>	tolerance for detection of singularity in the QR decomposition
<code>nmin</code>	minimum number of observations for an estimate; defaults to 3 times the number of covariates. This essentially truncates the computations near the tail of the data set, when <code>n</code> is small and the calculations can become numerically unstable.
<code>dfbeta</code>	should the array of <code>dfbeta</code> residuals be computed. This implies computation of the sandwich variance estimate. The residuals will always be computed if there is a <code>cluster</code> term in the model formula.
<code>taper</code>	allows for a smoothed variance estimate. $\text{Var}(x)$ , where <code>x</code> is the set of covariates, is an important component of the calculations for the Aalen regression model. At any given time point <code>t</code> , it is computed over all subjects who are still at risk at time <code>t</code> . The <code>taper</code> argument allows smoothing these estimates, for example <code>taper=(1:4)/4</code> would cause the variance estimate used at any event time to be a weighted average of the estimated variance matrices at the last 4 death times, with a weight of 1 for the current death time and decreasing to 1/4 for prior event times. The default value gives the standard Aalen model.
<code>test</code>	selects the weighting to be used, for computing an overall “average” coefficient vector over time and the subsequent test for equality to zero.
<code>model, x, y</code>	should copies of the model frame, the <code>x</code> matrix of predictors, or the response vector <code>y</code> be included in the saved result.

### Details

The Aalen model assumes that the cumulative hazard  $H(t)$  for a subject can be expressed as  $a(t) + X B(t)$ , where  $a(t)$  is a time-dependent intercept term,  $X$  is the vector of covariates for the subject (possibly time-dependent), and  $B(t)$  is a time-dependent matrix of coefficients. The estimates are inherently non-parametric; a fit of the model will normally be followed by one or more plots of the estimates.

The estimates may become unstable near the tail of a data set, since the increment to  $B$  at time `t` is based on the subjects still at risk at time `t`. The `tolerance` and/or `nmin` parameters may act to truncate the estimate before the last death. The `taper` argument can also be used to smooth out the tail of the curve. In practice, the addition of a taper such as 1:10 appears to have little effect on death times when `n` is still reasonably large, but can considerably dampen wild oscillations in the tail of the plot.

### Value

an object of class "aareg" representing the fit.

### References

- Aalen, O.O. (1989). A linear regression model for the analysis of life times. *Statistics in Medicine*, 8:907-925.
- Aalen, O.O (1993). Further results on the non-parametric linear model in survival analysis. *Statistics in Medicine*. 12:1569-1588.

### See Also

`print.aareg`, `summary.aareg`, `plot.aareg`

**Examples**

```

# Fit a model to the lung cancer data set
lfit <- aareg(Surv(time, status) ~ age + sex + ph.ecog, data=lung,
             nmin=1)

## Not run:
lfit
Call:
aareg(formula = Surv(time, status) ~ age + sex + ph.ecog, data = lung, nmin = 1
      )

n=227 (1 observations deleted due to missing values)
138 out of 138 unique event times used

              slope      coef se(coef)      z      p
Intercept  5.26e-03  5.99e-03 4.74e-03  1.26 0.207000
age        4.26e-05  7.02e-05 7.23e-05  0.97 0.332000
sex       -3.29e-03 -4.02e-03 1.22e-03 -3.30 0.000976
ph.ecog    3.14e-03  3.80e-03 1.03e-03  3.70 0.000214

Chisq=26.73 on 3 df, p=6.7e-06; test weights=aalen

plot(lfit[4], ylim=c(-4,4)) # Draw a plot of the function for ph.ecog

## End(Not run)
lfit2 <- aareg(Surv(time, status) ~ age + sex + ph.ecog, data=lung,
              nmin=1, taper=1:10)
## Not run: lines(lfit2[4], col=2) # Nearly the same, until the last point

# A fit to the multiple-infection data set of children with
# Chronic Granulomatous Disease. See section 8.5 of Therneau and Grambsch.
fita2 <- aareg(Surv(tstart, tstop, status) ~ treat + age + inherit +
              steroids + cluster(id), data=cgd)

## Not run:
n= 203
69 out of 70 unique event times used

              slope      coef se(coef) robust se      z      p
Intercept    0.004670  0.017800 0.002780  0.003910  4.55 5.30e-06
treatrIFN-g -0.002520 -0.010100 0.002290  0.003020 -3.36 7.87e-04
age          -0.000101 -0.000317 0.000115  0.000117 -2.70 6.84e-03
inheritautosomal 0.001330  0.003830 0.002800  0.002420  1.58 1.14e-01
steroids     0.004620  0.013200 0.010600  0.009700  1.36 1.73e-01

Chisq=16.74 on 4 df, p=0.0022; test weights=aalen

## End(Not run)

```

aml

*Acute Myelogenous Leukemia survival data***Description**

Survival in patients with Acute Myelogenous Leukemia. The question at the time was whether the standard course of chemotherapy should be extended ('maintenance') for additional cycles.



**Usage**

```
aml
leukemia
```

**Format**

```
time:  survival or censoring time
status: censoring status
x:     maintenance chemotherapy given? (factor)
```

**Source**

Rupert G. Miller (1997), *Survival Analysis*. John Wiley & Sons. ISBN: 0-471-25218-2.

---

anova.coxph	<i>Analysis of Deviance for a Cox model.</i>
-------------	--

---

**Description**

Compute an analysis of deviance table for one or more Cox model fits.

**Usage**

```
## S3 method for class 'coxph':
anova(object, ..., test = 'Chisq')
```

**Arguments**

object	An object of class <code>coxph</code>
...	Further <code>coxph</code> objects
test	a character string. The appropriate test is a chisquare, all other choices result in no test being done.

**Details**

Specifying a single object gives a sequential analysis of deviance table for that fit. That is, the reductions in the model log-likelihood as each term of the formula is added in turn are given in as the rows of a table, plus the log-likelihoods themselves. A robust variance estimate is normally used in situations where the model may be mis-specified, e.g., multiple events per subject. In this case a comparison of partial-likelihood values does not make sense, and `anova` will refuse to print results.

If more than one object is specified, the table has a row for the degrees of freedom and loglikelihood for each model. For all but the first model, the change in degrees of freedom and loglik is also given. (This only make statistical sense if the models are nested.) It is conventional to list the models from smallest to largest, but this is up to the user.

The table will optionally contain test statistics (and P values) comparing the reduction in loglik for each row.

**Value**

An object of class "anova" inheriting from class "data.frame".

**Warning**

The comparison between two or more models by `anova` or will only be valid if they are fitted to the same dataset. This may be a problem if there are missing values.

**See Also**

[coxph](#), [anova](#).

**Examples**

```
fit <- coxph(Surv(futime, fustat) ~ resid.ds *rx + ecog.ps, data = ovarian)
anova(fit)
fit2 <- coxph(Surv(futime, fustat) ~ resid.ds +rx + ecog.ps, data=ovarian)
anova(fit2, fit)
```

---

attrassign

---

*Create new-style "assign" attribute*


---

**Description**

The "assign" attribute on model matrices describes which columns come from which terms in the model formula. It has two versions. R uses the original version, but the alternate version found in S-plus is sometimes useful.

**Usage**

```
## Default S3 method:
attrassign(object, tt, ...)
## S3 method for class 'lm':
attrassign(object, ...)
```

**Arguments**

object	model matrix or linear model object
tt	terms object
...	ignored

**Details**

For instance consider the following

```
survreg(Surv(time, status) ~ age + sex + factor(ph.ecog), lung)
```

R gives the compact for for assign, a vector (0, 1, 2, 3, 3, 3); which can be read as “the first column of the X matrix (intercept) goes with none of the terms, the second column of X goes with term 1 of the model equation, the third column of X with term 2, and columns 4-6 with term 3”.

The alternate (S-Plus default) form is a list

```
$(Intercept)      1
$age              2
$sex              3
$factor(ph.ecog) 4 5 6
```

### Value

A list with names corresponding to the term names and elements that are vectors indicating which columns come from which terms

### See Also

[terms,model.matrix](#)

### Examples

```
formula <- Surv(time,status)~factor(edema)
tt <- terms(formula)
mf <- model.frame(tt,data=pbcc)
mm <- model.matrix(tt,mf)
## a few rows of data
mm[1:3,]
## old-style assign attribute
attr(mm,"assign")
## alternate style assign attribute
attrassign(mm,tt)
```

---

basehaz

*Compute the baseline survival curve for a Cox model*

---

### Description

Compute the baseline survival curve for a Cox model.

### Usage

```
basehaz(fit, centered = TRUE)
```

### Arguments

fit	The result of a <code>coxph</code> fit.
centered	If TRUE, the resultant curve is for a hypothetical subject whose covariate values are the corresponding means from the original data, otherwise for a hypothetical subject with a mean vector of zero.

## Details

This function exists primarily because users will look for the phrase 'baseline hazard' (often SAS converts looking for familiar keywords.) The primary function for creating a survival curve is `survfit`, which this calls. See that manual page for more options, including confidence limits and the ability to use other covariate vectors. The result of `survfit` also has print, plot and summary methods that make it far more useful.

## Value

a data frame with components

<code>time</code>	The sorted vector of unique time points (those at which an event occurred)
<code>hazard</code>	The baseline hazard function
<code>strata</code>	If <code>fit</code> was a stratified Cox model, the strata. There will be one survival curve per strata.

## See Also

[survfit](#)

---

`bladder`

*Bladder Cancer Recurrences*

---

## Description

Data on recurrences of bladder cancer, used by many people to demonstrate methodology for recurrent event modelling.

`Bladder1` is the full data set from the study. It contains all three treatment arms and all recurrences for 118 subjects; the maximum observed number of recurrences is 9.

`Bladder` is the data set that appears most commonly in the literature. It uses only the 85 subjects with nonzero follow-up who were assigned to either thiotepa or placebo. The status variable is 1 for recurrence and 0 for everything else (including death for any reason). The data set is laid out in the competing risks format of the paper by Wei, Lin, and Weissfeld.

`Bladder2` uses the same subset of subjects as `bladder`, but formatted in the (start, stop] or Anderson-Gill style. Note that in transforming from the WLW to the AG style data set there is a quite common programming mistake that leads to extra follow-up time for 12 subjects (all those with more than 4 recurrences); this includes some earlier releases of the data in R.

## Usage

```
bladder1
bladder
bladder2
```

**Format**

## bladder1

id: Patient id  
 treatment: Placebo, pyridoxine (vitamin B6), or thiotepa  
 number: Initial number of tumours (8=8 or more)  
 size: Size (cm) of largest initial tumour  
 recur: Number of recurrences  
 start,stop: The start and end time of each time interval  
 status: End of interval code, 0=censored, 1=recurrence,  
 2=death from bladder disease, 3=death other/unknown cause  
 rtumor: Number of tumors found at the time of a recurrence  
 rsize: Size of largest tumor at a recurrence  
 enum: Event number (observation number within patient)

## bladder

id: Patient id  
 rx: Treatment 1=placebo 2=thiotepa  
 number: Initial number of tumours (8=8 or more)  
 size: size (cm) of largest initial tumour  
 stop: recurrence or censoring time  
 enum: which recurrence (up to 4)

## bladder2

id: Patient id  
 rx: Treatment 1=placebo 2=thiotepa  
 number: Initial number of tumours (8=8 or more)  
 size: size (cm) of largest initial tumour  
 start: start of interval (0 or previous recurrence time)  
 stop: recurrence or censoring time  
 enum: which recurrence (up to 4)

**Source**

Andrews DF, Hertzberg AM (1985), *DATA: A Collection of Problems from Many Fields for the Student and Research Worker*, New York: Springer-Verlag.

LJ Wei, DY Lin, L Weissfeld (1989), Regression analysis of multivariate incomplete failure time data by modeling marginal distributions. *Journal of the American Statistical Association*, **84**.

## Description

Returns estimates and standard errors from relative risk regression fit to data from case-cohort studies. A choice is available among the Prentice, Self-Prentice and Lin-Ying methods for unstratified data. For stratified data the choice is between Borgan I, a generalization of the Self-Prentice estimator for unstratified case-cohort data, and Borgan II, a generalization of the Lin-Ying estimator.

## Usage

```
cch(formula, data = sys.parent(), subcoh, id, stratum=NULL, cohort.size,
    method =c("Prentice", "SelfPrentice", "LinYing", "I.Borgan", "II.Borgan"),
    robust=FALSE)
```

## Arguments

<code>formula</code>	A formula object that must have a <code>Surv</code> object as the response. The <code>Surv</code> object must be of type <code>"right"</code> , or of type <code>"counting"</code> .
<code>subcoh</code>	Vector of indicators for subjects sampled as part of the sub-cohort. Code 1 or TRUE for members of the sub-cohort, 0 or FALSE for others. If <code>data</code> is a data frame then <code>subcoh</code> may be a one-sided formula.
<code>id</code>	Vector of unique identifiers, or formula specifying such a vector.
<code>stratum</code>	A vector of stratum indicators or a formula specifying such a vector
<code>cohort.size</code>	Vector with size of each stratum original cohort from which subcohort was sampled
<code>data</code>	An optional data frame in which to interpret the variables occurring in the formula.
<code>method</code>	Three procedures are available. The default method is "Prentice", with options for "SelfPrentice" or "LinYing".
<code>robust</code>	For "LinYing" only, if <code>robust=TRUE</code> , use design-based standard errors even for phase I

## Details

Implements methods for case-cohort data analysis described by Therneau and Li (1999). The three methods differ in the choice of "risk sets" used to compare the covariate values of the failure with those of others at risk at the time of failure. "Prentice" uses the sub-cohort members "at risk" plus the failure if that occurs outside the sub-cohort and is score unbiased. "SelfPren" (Self-Prentice) uses just the sub-cohort members "at risk". These two have the same asymptotic variance-covariance matrix. "LinYing" (Lin-Ying) uses the all members of the sub-cohort and all failures outside the sub-cohort who are "at risk". The methods also differ in the weights given to different score contributions.

The `data` argument must not have missing values for any variables in the model. There must not be any censored observations outside the subcohort.

## Value

An object of class "cch" incorporating a list of estimated regression coefficients and two estimates of their asymptotic variance-covariance matrix.

<code>coef</code>	regression coefficients.
<code>naive.var</code>	Self-Prentice model based variance-covariance matrix.
<code>var</code>	Lin-Ying empirical variance-covariance matrix.

**Author(s)**

Norman Breslow, modified by Thomas Lumley

**References**

Prentice, RL (1986). A case-cohort design for epidemiologic cohort studies and disease prevention trials. *Biometrika* 73: 1–11.

Self, S and Prentice, RL (1988). Asymptotic distribution theory and efficiency results for case-cohort studies. *Annals of Statistics* 16: 64–81.

Lin, DY and Ying, Z (1993). Cox regression with incomplete covariate measurements. *Journal of the American Statistical Association* 88: 1341–1349.

Barlow, WE (1994). Robust variance estimation for the case-cohort design. *Biometrics* 50: 1064–1072

Therneau, TM and Li, H (1999). Computing the Cox model for case-cohort designs. *Lifetime Data Analysis* 5: 99–112.

Borgan, O, Langholz, B, Samuelsen, SO, Goldstein, L and Pogoda, J (2000) Exposure stratified case-cohort designs. *Lifetime Data Analysis* 6, 39-58.

**See Also**

twophase and svycoxph in the "survey" package for more general two-phase designs. <http://faculty.washington.edu/tlumley/survey/>

**Examples**

```
## The complete Wilms Tumor Data
## (Breslow and Chatterjee, Applied Statistics, 1999)
## subcohort selected by simple random sampling.
##

subcoh <- nwtco$in.subcohort
selccoh <- with(nwtco, rel==1|subcoh==1)
ccoh.data <- nwtco[selccoh,]
ccoh.data$subcohort <- subcoh[selccoh]
## central-lab histology
ccoh.data$histol <- factor(ccoh.data$histol, labels=c("FH", "UH"))
## tumour stage
ccoh.data$stage <- factor(ccoh.data$stage, labels=c("I", "II", "III", "IV"))
ccoh.data$age <- ccoh.data$age/12 # Age in years

##
## Standard case-cohort analysis: simple random subcohort
##

fit.ccP <- cch(Surv(edrel, rel) ~ stage + histol + age, data =ccoh.data,
  subcoh = ~subcohort, id=~seqno, cohort.size=4028)

fit.ccP

fit.ccSP <- cch(Surv(edrel, rel) ~ stage + histol + age, data =ccoh.data,
  subcoh = ~subcohort, id=~seqno, cohort.size=4028, method="SelfPren")
```

```
summary(fit.ccSP)

##
## (post-)stratified on instit
##
stratsizes<-table(nwtco$instit)
fit.BI<- cch(Surv(edrel, rel) ~ stage + histol + age, data =ccoh.data,
  subcoh = ~subcohort, id=~seqno, stratum=~instit, cohort.size=stratsizes,
  method="I.Borgan")

summary(fit.BI)
```

cgd

*Chronic Granulomatous Disease data***Description**

Data are from a placebo controlled trial of gamma interferon in chronic granulomatous disease (CGD). Uses the complete data on time to first serious infection observed through end of study for each patient, which includes the initial serious infections observed through the 7/15/89 interim analysis data cutoff, plus the residual data on occurrence of initial serious infections between the interim analysis cutoff and the final blinded study visit for each patient. Only one patient was taken off on the day of his last infection.

**Usage**

cgd

**Format**

id:	subject identification number
center:	enrolling center
random:	date of randomization
treatment:	placebo or gamma interferon
sex:	
age:	age in years, at study entry
height:	height in cm at study entry
weight:	weight in kg at study entry
inherit:	pattern of inheritance
steroids:	use of steroids at study entry, 1=yes
propylac:	use of prophylactic antibiotics at study entry
hos.cat:	a categorization of the centers into 4 groups
tstart, tstop:	start and end of each time interval
status:	1=the interval ends with an infection
enum:	observation number within subject



**Source**

Fleming and Harrington, Counting Processes and Survival Analysis, appendix D.2.

---

`clogit`*Conditional logistic regression*

---

**Description**

Estimates a logistic regression model by maximising the conditional likelihood. Uses a model formula of the form `case.status~exposure+strata(matched.set)`. The default is to use the exact conditional likelihood, a commonly used approximate conditional likelihood is provided for compatibility with older software.

**Usage**

```
clogit(formula, data, method=c("exact", "approximate"), na.action=getOption("na.
```

**Arguments**

<code>formula</code>	Model formula
<code>data</code>	data frame
<code>method</code>	correct or approximate conditonal likelihood?
<code>na.action</code>	missing value handling
<code>subset</code>	subset of records to use
<code>control</code>	control values

**Value**

An object of class "clogit", which is a wrapper for a "coxph" object.

**Author(s)**

Thomas Lumley

**See Also**

[strata](#), [coxph](#), [glm](#)

**Examples**

```
## Not run: clogit(case~spontaneous+induced+strata(stratum), data=infert)
```

---

cluster	<i>Identify clusters.</i>
---------	---------------------------

---

**Description**

This is a special function used in the context of survival models. It identifies correlated groups of observations, and is used on the right hand side of a formula. Using `cluster()` in a formula implies that robust sandwich variance estimators are desired.

**Usage**

```
cluster(x)
```

**Arguments**

`x` A character, factor, or numeric variable.

**Details**

The function's only action is semantic, to mark a variable as the cluster indicator. The resulting variance is what is known as the "working independence" variance in a GEE model.

**Value**

`x`

**See Also**

[coxph](#), [survreg](#)

**Examples**

```
marginal.model <- coxph(Surv(time, status) ~ rx + cluster(litter), rats)
frailty.model <- coxph(Surv(time, status) ~ rx + frailty(litter), rats)
```

---

colon	<i>Chemotherapy for Stage B/C colon cancer</i>
-------	--

---

**Description**

These are data from one of the first successful trials of adjuvant chemotherapy for colon cancer. Levamisole is a low-toxicity compound previously used to treat worm infestations in animals; 5-FU is a moderately toxic (as these things go) chemotherapy agent. There are two records per person, one for recurrence and one for death

**Usage**

```
colon
```

**Format**

id: id  
 study: 1 for all patients  
 rx: Treatment - Obs(ervation), Lev(amisole), Lev(amisole)+5-FU  
 sex: 1=male  
 age: in years  
 obstruct: obstruction of colon by tumour  
 perfor: perforation of colon  
 adhere: adherence to nearby organs  
 nodes: number of lymph nodes with detectable cancer  
 time: days until event or censoring  
 status: censoring status  
 differ: differentiation of tumour (1=well, 2=moderate, 3=poor)  
 extent: Extent of local spread (1=submucosa, 2=muscle, 3=serosa, 4=contiguous structures)  
 surg: time from surgery to registration (0=short, 1=long)  
 node4: more than 4 positive lymph nodes  
 etype: event type: 1=recurrence,2=death

## Source

Danyu Lin

---

cox.zph

*Test the Proportional Hazards Assumption of a Cox Regression*

---

## Description

Test the proportional hazards assumption for a Cox regression model fit (coxph).

## Usage

```
cox.zph(fit, transform="km", global=TRUE)
```

## Arguments

fit the result of fitting a Cox regression model, using the `coxph` function.  
 transform a character string specifying how the survival times should be transformed before the test is performed. Possible values are "km", "rank", "identity" or a function of one argument.  
 global should a global chi-square test be done, in addition to the per-variable tests.

## Value

an object of class "cox.zph", with components:

table a matrix with one row for each variable, and optionally a last row for the global test. Columns of the matrix contain the correlation coefficient between transformed survival time and the scaled Schoenfeld residuals, a chi-square, and the two-sided p-value. For the global test there is no appropriate correlation, so an NA is entered into the matrix as a placeholder.

<code>x</code>	the transformed time axis.
<code>y</code>	the matrix of scaled Schoenfeld residuals. There will be one column per variable and one row per event. The row labels contain the original event times (for the identity transform, these will be the same as <code>x</code> ).
<code>call</code>	the calling sequence for the routine.  The computations require the original <code>x</code> matrix of the Cox model fit. Thus it saves time if the <code>x=TRUE</code> option is used in <code>coxph</code> . This function would usually be followed by both a plot and a print of the result. The plot gives an estimate of the time-dependent coefficient $\beta(t)$ . If the proportional hazards assumption is true, $\beta(t)$ will be a horizontal line. The printout gives a test for <code>slope=0</code> .

## References

P. Grambsch and T. Therneau (1994), Proportional hazards tests and diagnostics based on weighted residuals. *Biometrika*, **81**, 515-26.

## See Also

[coxph](#), [Surv](#).

## Examples

```
fit <- coxph(Surv(futime, fustat) ~ age + ecog.ps,
             data=ovarian)
temp <- cox.zph(fit)
print(temp)                # display the results
plot(temp)                 # plot curves
```

---

coxph

*Fit Proportional Hazards Regression Model*

---

## Description

Fits a Cox proportional hazards regression model. Time dependent variables, time dependent strata, multiple events per subject, and other extensions are incorporated using the counting process formulation of Andersen and Gill.

## Usage

```
coxph(formula, data=, weights, subset,
       na.action, init, control,
       method=c("efron", "breslow", "exact"),
       singular.ok=TRUE, robust=FALSE,
       model=FALSE, x=FALSE, y=TRUE, ...)
```

**Arguments**

<code>formula</code>	a formula object, with the response on the left of a <code>~</code> operator, and the terms on the right. The response must be a survival object as returned by the <code>Surv</code> function.
<code>data</code>	a <code>data.frame</code> in which to interpret the variables named in the <code>formula</code> , or in the <code>subset</code> and the <code>weights</code> argument.
<code>weights</code>	vector of case weights. If <code>weights</code> is a vector of integers, then the estimated coefficients are equivalent to estimating the model from data with the individual cases replicated as many times as indicated by <code>weights</code> .
<code>subset</code>	expression indicating which subset of the rows of data should be used in the fit. All observations are included by default.
<code>na.action</code>	a missing-data filter function. This is applied to the <code>model.frame</code> after any <code>subset</code> argument has been used. Default is <code>options()\$na.action</code> .
<code>init</code>	vector of initial values of the iteration. Default initial value is zero for all variables.
<code>control</code>	Object of class <code>coxph.control</code> specifying iteration limit and other control options. Default is <code>coxph.control(...)</code> .
<code>method</code>	a character string specifying the method for tie handling. If there are no tied death times all the methods are equivalent. Nearly all Cox regression programs use the Breslow method by default, but not this one. The Efron approximation is used as the default here, as it is much more accurate when dealing with tied death times, and is as efficient computationally. The exact method computes the exact partial likelihood, which is equivalent to a conditional logistic model. If there are a large number of ties the computational time will be excessive.
<code>singular.ok</code>	logical value indicating how to handle collinearity in the model matrix. If <code>TRUE</code> , the program will automatically skip over columns of the X matrix that are linear combinations of earlier columns. In this case the coefficients for such columns will be NA, and the variance matrix will contain zeros. For ancillary calculations, such as the linear predictor, the missing coefficients are treated as zeros.
<code>robust</code>	if <code>TRUE</code> a robust variance estimate is returned. Default is <code>TRUE</code> if the model includes a <code>cluster</code> operative, <code>FALSE</code> otherwise.
<code>model</code>	logical value: if <code>TRUE</code> , the model frame is returned in component <code>model</code> .
<code>x</code>	logical value: if <code>TRUE</code> , the model frame is returned in component <code>x</code> .
<code>y</code>	logical value: if <code>TRUE</code> , the model frame is returned in component <code>y</code> .
<code>...</code>	Other arguments will be passed to <code>coxph.control</code>

**Details**

The proportional hazards model is usually expressed in terms of a single survival time value for each person, with possible censoring. Andersen and Gill reformulated the same problem as a counting process; as time marches onward we observe the events for a subject, rather like watching a Geiger counter. The data for a subject is presented as multiple rows or "observations", each of which applies to an interval of observation (start, stop].

**Value**

an object of class "coxph" representing the fit. See `coxph.object` for details.

### Side Effects

Depending on the call, the `predict`, `residuals`, and `survfit` routines may need to reconstruct the `x` matrix created by `coxph`. Differences in the environment, such as which data frames are attached or the value of `options()$contrasts`, may cause this computation to fail or worse, to be incorrect. See the survival overview document for details.

### Special terms

There are two special terms that may be used in the model equation. A `strata` term identifies a stratified Cox model; separate baseline hazard functions are fit for each strata. The `cluster` term is used to compute a robust variance for the model. The term `+ cluster(id)` where each value of `id` is unique is equivalent to specifying the `robust=T` argument, and produces an approximate jackknife estimate of the variance. If the `id` variable were not unique, but instead identifies clusters of correlated observations, then the variance estimate is based on a grouped jackknife.

### Convergence

In certain data cases the actual MLE estimate of a coefficient is infinity, e.g., a dichotomous variable where one of the groups has no events. When this happens the associated coefficient grows at a steady pace and a race condition will exist in the fitting routine: either the log likelihood converges, the information matrix becomes effectively singular, an argument to `exp` becomes too large for the computer hardware, or the maximum number of interactions is exceeded. (Nearly always the first occurs.) The routine attempts to detect when this has happened, not always successfully. The primary consequence for the user is that the Wald statistic, `coefficient/se(coefficient)`, is not valid in this case and should be ignored; the likelihood ratio and Wald tests remain valid however.

### PENALISED REGRESSION

`coxph` can now maximise a penalised partial likelihood with arbitrary user-defined penalty. Supplied penalty functions include ridge regression ([ridge](#)), smoothing splines ([pspline](#)), and frailty models ([frailty](#)).

### References

Andersen, P. and Gill, R. (1982). Cox's regression model for counting processes, a large sample study. *Annals of Statistics* **10**, 1100-1120.

Therneau, T., Grambsch, P., Modeling Survival Data: Extending the Cox Model. Springer-Verlag, 2000.

### See Also

[cluster](#), [strata](#), [Surv](#), [survfit](#), [pspline](#), [frailty](#), [ridge](#).

### Examples

```
# Create the simplest test data set
test1 <- list(time=c(4,3,1,1,2,2,3),
             status=c(1,1,1,0,1,1,0),
             x=c(0,2,1,1,1,0,0),
             sex=c(0,0,0,0,1,1,1))
# Fit a stratified model
coxph(Surv(time, status) ~ x + strata(sex), test1)
# Create a simple data set for a time-dependent model
test2 <- list(start=c(1,2,5,2,1,7,3,4,8,8),
```

```

      stop=c(2,3,6,7,8,9,9,9,14,17),
      event=c(1,1,1,1,1,1,1,0,0,0),
      x=c(1,0,0,1,0,1,1,1,0,0))
summary(coxph(Surv(start, stop, event) ~ x, test2))

#
# Create a simple data set for a time-dependent model
#
test2 <- list(start=c(1, 2, 5, 2, 1, 7, 3, 4, 8, 8),
              stop =c(2, 3, 6, 7, 8, 9, 9, 9,14,17),
              event=c(1, 1, 1, 1, 1, 1, 1, 0, 0, 0),
              x     =c(1, 0, 0, 1, 0, 1, 1, 1, 0, 0) )

summary( coxph( Surv(start, stop, event) ~ x, test2))

# Fit a stratified model, clustered on patients

bladder1 <- bladder[bladder$enum < 5, ]
coxph(Surv(stop, event) ~ (rx + size + number) * strata(enum) +
      cluster(id), bladder1)

```

---

coxph.control

*Ancillary arguments for controlling coxph fits*


---

## Description

This is used to set various numeric parameters controlling a Cox model fit. Typically it would only be used in a call to `coxph`.

## Usage

```
coxph.control(eps = 1e-09, toler.chol = .Machine$double.eps^0.75,
              iter.max = 20, toler.inf = sqrt(eps), outer.max = 10)
```

## Arguments

<code>eps</code>	Iteration continues until the relative change in the log partial likelihood is less than <code>eps</code> . Must be positive.
<code>toler.chol</code>	Tolerance for detection of singularity during a Cholesky decomposition of the variance matrix, i.e., for detecting a redundant predictor variable.
<code>iter.max</code>	Maximum number of iterations to attempt for convergence.
<code>toler.inf</code>	Tolerance criteria for the warning message about a possible infinite coefficient value.
<code>outer.max</code>	For a penalized coxph model, e.g. with pspline terms, there is an outer loop of iteration to determine the penalty parameters; maximum number of iterations for this outer loop.

## Value

a list containing the values of each of the above constants

**Author(s)**

Terry Therneau

**See Also**[coxph](#)

coxph.detail

*Details of a Cox Model Fit***Description**

Returns the individual contributions to the first and second derivative matrix, at each unique event time.

**Usage**

```
coxph.detail(object, riskmat=FALSE)
```

**Arguments**

object	a Cox model object, i.e., the result of <code>coxph</code> .
riskmat	include the at-risk indicator matrix in the output?

**Details**

This function may be useful for those who wish to investigate new methods or extensions to the Cox model. The example below shows one way to calculate the Schoenfeld residuals.

**Value**

a list with components

time	the vector of unique event times
nevent	the number of events at each of these time points.
means	a matrix with one row for each event time and one column for each variable in the Cox model, containing the weighted mean of the variable at that time, over all subjects still at risk at that time. The weights are the risk weights $\exp(x \%*\% \text{fit}\$\text{coef})$ .
nrisk	number of subjects at risk.
hazard	the hazard increment.
score	the contribution to the score vector (first derivative of the log partial likelihood) at each time point.
imat	the contribution to the information matrix (second derivative of the log partial likelihood) at each time point.
varhaz	the variance of the hazard increment.
x, y	copies of the input data.
strata	only present for a stratified Cox model, this is a table giving the number of time points of component <code>time</code> that were contributed by each of the strata.



`riskmat` a matrix with one row for each time and one column for each observation containing a 0/1 value to indicate whether that observation was (1) or was not (0) at risk at the given time point.

### See Also

[coxph](#), [residuals.coxph](#)

### Examples

```
fit <- coxph(Surv(futime,fustat) ~ age + rx + ecog.ps, ovarian, x=TRUE)
fitd <- coxph.detail(fit)
events <- fit$y[,2]==1
etime <- fit$y[events,1] #the event times --- may have duplicates
indx <- match(etime, fitd$time)
sresid <- fit$x[events,] - fitd$means[indx,]
```

---

coxph.object

*Proportional Hazards Regression Object*

---

### Description

This class of objects is returned by the `coxph` class of functions to represent a fitted proportional hazards model. Objects of this class have methods for the functions `print`, `summary`, `residuals`, `predict` and `survfit`.

### Arguments

`coefficients` the coefficients of the linear predictor, which multiply the columns of the model matrix. If the model is over-determined there will be missing values in the vector corresponding to the redundant columns in the model matrix.

`var` the variance matrix of the coefficients. Rows and columns corresponding to any missing coefficients are set to zero.

`naive.var` this component will be present only if the `robust` option was true. If so, the `var` component will contain the robust estimate of variance, and this component will contain the ordinary estimate.

`loglik` a vector of length 2 containing the log-likelihood with the initial values and with the final values of the coefficients.

`score` value of the efficient score test, at the initial value of the coefficients.

`rscore` the robust log-rank statistic, if a robust variance was requested.

`wald.test` the Wald test of whether the final coefficients differ from the initial values.

`iter` number of iterations used.

`linear.predictors` the vector of linear predictors, one per subject.

`residuals` the martingale residuals.

`means` vector of column means of the X matrix. Subsequent survival curves are adjusted to this value.

`n` the number of observations used in the fit.

<code>weights</code>	the vector of case weights, if one was used.
<code>method</code>	the computation method used.
<code>na.action</code>	the <code>na.action</code> attribute, if any, that was returned by the <code>na.action</code> routine. The object will also contain the following, for documentation see the <code>lm</code> object: <code>terms</code> , <code>assign</code> , <code>formula</code> , <code>call</code> , and, optionally, <code>x</code> , <code>y</code> , and/or <code>frame</code> .

### Components

The following components must be included in a legitimate `coxph` object.

### See Also

[coxph](#), [coxph.detail](#), [cox.zph](#), [residuals.coxph](#), [survfit](#), [survreg](#).

---

dsurvreg

*Distributions available in survreg.*

---

### Description

Density, cumulative probability, and quantiles for the set of distributions supported by the `survreg` function.

### Usage

```
dsurvreg(x, mean, scale=1, distribution='weibull', parms)
psurvreg(q, mean, scale=1, distribution='weibull', parms)
qsurvreg(p, mean, scale=1, distribution='weibull', parms)
```

### Arguments

<code>x</code>	vector of quantiles. Missing values (NAs) are allowed.
<code>q</code>	vector of quantiles. Missing values (NAs) are allowed.
<code>p</code>	vector of probabilities. Missing values (NAs) are allowed.
<code>mean</code>	vector of means. This is replicated to be the same length as <code>p</code> or <code>q</code> .
<code>scale</code>	vector of (positive) scale factors. This is replicated to be the same length as <code>p</code> or <code>q</code> .
<code>distribution</code>	character string giving the name of the distribution. This must be one of the elements of <code>survreg.distributions</code>
<code>parms</code>	optional parameters, if any, of the distribution. For the t-distribution this is the degrees of freedom.

### Details

Elements of `q` or `p` that are missing will cause the corresponding elements of the result to be missing.

The `mean` and `scale` values are as they would be for `survreg`. In particular, if the distribution is one that involves a transformation, then they are the mean and scale of the transformed distribution. For example, the Weibull distribution is fit using the Extreme value distribution along with a log transformation. Letting  $F(t) = 1 - \exp[-(at)^p]$  be the cumulative distribution of the Weibull, the mean corresponds to  $-\log(a)$  and the scale to  $1/p$  (Kalbfleish and Prentice, section 2.2.2).

**Value**

density (`dsurvreg`), probability (`psurvreg`), quantile (`qsurvreg`), or for the requested distribution with mean and scale parameters `mean` and `sd`.

**References**

Kalbfleish, J. D. and Prentice, R. L. (1970). *The Statistical Analysis of Failure Time Data* Wiley, New York.

**See Also**

[survreg](#), [Normal](#)

**Examples**

```
# List of distributions available
names(survreg.distributions)
## Not run:
[1] "extreme"      "logistic"     "gaussian"     "weibull"     "exponential"
[6] "rayleigh"    "loggaussian" "lognormal"    "loglogistic" "t"

## End(Not run)
# Compare results
all.equal(dsurvreg(1:10, 2, 5, dist='lognormal'), dlnorm(1:10, 2, 5))

# Hazard function for a Weibull distribution
x <- seq(.1, 3, length=30)
haz <- dsurvreg(x, 2, 3) / (1-psurvreg(x, 2, 3))
## Not run:
plot(x, haz, log='xy', ylab="Hazard") #line with slope (1/scale -1)

## End(Not run)
```

---

frailty

*Random effects terms*

---

**Description**

The frailty function allows one to add a simple random effects term to a Cox or survreg model.

**Usage**

```
frailty(x, distribution="gamma", ...)
frailty.gamma(x, sparse = (nclass > 5), theta, df, eps = 1e-05, method = c("em",
frailty.gaussian(x, sparse = (nclass > 5), theta, df, method = c("reml", "aic", "d
frailty.t(x, sparse = (nclass > 5), theta, df, eps = 1e-05, tdf = 5, method = c("
```

**Arguments**

<code>x</code>	the variable to be entered as a random effect. It is always treated as a factor.
<code>distribution</code>	either the <code>gamma</code> , <code>gaussian</code> or <code>t</code> distribution may be specified. The routines <code>frailty.gamma</code> , <code>frailty.gaussian</code> and <code>frailty.t</code> do the actual work.
<code>...</code>	Arguments for specific distribution, including (but not limited to)
<code>sparse</code>	cutoff for using a sparse coding of the data matrix. If the total number of levels of <code>x</code> is larger than this value, then a sparse matrix approximation is used. The correct cutoff is still a matter of exploration: if the number of levels is very large (thousands) then the non-sparse calculation may not be feasible in terms of both memory and compute time. Likewise, the accuracy of the sparse approximation appears to be related to the maximum proportion of subjects in any one class, being best when no one class has a large membership.
<code>theta</code>	if specified, this fixes the variance of the random effect. If not, the variance is a parameter, and a best solution is sought. Specifying this implies <code>method='fixed'</code> .
<code>df</code>	if specified, this fixes the degrees of freedom for the random effect. Specifying this implies <code>method='df'</code> . Only one of <code>theta</code> or <code>df</code> should be specified.
<code>method</code>	the method used to select a solution for <code>theta</code> , the variance of the random effect. The <code>fixed</code> corresponds to a user-specified value, and no iteration is done. The <code>df</code> selects the variance such that the degrees of freedom for the random effect matches a user specified value. The <code>aic</code> method seeks to maximize Akiake's information criteria $2*(\text{partial likelihood} - \text{df})$ . The <code>ml</code> and <code>reml</code> methods are specific to Cox models with <code>gamma</code> and <code>gaussian</code> random effects, respectively. Please see further discussion below.
<code>tdf</code>	the degrees of freedom for the <code>t</code> -distribution.
<code>eps</code>	convergence criteria for the iteration on <code>theta</code> .

**Details**

The `frailty` plugs into the general penalized modeling framework provided by the `coxph` and `survreg` routines. This framework deals with likelihood, penalties, and degrees of freedom; these aspects work well with either parent routine.

Therneau, Grambsch, and Pankratz show how maximum likelihood estimation for the Cox model with a `gamma` frailty can be accomplished using a general penalized routine, and Ripatti and Palmgren work through a similar argument for the Cox model with a `gaussian` frailty. Both of these are specific to the Cox model. Use of `gamma/ml` or `gaussian/reml` with `survreg` does not lead to valid results.

The extensible structure of the penalized methods is such that the penalty function, such as `frailty` or `pspine`, is completely separate from the modeling routine. The strength of this is that a user can plug in any penalization routine they choose. A weakness is that it is very difficult for the modeling routine to know whether a sensible penalty routine has been supplied.

For Cox models the `coxme` package has replaced superseded this method.

**Value**

this function is used in the model statement of either `coxph` or `survreg`. It's results are used internally.

**References**

S Ripatti and J Palmgren, Estimation of multivariate frailty models using penalized partial likelihood, *Biometrics*, 56:1016-1022, 2000.

T Therneau, P Grambsch and VS Pankratz, Penalized survival models and frailty, *J Computational and Graphical Statistics*, 12:156-175, 2003.

**See Also**

[coxph](#), [survreg](#)

**Examples**

```
# Random institutional effect
coxph(Surv(time, status) ~ age + frailty(inst, df=4), lung)

# Litter effects for the rats data
rfit2a <- survreg(Surv(time, status) ~ rx +
                 frailty.gaussian(litter, df=13, sparse=FALSE), rats )
rfit2b <- survreg(Surv(time, status) ~ rx +
                 frailty.gaussian(litter, df=13, sparse=TRUE), rats )
```

---

heart

*Stanford Heart Transplant data*

---

**Description**

Survival of patients on the waiting list for the Stanford heart transplant program.

**Usage**

```
heart
jasa
jasa1
```

**Format**

jasa: original data

birth.dt:	birth date
accept.dt:	acceptance into program
tx.date:	transplant date
fu.date:	end of followup
fustat:	dead or alive
surgery:	prior bypass surgery
age:	age (in days)
futime:	followup time
wait.time:	time before transplant
transplant:	transplant indicator
mismatch:	mismatch score
hla.a2:	particular type of mismatch
mscore:	another mismatch score
reject:	rejection occurred

jasal, heart: processed data

start, stop, event:	Entry and exit time and status for this interval of time
age:	age-48 years
year:	year of acceptance (in years after 1 Nov 1967)
surgery:	prior bypass surgery 1=yes
transplant:	received transplant 1=yes
id:	patient id

### Source

J Crowley and M Hu (1977), Covariance analysis of heart transplant survival data. *Journal of the American Statistical Association*, **72**, 27–36.

### See Also

[stanford2](#)

---

is.ratetable	Verify that an object is of class ratetable.
--------------	--

---

### Description

The function verifies not only the `class` attribute, but the structure of the object.

### Usage

```
is.ratetable(x, verbose=FALSE)
```

### Arguments

x	the object to be verified.
verbose	if TRUE and the object is not a ratetable, then return a character string describing the way(s) in which x fails to be a proper ratetable object.

### Details

Rate tables are used by the `pyears` and `survexp` functions, and normally contain death rates for some population, categorized by age, sex, or other variables. They have a fairly rigid structure, and the `verbose` option can help in creating a new rate table.

### Value

returns TRUE if x is a ratetable, and FALSE or a description if it is not.

### See Also

[pyears](#), [survexp](#).

### Examples

```
is.ratetable(survexp.us) # True
is.ratetable(cancer)    # False
```

---

 kidney

*Kidney catheter data*


---

### Description

Data on the recurrence times to infection, at the point of insertion of the catheter, for kidney patients using portable dialysis equipment. Catheters may be removed for reasons other than infection, in which case the observation is censored. Each patient has exactly 2 observations.

This data has often been used to illustrate the use of random effects (frailty) in a survival model. However, one of the males (id 21) is a large outlier, with much longer survival than his peers. If this observation is removed no evidence remains for a random subject effect.

### Format

```

patient:  id
time:    time
status:  event status
age:     in years
sex:     1=male, 2=female
disease: disease type (0=GN, 1=AN, 2=PKD, 3=Other)
frail:   frailty estimate from original paper
  
```

### Note

The original paper ignored the issue of tied times and so is not exactly reproduced by the survival package.

### Source

CA McGilchrist, CW Aisbett (1991), Regression with frailty in survival analysis. *Biometrics* **47**, 461–66.

### Examples

```

kfit <- coxph(Surv(time, status)~ age + sex + disease + frailty(id), kidney)
kfit0 <- coxph(Surv(time, status)~ age + sex + disease, kidney)
kfitml <- coxph(Surv(time, status) ~ age + sex + disease +
  frailty(id, dist='gauss'), kidney)
  
```

---

 lines.survfit

*Add Lines or Points to a Survival Plot*


---

### Description

Often used to add the expected survival curve(s) to a Kaplan-Meier plot generated with `plot.survfit`.

**Usage**

```
## S3 method for class 'survfit':
lines(x, type="s", mark=3, col=1, lty=1,
      lwd=1, mark.time=TRUE,
      xscale=1, firstx=0, firsty=1, xmax, fun, conf.int=FALSE, ...)
## S3 method for class 'survfit':
points(x, ...)
```

**Arguments**

<code>x</code>	a survival object, generated from the <code>survfit</code> or <code>survexp</code> functions.
<code>type</code>	the line type, as described in <code>lines</code> . The default is a step function for <code>survfit</code> objects, and a connected line for <code>survexp</code> objects.
<code>mark, col, lty, lwd</code>	vectors giving the mark symbol, color, line type and line width for the added curves.
<code>...</code>	other graphical parameters
<code>mark.time</code>	controls the labeling of the curves. If <code>FALSE</code> , no labeling is done. If <code>TRUE</code> , then curves are marked at each censoring time. If <code>mark.time</code> is a numeric vector, then curves are marked at the specified time points.
<code>xscale</code>	a number used to divide the x values. If time was originally in days, a value of 365.25 would give a plotted scale in years.
<code>firstx, firsty</code>	the starting point for the survival curves. If either of these is set to <code>NA</code> or <code>&lt;</code> blank <code>&gt;</code> the plot will start at the first time point of the curve.
<code>xmax</code>	the maximum horizontal plot coordinate. This shortens the curve before plotting it, so unlike using the <code>xlim</code> graphical parameter, warning messages about out of bounds points are not generated.
<code>fun</code>	an arbitrary function defining a transformation of the survival curve. For example <code>fun=log</code> is an alternative way to draw a log-survival curve (but with the axis labeled with $\log(S)$ values). Four often used transformations can be specified with a character argument instead: "log" is the same as using the <code>log=T</code> option, "event" plots cumulative events ( $f(y) = 1-y$ ), "cumhaz" plots the cumulative hazard function ( $f(y) = -\log(y)$ ) and "cloglog" creates a complimentary log-log survival plot ( $f(y) = \log(-\log(y))$ along with log scale for the x-axis).
<code>conf.int</code>	if <code>TRUE</code> , confidence bands for the curves are also plotted. If set to "only", then only the CI bands are plotted, and the curve itself is left off. This can be useful for fine control over the colors or line types of a plot.

**Value**

a list with components `x` and `y`, containing the coordinates of the last point on each of the curves (but not of the confidence limits). This may be useful for labeling.

**Side Effects**

one or more curves are added to the current plot.

**See Also**

[lines](#), [par](#), [plot.survfit](#), [survfit](#), [survexp](#).



**Examples**

```

fit <- survfit(Surv(time, status) ~ sex, pbc, subset=1:312)
plot(fit, mark.time=FALSE, xscale=365.25,
     xlab='Years', ylab='Survival')
lines(fit[1], lwd=2, xscale=365.24)      #darken the first curve and add marks

# Add expected survival curves for the two groups,
# based on the US census data
# The data set does not have entry date, use the midpoint of the study
efit <- survexp(~ ratetable(sex=sex, age=age*365.35, year=as.Date('1979/1/1')) +
               sex, data=pbcc, times=(0:24)*182)
temp <- lines(efit, lty=2, xscale=365.24, lwd=2:1)
text(temp, c("Male", "Female"), adj= -.1) #labels just past the ends
title(main="Primary Biliary Cirrhosis, Observed and Expected")

```

---

lung

*NCCTG Lung Cancer Data*


---

**Description**

Survival in patients with advanced lung cancer from the North Central Cancer Treatment Group. Performance scores rate how well the patient can perform usual daily activities.

**Usage**

```

lung
cancer

```

**Format**

inst:	Institution code
time:	Survival time in days
status:	censoring status 1=censored, 2=dead
age:	Age in years
sex:	Male=1 Female=2
ph.ecog:	ECOG performance score (0=good 5=dead)
ph.karno:	Karnofsky performance score (bad=0-good=100) rated by physician
pat.karno:	Karnofsky performance score as rated by patient
meal.cal:	Calories consumed at meals
wt.loss:	Weight loss in last six months

**Source**

Terry Therneau

## References

Loprinzi CL, Laurie JA, Wieand HS, Krook JE, Novotny PJ, Kugler JW, Bartel J, Law M, Bateman M, Klatt NE, et al. Prospective evaluation of prognostic variables from patient-completed questionnaires. North Central Cancer Treatment Group. *Journal of Clinical Oncology*. 12(3):601-7, 1994.

---

 mgus

*Monoclonal gammopathy data*


---

## Description

Natural history of 241 subjects with monoclonal gammopathy of undetermined significance (MGUS).

## Usage

mgus  
mgus1  
mgus2

## Format

mgus: A data frame with 241 observations on the following 12 variables.

id: subject id  
 age: age in years  
 sex: male or female  
 dxyr: year of diagnosis  
 pcdx: for subjects who progress to a plasma cell malignancy  
 the subtype of malignancy: multiple myeloma (MM) is the most common, followed by amyloidosis (AM), macroglobulinemia (MA), and other lymphoprolifative (LP)  
 pctime: days from MGUS until diagnosis of a plasma cell malignancy  
 futime: days from diagnosis to last follow-up  
 death: 1= follow-up is until death  
 alb: albumin level at MGUS diagnosis  
 creat: creatinine at MGUS diagnosis  
 hgb: hemoglobin at MGUS diagnosis  
 mspike: size of the monoclonal protien spike at diagnosis

mgus1: The same data set in start,stop format. Contains the id, age, sex, and laboratory variable described above along with

start, stop: sequential intervals of time for each subject  
 status: =1 if the interval ends in an event  
 event: the event type

mgus2: The mgus data, but formatted in the competing risks style. Each subject has three observa-

tions, one for time to death, one for time to MM, and one for time to a PC malignancy other than MM. Contains the id, age, sex, and laboratory variable described above along with

time: time to event or censoring  
 status: 1 if the event occurred, 0 otherwise  
 event: death, myeloma, or other

### Details

Plasma cells are responsible for manufacturing immunoglobulins, an important part of the immune defense. At any given time there are estimated to be about  $10^6$  different immunoglobulins in the circulation at any one time. When a patient has a plasma cell malignancy the distribution will become dominated by a single isotype, the product of the malignant clone, visible as a spike on a serum protein electrophoresis. Monoclonal gammopathy of undetermined significance (MGUS) is the presence of such a spike, but in a patient with no evidence of overt malignancy. This data set of 241 sequential subjects at Mayo Clinic was the groundbreaking study defining the natural history of such subjects.

### Source

Mayo Clinic data courtesy of Dr. Robert Kyle.

### References

R Kyle, Benign monoclonal gammopathy – after 20 to 35 years of follow-up, Mayo Clinic Proc 1993; 68:26-36.

---

model.frame.coxph *Model.frame method for coxph objects*

---

### Description

Recreate the model frame of a coxph fit.

### Usage

```
## S3 method for class 'coxph':
model.frame(formula, ...)
```

### Arguments

formula      the result of a coxph fit  
 ...          other arguments to model.frame

### Details

For details, see the manual page for the generic function. This function would rarely be called by a user, it is mostly used inside functions like `residual` that need to recreate the data set from a model in order to do further calculations.

**Value**

the model frame used in the original fit, or a parallel one for new data.

**Author(s)**

Terry Therneau

**See Also**

[model.frame](#)

---

model.matrix.coxph *Model.matrix method for coxph models*

---

**Description**

Reconstruct the model matrix for a cox model.

**Usage**

```
## S3 method for class 'coxph':  
model.matrix(object, data, contrast.arg = object$contrasts, ...)
```

**Arguments**

object	the result of a coxph model
data	optional, a data frame from which to obtain the data
contrast.arg	optional, a contrasts object describing how factors should be coded
...	other possible argument to model.frame

**Details**

for details see the documentation of the generic method.

**Value**

The model matrix for the fit

**Author(s)**

Terry Therneau

**See Also**

[model.matrix](#)

**Examples**

```
fit1 <- coxph(Surv(time, status) ~ age + factor(ph.ecog), data=lung)
linear.predictor <- model.matrix(fit1)

fit2 <- coxph(Surv(time, status) ~ age + factor(ph.ecog), data=lung,
              x=TRUE)
all.equal(model.matrix(fit1), fit2$x)
```

nwtco

*Data from the National Wilms's Tumor Study***Description**

Missing data/measurement error example. Tumor histology predicts survival, but prediction is stronger with central lab histology than with the local institution determination.

**Usage**

```
nwtco
```

**Format**

A data frame with 4028 observations on the following 9 variables.

```
seqno id number
instit Histology from local institution
histol Histology from central lab
stage Disease stage
study study
rel indicator for relapse
edrel time to relapse
age age in months
in.subcohort Included in the subcohort for the example in the paper
```

**Source**

<http://faculty.washington.edu/norm/software.html>

**References**

NE Breslow and N Chatterjee (1999), Design and analysis of two-phase studies with binary outcome applied to Wilms tumour prognosis. *Applied Statistics* **48**, 457–68.

**Examples**

```
with(nwtco, table(instit, histol))
anova(coxph(Surv(edrel, rel) ~ histol + instit, data=nwtco))
anova(coxph(Surv(edrel, rel) ~ instit + histol, data=nwtco))
```

---

ovarian

*Ovarian Cancer Survival Data*

---

### Description

Survival in a randomised trial comparing two treatments for ovarian cancer (? from an Eastern Cooperative Oncology Group study)

### Usage

ovarian

### Format

futime: survival or censoring time  
fustat: censoring status  
age: in years  
resid.ds: residual disease present (1=no,2=yes)  
rx: treatment group  
ecog.ps: ECOG performance status (1 is better, see reference)

### Source

Terry Therneau

### References

for ECOG performance status: [http://ecog.dfci.harvard.edu/~ecogdba/general/perf\\_stat.html](http://ecog.dfci.harvard.edu/~ecogdba/general/perf_stat.html)

---

pbc

*Mayo Clinic Primary Biliary Cirrhosis Data*

---

### Description

D This data is from the Mayo Clinic trial in primary biliary cirrhosis (PBC) of the liver conducted between 1974 and 1984. A total of 424 PBC patients, referred to Mayo Clinic during that ten-year interval, met eligibility criteria for the randomized placebo controlled trial of the drug D-penicillamine. The first 312 cases in the data set participated in the randomized trial and contain largely complete data. The additional 112 cases did not participate in the clinical trial, but consented to have basic measurements recorded and to be followed for survival. Six of those cases were lost to follow-up shortly after diagnosis, so the data here are on an additional 106 cases as well as the 312 randomized participants.

A nearly identical data set found in appendix D of Fleming and Harrington; this version has fewer missing values.

**Usage**

pbc

**Format**

age: in years  
 albumin: serum albumin (mg/dl)  
 alk.phos: alkaline phosphatase (U/liter)  
 ascites: presence of ascites  
 ast: aspartate aminotransferase, once called SGOT (U/ml)  
 bili: serum bilirubin (mg/dl)  
 chol: serum cholesterol (mg/dl)  
 copper: urine copper (ug/day)  
 edema: 0 no edema, 0.5 untreated or successfully treated  
         1 edema despite diuretic therapy  
 hepato: presence of hepatomegaly or enlarged liver  
 id: case number  
 platelet: platelet count  
 protime: standardised blood clotting time  
 sex: m/f  
 spiders: blood vessel malformations in the skin  
 stage: histologic stage of disease (needs biopsy)  
 status: status at endpoint, 0/1/2 for censored, transplant, dead  
 time: number of days between registration and the earlier of death,  
        transplantation, or study analysis in July, 1986  
 trt: 1/2/NA for D-penicillmain, placebo, not randomised  
 trig: triglycerides (mg/dl)

**Source**

T Therneau and P Grambsch (2000), *Modeling Survival Data: Extending the Cox Model*, Springer-Verlag, New York. ISBN: 0-387-98784-3.

pbcseq

*Mayo Clinic Primary Biliary Cirrhosis, sequential data***Description**

This data is a continuation of the PBC data set, and contains the follow-up laboratory data for each study patient. An analysis based on the data can be found in Murtagh, et. al.

The primary PBC data set contains only baseline measurements of the laboratory paramters. This data set contains multiple laboratory results, but only on the 312 randomized patients. Some baseline data values in this file differ from the original PBC file, for instance, the data errors in prothrombin time and age which were discovered after the original analysis (see Fleming and Harrington, figure 4.6.7).

One "feature" of the data deserves special comment. The last observation before death or liver transplant often has many more missing covariates than other data rows. The original clinical protocol for these patients specified visits at 6 months, 1 year, and annually thereafter. At these protocol visits lab values were obtained for a large pre-specified battery of tests. "Extra" visits, often undertaken because of worsening medical condition, did not necessarily have all this lab work. The missing values are thus potentially informative.

## Usage

pbc

## Format

id:	case number
age:	in years
sex:	m/f
trt:	1/2/NA for D-penicillmain, placebo, not randomised
time:	number of days between registration and the earlier of death, transplantation, or study analysis in July, 1986
status:	status at endpoint, 0/1/2 for censored, transplant, dead
day:	number of days between enrollment and this visit date all measurements below refer to this date
albumin:	serum albumin (mg/dl)
alk.phos:	alkaline phosphatase (U/liter)
ascites:	presence of ascites
ast:	aspartate aminotransferase, once called SGOT (U/ml)
bili:	serum bilirubin (mg/dl)
chol:	serum cholesterol (mg/dl)
copper:	urine copper (ug/day)
edema:	0 no edema, 0.5 untreated or successfully treated 1 edema despite diuretic therapy
hepato:	presence of hepatomegaly or enlarged liver
platelet:	platelet count
protime:	standardised blood clotting time
spiders:	blood vessel malformations in the skin
stage:	histologic stage of disease (needs biopsy)
trig:	triglycerides (mg/dl)

## Source

T Therneau and P Grambsch, "Modeling Survival Data: Extending the Cox Model", Springer-Verlag, New York, 2000. ISBN: 0-387-98784-3.

## References

Murtaugh PA. Dickson ER. Van Dam GM. Malinchoc M. Grambsch PM. Langworthy AL. Gips CH. "Primary biliary cirrhosis: prediction of short-term survival based on repeated patient visits." *Hepatology*. 20(1.1):126-34, 1994.

Fleming T and Harrington D., "Counting Processes and Survival Analysis", Wiley, New York, 1991.



---

plot.aareg                      *Plot an aareg object.*

---

### Description

Plot the estimated coefficient function(s) from a fit of Aalen's additive regression model.

### Usage

```
## S3 method for class 'aareg':
plot(x, se=TRUE, maxtime, type='s', ...)
```

### Arguments

x	the result of a call to the aareg function
se	if TRUE, standard error bands are included on the plot
maxtime	upper limit for the x-axis.
type	graphical parameter for the type of line, default is "steps".
...	other graphical parameters such as line type, color, or axis labels.

### Side Effects

A plot is produced on the current graphical device.

### References

Aalen, O.O. (1989). A linear regression model for the analysis of life times. *Statistics in Medicine*, 8:907-925.

### See Also

aareg

---

plot.cox.zph                      *Graphical Test of Proportional Hazards*

---

### Description

Displays a graph of the scaled Schoenfeld residuals, along with a smooth curve.

### Usage

```
## S3 method for class 'cox.zph':
plot(x, resid=TRUE, se=TRUE, df=4, nsmo=40, var, ...)
```

**Arguments**

x	result of the <code>cox.zph</code> function.
resid	a logical value, if <code>TRUE</code> the residuals are included on the plot, as well as the smooth fit.
se	a logical value, if <code>TRUE</code> , confidence bands at two standard errors will be added.
df	the degrees of freedom for the fitted natural spline, <code>df=2</code> leads to a linear fit.
nsmo	number of points used to plot the fitted spline.
var	the set of variables for which plots are desired. By default, plots are produced in turn for each variable of a model. Selection of a single variable allows other features to be added to the plot, e.g., a horizontal line at zero or a main title. This has been superseded by a subscripting method; see the example below.
...	additional graphical arguments passed to the <code>plot</code> function.

**Side Effects**

a plot is produced on the current graphics device.

**See Also**

[coxph](#), [cox.zph](#).

**Examples**

```
vfit <- coxph(Surv(time,status) ~ trt + factor(celltype) +
             karno + age, data=veteran, x=TRUE)
temp <- cox.zph(vfit)
plot(temp, var=5)      # Look at Karnofsky score, old way of doing plot
plot(temp[5])         # New way with subscripting
abline(0, 0, lty=3)
# Add the linear fit as well
abline(lm(temp$y[,5] ~ temp$x)$coefficients, lty=4, col=3)
title(main="VA Lung Study")
```

---

plot.survfit

*Plot Method for 'survfit'*

---

**Description**

A plot of survival curves is produced, one curve for each strata. The `log=T` option does extra work to avoid `log(0)`, and to try to create a pleasing result. If there are zeros, they are plotted by default at 0.8 times the smallest non-zero value on the curve(s).

**Usage**

```
## S3 method for class 'survfit':
plot(x, conf.int=, mark.time=TRUE,
     mark=3, col=1, lty=1, lwd=1, cex=1, log=FALSE, xscale=1, yscale=1,
     firstx=0, firsty=1, xmax, ymin=0, fun,
     xlab="", ylab="", xaxs="S", ...)
```

**Arguments**

<code>x</code>	an object of class <code>survfit</code> , usually returned by the <code>survfit</code> function.
<code>conf.int</code>	determines whether confidence intervals will be plotted. The default is to do so if there is only 1 curve, i.e., no strata.
<code>mark.time</code>	controls the labeling of the curves. If set to <code>FALSE</code> , no labeling is done. If <code>TRUE</code> , then curves are marked at each censoring time which is not also a death time. If <code>mark.time</code> is a numeric vector, then curves are marked at the specified time points.
<code>mark</code>	vector of mark parameters, which will be used to label the curves. The <code>lines</code> help file contains examples of the possible marks. The vector is reused cyclically if it is shorter than the number of curves.
<code>col</code>	a vector of integers specifying colors for each curve. The default value is 1.
<code>lty</code>	a vector of integers specifying line types for each curve. The default value is 1.
<code>lwd</code>	a vector of numeric values for line widths. The default value is 1.
<code>cex</code>	a numeric value specifying the size of the marks. This is not treated as a vector; all marks have the same size.
<code>log</code>	a logical value, if <code>TRUE</code> the y axis will be on a log scale. Alternately, one of the standard character strings "x", "y", or "xy" can be given to specific logarithmic horizontal and/or vertical axes.
<code>yscale</code>	a numeric value used to multiply the labels on the y axis. A value of 100, for instance, would be used to give a percent scale. Only the labels are changed, not the actual plot coordinates, so that adding a curve with <code>"lines(surv.exp(...))"</code> , say, will perform as it did without the <code>yscale</code> argument.
<code>xscale</code>	a numeric value used like <code>yscale</code> for labels on the x axis. A value of 365.25 will give labels in years instead of the original days.
<code>firstx, firsty</code>	the starting point for the survival curves. If either of these is set to <code>NA</code> the plot will start at the first time point of the curve. By default, the plot program obeys tradition by having the plot start at (0,0). If <code>start.time</code> argument is used in <code>survfit</code> , <code>firstx</code> is set to that value.
<code>xmax</code>	the maximum horizontal plot coordinate. This can be used to shrink the range of a plot. It shortens the curve before plotting it, so that unlike using the <code>xlim</code> graphical parameter, warning messages about out of bounds points are not generated.
<code>ymin</code>	lower boundary for y values. Survival curves are most often drawn in the range of 0-1, even if none of the curves approach zero. The parameter is ignored if the <code>fun</code> argument is present, or if it has been set to <code>NA</code> .
<code>fun</code>	an arbitrary function defining a transformation of the survival curve. For example <code>fun=log</code> is an alternative way to draw a log-survival curve (but with the axis labeled with $\log(S)$ values), and <code>fun=sqrt</code> would generate a curve on square root scale. Four often used transformations can be specified with a character argument instead: "log" is the same as using the <code>log=T</code> option, "event" plots cumulative events ( $f(y) = 1-y$ ), "cumhaz" plots the cumulative hazard function ( $f(y) = -\log(y)$ ), and "cloglog" creates a complimentary log-log survival plot ( $f(y) = \log(-\log(y))$ ) along with log scale for the x-axis.
<code>xlab</code>	label given to the x-axis.

ylab	label given to the y-axis.
xaxis	either "S" for a survival curve or a standard x axis style as listed in <code>par</code> . Survival curves are usually displayed with the curve touching the y-axis, but not touching the bounding box of the plot on the other 3 sides. Type "S" accomplishes this by manipulating the plot range and then using the "i" style internally.
...	for future methods

**Value**

a list with components `x` and `y`, containing the coordinates of the last point on each of the curves (but not the confidence limits). This may be useful for labeling.

**Bugs**

Survival curve objects created from a `coxph` model does not include the censoring times. Therefore, specifying `mark.time=T` does not work. If you want to mark censoring times on the curve(s) resulting from a `coxph` fit, provide a vector of times as the `mark.time` argument in the call to `plot.survfit` or `lines.survfit`.

**See Also**

`par`, `survfit`, `lines.survfit`.

**Examples**

```
leukemia.surv <- survfit(Surv(time, status) ~ x, data = aml)
plot(leukemia.surv, lty = 2:3)
legend(100, .9, c("Maintenance", "No Maintenance"), lty = 2:3)
title("Kaplan-Meier Curves\nfor AML Maintenance Study")
lsurv2 <- survfit(Surv(time, status) ~ x, aml, type='fleming')
plot(lsurv2, lty=2:3, fun="cumhaz",
     xlab="Months", ylab="Cumulative Hazard")
```

---

predict.coxph

*Predictions for a Cox model*

---

**Description**

Compute fitted values and regression terms for a model fitted by `coxph`

**Usage**

```
## S3 method for class 'coxph':
predict(object, newdata,
       type=c("lp", "risk", "expected", "terms"),
       se.fit=FALSE, na.action=na.pass, terms=names(object$assign), collapse, ...)
```

**Arguments**

object	the results of a coxph fit.
newdata	Optional new data at which to do predictions. If absent predictions are for the data frame used in the original fit.
type	the type of predicted value. Choices are the linear predictor ("lp"), the risk score exp(lp) ("risk"), the expected number of events given the covariates and follow-up time ("expected"), and the terms of the linear predictor ("terms").
se.fit	if TRUE, pointwise standard errors are produced for the predictions.
na.action	applies only when the newdata argument is present, and defines the missing value action for the new data. The default is to include all observations.
terms	if type="terms", this argument can be used to specify which terms should be included; the default is all.
collapse	optional vector of subject identifiers. If specified, the output will contain one entry per subject rather than one entry per observation.
...	For future methods

**Value**

a vector or matrix of predictions, or a list containing the predictions (element "fit") and their standard errors (element "se.fit") if the se.fit option is TRUE.

**See Also**

[predict.coxph](#), [termplot](#)

**Examples**

```
fit <- coxph(Surv(time, status) ~ age + ph.ecog + strata(inst), lung)
mresid <- lung$status - predict(fit, type='expected') #Martingale resid
predict(fit, type="lp")
predict(fit, type="risk")
predict(fit, type="expected")
predict(fit, type="terms")
predict(fit, type="lp", se.fit=TRUE)
predict(fit, type="risk", se.fit=TRUE)
predict(fit, type="expected", se.fit=TRUE)
predict(fit, type="terms", se.fit=TRUE)
```

---

predict.survreg      *Predicted Values for a 'survreg' Object*

---

**Description**

Predicted values for a survreg object

**Usage**

```
## S3 method for class 'survreg':
predict(object, newdata,
        type=c("response", "link", "lp", "linear", "terms", "quantile",
              "uquantile"),
        se.fit=FALSE, terms=NULL, p=c(0.1, 0.9), na.action=na.pass, ...)
```

**Arguments**

object	result of a model fit using the <code>survreg</code> function.
newdata	data for prediction. If absent predictions are for the subjects used in the original fit.
type	the type of predicted value. This can be on the original scale of the data (response), the linear predictor ("linear", with "lp" as an allowed abbreviation), a predicted quantile on the original scale of the data ("quantile"), a quantile on the linear predictor scale ("uquantile"), or the matrix of terms for the linear predictor ("terms"). At this time "link" and linear predictor ("lp") are identical.
se.fit	if TRUE, include the standard errors of the prediction in the result.
terms	subset of terms. The default for residual type "terms" is a matrix with one column for every term (excluding the intercept) in the model.
p	vector of percentiles. This is used only for quantile predictions.
na.action	applies only when the <code>newdata</code> argument is present, and defines the missing value action for the new data. The default is to include all observations.
...	for future methods

**Value**

a vector or matrix of predicted values.

**References**

Escobar and Meeker (1992). Assessing influence in regression analysis with censored data. *Biometrics*, 48, 507-528.

**See Also**

[survreg](#), [residuals.survreg](#)

**Examples**

```
# Draw figure 1 from Escobar and Meeker
fit <- survreg(Surv(time,status) ~ age + age^2, data=stanford2,
              dist='lognormal')
plot(stanford2$age, stanford2$time, xlab='Age', ylab='Days',
     xlim=c(0,65), ylim=c(.01, 10^6), log='y')
pred <- predict(fit, newdata=list(age=1:65), type='quantile',
              p=c(.1, .5, .9))
matlines(1:65, pred, lty=c(2,1,2), col=1)

# Predicted Weibull survival curve for a lung cancer subject with
# ECOG score of 2
```

```

lfit <- survreg(Surv(time, status) ~ ph.ecog, data=lung)
pct <- 1:98/100 # The 100th percentile of predicted survival is at +infinity
ptime <- predict(lfit, newdata=data.frame(ph.ecog=2), type='quantile',
                p=pct, se=TRUE)
matplot(cbind(ptime$fit, ptime$fit + 2*ptime$se.fit,
              ptime$fit - 2*ptime$se.fit)/30.5, 1-pct,
        xlab="Months", ylab="Survival", type='l', lty=c(1,2,2), col=1)

```

---

```
print.aareg      Print an aareg object
```

---

## Description

Print out a fit of Aalen's additive regression model

## Usage

```
## S3 method for class 'aareg':
print(x, maxtime, test=c("aalen", "nrisk"), scale=1, ...)
```

## Arguments

<code>x</code>	the result of a call to the <code>aareg</code> function
<code>maxtime</code>	the upper time point to be used in the test for non-zero slope
<code>test</code>	the weighting to be used in the test for non-zero slope. The default weights are based on the variance of each coefficient, as a function of time. The alternative weight is proportional to the number of subjects still at risk at each time point.
<code>scale</code>	scales the coefficients. For some data sets, the coefficients of the Aalen model will be very small ( $10^{-4}$ ); this simply multiplies the printed values by a constant, say $1e6$ , to make the printout easier to read.
<code>...</code>	for future methods

## Details

The estimated increments in the coefficient estimates can become quite unstable near the end of follow-up, due to the small number of observations still at risk in a data set. Thus, the test for slope will sometimes be more powerful if this last 'tail' is excluded.

## Value

the calling argument is returned.

## Side Effects

the results of the fit are displayed.

## References

Aalen, O.O. (1989). A linear regression model for the analysis of life times. *Statistics in Medicine*, 8:907-925.

**See Also**

aareg

---

`print.summary.coxph`*Print method for summary.coxph objects*

---

**Description**

Produces a printed summary of a fitted coxph model

**Usage**

```
## S3 method for class 'summary.coxph':
print(x, digits=max(getOption("digits") - 3, 3),
      signif.stars = getOption("show.signif.stars"), ...)
```

**Arguments**

<code>x</code>	the result of a call to <code>summary.coxph</code>
<code>digits</code>	significant digits to print
<code>signif.stars</code>	Show stars to highlight small p-values
<code>...</code>	For future methods

---

`print.summary.survfit`*Print Survfit Summary*

---

**Description**Prints the result of `summary.survfit`.**Usage**

```
## S3 method for class 'summary.survfit':
print(x, digits = max(options() $digits-4, 3), ...)
```

**Arguments**

<code>x</code>	an object of class "summary.survfit", which is the result of the <code>summary.survfit</code> function.
<code>digits</code>	the number of digits to use in printing the numbers.
<code>...</code>	for future methods

**Value**

x, with the invisible flag set to prevent printing.



**Side Effects**

prints the summary created by `summary.survfit`.

**See Also**

`options`, `print`, `summary.survfit`.

---

`print.survfit`      *Print a Short Summary of a Survival Curve*

---

**Description**

Print number of observations, number of events, the restricted mean survival and its standard error, and the median survival with confidence limits for the median.

**Usage**

```
## S3 method for class 'survfit':
print(x, scale=1, digits = max(options()$digits - 4, 3),
      print.rmean=getOption("survfit.print.rmean"),
      rmean = getOption('survfit.rmean'),...)
```

**Arguments**

<code>x</code>	the result of a call to the <code>survfit</code> function.
<code>scale</code>	a numeric value to rescale the survival time, e.g., if the input data to <code>survfit</code> were in days, <code>scale=365</code> would scale the printout to years.
<code>digits</code>	Number of digits to print
<code>print.rmean, rmean</code>	Options for computation and display of the restricted mean.
<code>...</code>	for future results

**Details**

The mean and its variance are based on a truncated estimator. That is, if the last observation(s) is not a death, then the survival curve estimate does not go to zero and the mean is undefined. There are four possible approaches, which are selected by the `rmean` option. The first is to set the upper limit to a constant, e.g., `rmean=365`. In this case the reported mean would be the expected number of days, out of the first 365, that would be experienced by each group. This is useful if interest focuses on a fixed period. Other options are `"none"` (no estimate), `"common"` and `"individual"`. For the last of these, the mean is computed as the area under the curve, over the range from 0 to the maximum observed time for that curve. Since the end point is random, values for different curves are not comparable and the printed standard errors are an underestimate as they do not take into account this random variation. This option is provided mainly for backwards compatibility, as this estimate was the default (only) one in earlier releases of the code. The `"common"` option uses the maximum time for all curves in the object as a common upper limit for the auc calculation.

The median and its confidence interval are defined by drawing a horizontal line at 0.5 on the plot of the survival curve and its confidence bands. The intersection of the line with the lower CI band defines the lower limit for the median's interval, and similarly for the upper band. If any of the intersections is not a point, then we use the smallest point of intersection, e.g., if the survival curve were exactly equal to 0.5 over an interval.

**Value**

`x`, with the invisible flag set to prevent printing.

**Side Effects**

he number of observations, the number of events, the median survival with its confidence interval, and optionally the restricted mean survival (`rmean`) and its standard error, are printed. If there are multiple curves, there is one line of output for each.

**References**

Miller, Rupert G., Jr. (1981). *Survival Analysis*. New York:Wiley, p 71.

**See Also**

[summary.survfit](#).

---

pspline

*Smoothing splines using a pspline basis*

---

**Description**

Specifies a penalised spline basis for the predictor. This is done by fitting a comparatively small set of splines and penalising the integrated second derivative. Traditional smoothing splines use one basis per observation, but several authors have pointed out that the final results of the fit are indistinguishable for any number of basis functions greater than about 2-3 times the degrees of freedom. Eilers and Marx point out that if the basis functions are evenly spaced, this leads to significant computational simplifications.

**Usage**

```
pspline(x, df=4, theta, nterm=2.5 * df, degree=3, eps=0.1, method, ...)
```

**Arguments**

<code>x</code>	predictor. The function does not apply to factor variables.
<code>df</code>	the desired degrees of freedom. One of the arguments <code>df</code> or <code>theta</code> must be given, but not both. If <code>df=0</code> , then the AIC = (loglik -df) is used to choose an "optimal" degrees of freedom. If AIC is chosen, then an optional argument <code>'caic=T'</code> can be used to specify the corrected AIC of Hurvich et. al.
<code>theta</code>	roughness penalty for the fit. It is a monotone function of the degrees of freedom, with <code>theta=1</code> corresponding to a linear fit and <code>theta=0</code> to an unconstrained fit of <code>nterm</code> degrees of freedom.
<code>nterm</code>	number of splines in the basis
<code>degree</code>	degree of splines
<code>eps</code>	accuracy for <code>df</code>
<code>method</code>	the method for choosing the tuning parameter <code>theta</code> . If <code>theta</code> is given, then <code>'fixed'</code> is assumed. If the degrees of freedom is given, then <code>'df'</code> is assumed. If <code>method='aic'</code> then the degrees of freedom is chosen automatically using Akaike's information criterion.
<code>...</code>	optional arguments to the control function

**Value**

Object of class `coxph.penalty` containing the spline basis, with the appropriate attributes to be recognized as a penalized term by the `coxph` or `survreg` functions.

**References**

Eilers, Paul H. and Marx, Brian D. (1996). Flexible smoothing with B-splines and penalties. *Statistical Science*, 11, 89-121.

Hurvich, C.M. and Simonoff, J.S. and Tsai, Chih-Ling (1998). Smoothing parameter selection in nonparametric regression using an improved Akaike information criterion, *JRSSB*, volume 60, 271-293.

**See Also**

`coxph`, `survreg`, `ridge`, `frailty`

**Examples**

```
lfit6 <- survreg(Surv(time, status)~pspline(age, df=2), cancer)
plot(cancer$age, predict(lfit6), xlab='Age', ylab="Spline prediction")
title("Cancer Data")
fit0 <- coxph(Surv(time, status) ~ ph.ecog + age, cancer)
fit1 <- coxph(Surv(time, status) ~ ph.ecog + pspline(age,3), cancer)
fit3 <- coxph(Surv(time, status) ~ ph.ecog + pspline(age,8), cancer)
fit0
fit1
fit3
```

---

pyears

*Person Years*

---

**Description**

This function computes the person-years of follow-up time contributed by a cohort of subjects, stratified into subgroups. It also computes the number of subjects who contribute to each cell of the output table, and optionally the number of events and/or expected number of events in each cell.

**Usage**

```
pyears(formula, data, weights, subset, na.action,
       ratetable=survexp.us, scale=365.25, expect=c('event', 'pyears'),
       model=FALSE, x=FALSE, y=FALSE, data.frame=FALSE)
```

**Arguments**

`formula` a formula object. The response variable will be a vector of follow-up times for each subject, or a `Surv` object containing the survival time and an event indicator. The predictors consist of optional grouping variables separated by `+` operators (exactly as in `survfit`), time-dependent grouping variables such as `age` (specified with `tcut`), and optionally a `ratetable` term. This latter matches each subject to his/her expected cohort.

<code>data</code>	a data frame in which to interpret the variables named in the <code>formula</code> , or in the <code>subset</code> and the <code>weights</code> argument.
<code>weights</code>	case weights.
<code>subset</code>	expression saying that only a subset of the rows of the data should be used in the fit.
<code>na.action</code>	a missing-data filter function, applied to the <code>model.frame</code> , after any <code>subset</code> argument has been used. Default is <code>options()\$na.action</code> .
<code>ratetable</code>	a table of event rates, such as <code>survexp.uswhite</code> .
<code>scale</code>	a scaling for the results. As most rate tables are in units/day, the default value of 365.25 causes the output to be reported in years.
<code>expect</code>	should the output table include the expected number of events, or the expected number of person-years of observation. This is only valid with a rate table.
<code>data.frame</code>	return a data frame rather than a set of arrays.
<code>model, x, y</code>	If any of these is true, then the model frame, the model matrix, and/or the vector of response times will be returned as components of the final result.

### Details

Because `pyears` may have several time variables, it is necessary that all of them be in the same units. For instance, in the call

```
py <- pyears(futime ~ rx + ratetable(age=age, sex=sex, year=entry.dt))
```

with a `ratetable` whose natural unit is days, it is important that `futime`, `age` and `entry.dt` all be in days. Given the wide range of possible inputs, it is difficult for the routine to do sanity checks of this aspect.

A special function `tcut` is needed to specify time-dependent cutpoints. For instance, assume that `age` is in years, and that the desired final arrays have as one of their margins the age groups 0-2, 2-10, 10-25, and 25+. A subject who enters the study at age 4 and remains under observation for 10 years will contribute follow-up time to both the 2-10 and 10-25 subsets. If `cut(age, c(0, 2, 10, 25, 100))` were used in the formula, the subject would be classified according to his starting age only. The `tcut` function has the same arguments as `cut`, but produces a different output object which allows the `pyears` function to correctly track the subject.

The results of `pyears` are normally used as input to further calculations. The `print` routine, therefore, is designed to give only a summary of the table.

The example below is from a study of hip fracture rates from 1930 - 1990 in Rochester, Minnesota. Survival post hip fracture has increased over that time, but so has the survival of elderly subjects in the population at large. A model of relative survival helps to clarify what has happened: Poisson regression is used, but replacing exposure time with expected exposure (for an age and sex matched control). Death rates change with age, of course, so the result is carved into 1 year increments of time. Males and females were done separately.

### Value

a list with components:

<code>pyears</code>	an array containing the person-years of exposure. (Or other units, depending on the rate table and the scale). The dimension and dimnames of the array correspond to the variables on the right hand side of the model equation.
---------------------	--

n	an array containing the number of subjects who contribute time to each cell of the <code>pyears</code> array.
event	an array containing the observed number of events. This will be present only if the response variable is a <code>Surv</code> object.
expected	an array containing the expected number of events (or person years if <code>expect="pyears"</code> ). This will be present only if there was a <code>ratetable</code> term.
data	if the <code>data.frame</code> option was set, a data frame containing the variables <code>n</code> , <code>event</code> , <code>pyears</code> and <code>event</code> that supplants the four arrays listed above, along with variables corresponding to each dimension. There will be one row for each cell in the arrays.
offtable	the number of person-years of exposure in the cohort that was not part of any cell in the <code>pyears</code> array. This is often useful as an error check; if there is a mismatch of units between two variables, nearly all the person years may be off table.
summary	a summary of the rate-table matching. This is also useful as an error check.
call	an image of the call to the function.
na.action	the <code>na.action</code> attribute contributed by an <code>na.action</code> routine, if any.

### See Also

[ratetable](#), [survexp](#), [Surv](#).

### Examples

```
# Look at progression rates jointly by calendar date and age
#
temp.yr <- tcut(mgus$dxyr, 55:92, labels=as.character(55:91))
temp.age <- tcut(mgus$age, 34:101, labels=as.character(34:100))
ptime <- ifelse(is.na(mgus$pctime), mgus$futime, mgus$pctime)
pstat <- ifelse(is.na(mgus$pctime), 0, 1)
pfit <- pyears(Surv(ptime/365.25, pstat) ~ temp.yr + temp.age + sex, mgus,
  data.frame=TRUE)
# Turn the factor back into numerics for regression
tdata <- pfit$data
tdata$age <- as.numeric(as.character(tdata$temp.age))
tdata$year <- as.numeric(as.character(tdata$temp.yr))
fit1 <- glm(event ~ year + age + sex + offset(log(pyears)),
  data=tdata, family=poisson)
## Not run:
# fit a gam model
gfit.m <- gam(y ~ s(age) + s(year) + offset(log(time)),
  family = poisson, data = tdata)
## End(Not run)

# Example #2 Create the hearta data frame:
hearta <- by(heart, heart$id,
  function(x)x[x$stop == max(x$stop),])
hearta <- do.call("rbind", hearta)
# Produce pyears table of death rates on the surgical arm
# The first is by age at randomization, the second by current age
fit1 <- pyears(Surv(stop/365.25, event) ~ cut(age + 48, c(0,50,60,70,100)) +
  surgery, data = hearta, scale = 1)
```

```
fit2 <- pyears(Surv(stop/365.25, event) ~ tcut(age + 48, c(0,50,60,70,100)) +
  surgery, data = hearta, scale = 1)
fit1$event/fit1$pyears #death rates on the surgery and non-surg arm
fit2$event/fit2$pyears #death rates on the surgery and non-surg arm
```

---

ratetable	<i>Ratetable reference in formula</i>
-----------	---------------------------------------

---

## Description

This function matches variable names in data to those in a ratetable for [survexp](#)

## Usage

```
ratetable(...)
```

## Arguments

... tags matching dimensions of the ratetable and variables in the data frame (see example)

## Value

A data frame

## See Also

[survexp](#), [survexp.us](#), [is.ratetable](#)

## Examples

```
fit <- survfit(Surv(time, status) ~ sex, pbc, subset=1:312)

# The data set does not have entry date, use the midpoint of the study
efit <- survexp(~ ratetable(sex=sex, age=age*365.35, year=as.Date('1979/1/1')) +
  sex, data=pbcc, times=(0:24)*182)
## Not run:
plot(fit, mark.time=F, xscale=365.25, xlab="Years post diagnosis",
  ylab="Survival")
lines(efit, col=2, xscale=365.25) # Add the expected survival line

## End(Not run)
```

ratetables

*Census Data Sets for the Expected Survival and Person Years Functions***Description**

Census data sets for the expected survival and person years functions.

**Details**

**us** total United States population, by age and sex, 1960 to 1980.

**uswhite** United States white population, by age and sex, 1950 to 1980. This is no longer included, but can be extracted from `survexp.usr` as shown in the examples.

**usr** United States population, by age, sex and race, 1960 to 1980. Race is white, nonwhite, or black. For 1960 and 1970 the black population values were not reported separately, so the nonwhite values were used.

**mn** total Minnesota population, by age and sex, 1970 and 1980.

**mnwhite** Minnesota white population, by age and sex, 1960 to 1980.

**fl** total Florida population, by age and sex, 1970 and 1980.

**flr** Florida population, by age, sex and race, 1970-1980. Race is white, nonwhite, or black. For 1970 the black population values were not reported separately, so the nonwhite values were used.

**az** total Arizona population, by age and sex, 1970 and 1980.

**azr** Arizona population, by age, sex and race, 1970-1980. Race is white versus nonwhite. For 1970 the nonwhite population values were not reported separately. In order to make the rate table be a matrix, the 1980 values were repeated. (White and non-white values are quite different).

Each of these tables contains the daily hazard rate for a matched subject from the population, defined as  $-\log(1 - q)/365.24$  where  $q$  is the 1 year probability of death as reported in the original tables. For age 25 in 1970, for instance,  $p = 1 - q$  is the probability that a subject who becomes 25 years of age in 1970 will achieve his/her 26th birthday. The tables are recast in terms of hazard per day entirely for computational convenience. (The fraction .24 in the denominator is based on 24 leap years per century.)

Each table is stored as an array, with additional attributes, and can be subset and manipulated as standard S arrays. Interpolation between calendar years is done “on the fly” by the `survexp` routine.

Some of the deficiencies, e.g., 1970 Arizona non-white, are a result of local (Mayo Clinic) conditions. The data probably exists, but we don't have a copy it in the library.

The tables have been augmented to contain extrapolated values for 1990 and 2000. The details can be found in Mayo Clinic Biostatistics technical report 63 at <http://www.mayo.edu/hsr/techrpt.html>.

**Examples**

```
survexp.uswhite <- survexp.usr[,,"white",]
```

rats

*Rat data from Gail et al.***Description**

48 rats were injected with a carcinogen, and then randomized to either drug or placebo. The number of tumors ranges from 0 to 13; all rats were censored at 6 months after randomization.

**Usage**

rats

**Format**

rat:	id
rx:	treatment,(1=drug, 0=control)
observation:	within rat
start:	entry time
stop:	exit time
status:	event status

**Source**

MH Gail, TJ Santner, and CC Brown (1980), An analysis of comparative carcinogenesis experiments based on multiple times to tumor. *Biometrics* **36**, 255–266.

residuals.coxph

*Calculate Residuals for a 'coxph' Fit***Description**

Calculates martingale, deviance, score or Schoenfeld residuals for a Cox proportional hazards model.

**Usage**

```
## S3 method for class 'coxph':
residuals(object,
  type=c("martingale", "deviance", "score", "schoenfeld",
        "dfbeta", "dfbetas", "scaledsch", "partial"),
  collapse=FALSE, weighted=FALSE, ...)
## S3 method for class 'coxph.null':
residuals(object,
  type=c("martingale", "deviance", "score", "schoenfeld"),
  collapse=FALSE, weighted=FALSE, ...)
```



**Arguments**

object	an object inheriting from class <code>coxph</code> , representing a fitted Cox regression model. Typically this is the output from the <code>coxph</code> function.
type	character string indicating the type of residual desired. Possible values are "martingale", "deviance", "score", "schoenfeld", "dfbeta", "dfbetas", and "scaledsch". Only enough of the string to determine a unique match is required.
collapse	vector indicating which rows to collapse (sum) over. In time-dependent models more than one row data can pertain to a single individual. If there were 4 individuals represented by 3, 1, 2 and 4 rows of data respectively, then <code>collapse=c(1,1,1, 2, 3,3, 4,4,4,4)</code> could be used to obtain per subject rather than per observation residuals.
weighted	if TRUE and the model was fit with case weights, then the weighted residuals are returned.
...	other unused arguments

**Value**

For martingale and deviance residuals, the returned object is a vector with one element for each subject (without `collapse`). For score residuals it is a matrix with one row per subject and one column per variable. The row order will match the input data for the original fit. For Schoenfeld residuals, the returned object is a matrix with one row for each event and one column per variable. The rows are ordered by time within strata, and an attribute `strata` is attached that contains the number of observations in each strata. The scaled Schoenfeld residuals are used in the `cox.zph` function.

The score residuals are each individual's contribution to the score vector. Two transformations of this are often more useful: `dfbeta` is the approximate change in the coefficient vector if that observation were dropped, and `dfbetas` is the approximate change in the coefficients, scaled by the standard error for the coefficients.

**NOTE**

For deviance residuals, the status variable may need to be reconstructed. For score and Schoenfeld residuals, the X matrix will need to be reconstructed.

**References**

T. Therneau, P. Grambsch, and T. Fleming. "Martingale based residuals for survival models", *Biometrika*, March 1990.

**See Also**

[coxph](#)

**Examples**

```
fit <- coxph(Surv(start, stop, event) ~ (age + surgery)* transplant,
            data=heart)
mresid <- resid(fit, collapse=heart$id)
```

---

residuals.survreg *Compute Residuals for 'survreg' Objects*


---

## Description

This is a method for the function [residuals](#) for objects inheriting from class `survreg`.

## Usage

```
## S3 method for class 'survreg':
residuals(object, type=c("response", "deviance", "dfbeta", "dfbetas",
"working", "ldcase", "ldresp", "ldshape", "matrix"), rsigma=TRUE,
collapse=FALSE, weighted=FALSE, ...)
```

## Arguments

<code>object</code>	an object inheriting from class <code>survreg</code> .
<code>type</code>	type of residuals, with choices of "response", "deviance", "dfbeta", "dfbetas", "working", "ldcase", "lsresp", "ldshape", and "matrix". See the LaTeX documentation ( <a href="#">survival/doc/survival.ps.gz</a> ) for more detail.
<code>rsigma</code>	include the scale parameters in the variance matrix, when doing computations. (I can think of no good reason not to).
<code>collapse</code>	optional vector of subject groups. If given, this must be of the same length as the residuals, and causes the result to be per group residuals.
<code>weighted</code>	give weighted residuals? Normally residuals are unweighted.
<code>...</code>	other unused arguments

## Value

A vector or matrix of residuals is returned. Response residuals are on the scale of the original data, working residuals are on the scale of the linear predictor, and deviance residuals are on log-likelihood scale. The `dfbeta` residuals are a matrix, where the *i*th row gives the approximate change in the coefficients due to the addition of subject *i*. The `dfbetas` matrix contains the `dfbeta` residuals, with each column scaled by the standard deviation of that coefficient.

The `matrix` type produces a matrix based on derivatives of the log-likelihood function. Let  $L$  be the log-likelihood,  $p$  be the linear predictor  $X\beta$ , and  $s$  be  $\log(\sigma)$ . Then the 6 columns of the matrix are  $L$ ,  $dL/dp$ ,  $\partial^2 L/\partial p^2$ ,  $dL/ds$ ,  $\partial^2 L/\partial s^2$  and  $\partial^2 L/\partial p \partial s$ . Diagnostics based on these quantities are discussed in an article by Escobar and Meeker. The main ones are the likelihood displacement residuals for perturbation of a case weight (`ldcase`), the response value (`ldresp`), and the shape.

## References

Escobar, L. A. and Meeker, W. Q. (1992). Assessing influence in regression analysis with censored data. *Biometrics* **48**, 507-528.

## See Also

[predict.survreg](#)

**Examples**

```
fit <- survreg(Surv(time, status) ~x, aml)
rr <- residuals(fit, type='matrix')
```

---

 ridge

*Ridge regression*


---

**Description**

When used in a [coxph](#) or [survreg](#) model formula, specifies a ridge regression term. The likelihood is penalised by  $\theta/2$  time the sum of squared coefficients. If `scale=T` the penalty is calculated for coefficients based on rescaling the predictors to have unit variance. If `df` is specified then  $\theta$  is chosen based on an approximate degrees of freedom.

**Usage**

```
ridge(..., theta, df=nvar/2, eps=0.1, scale=TRUE)
```

**Arguments**

<code>...</code>	predictors to be ridged
<code>theta</code>	penalty is $\theta/2$ time sum of squared coefficients
<code>df</code>	Approximate degrees of freedom
<code>eps</code>	Accuracy required for <code>df</code>
<code>scale</code>	Scale variables before applying penalty?

**Value**

An object of class `coxph.penalty` containing the data and control functions.

**References**

Gray (1992) "Flexible methods of analysing survival data using splines, with applications to breast cancer prognosis" JASA 87:942–951

**See Also**

[coxph](#), [survreg](#), [pspline](#), [frailty](#)

**Examples**

```
coxph(Surv(futime, fustat) ~ rx + ridge(age, ecog.ps, theta=1),
      ovarian)

lfit0 <- survreg(Surv(time, status) ~1, cancer)
lfit1 <- survreg(Surv(time, status) ~ age + ridge(ph.ecog, theta=5), cancer)
lfit2 <- survreg(Surv(time, status) ~ sex + ridge(age, ph.ecog, theta=1), cancer)
lfit3 <- survreg(Surv(time, status) ~ sex + age + ph.ecog, cancer)
```

---

`stanford2`*More Stanford Heart Transplant data*

---

**Description**

This contains the Stanford Heart Transplant data in a different format. The main data set is in [heart](#).

**Usage**`stanford2`**Format**

<code>id:</code>	ID number
<code>time:</code>	survival or censoring time
<code>status:</code>	censoring status
<code>age:</code>	in years
<code>t5:</code>	T5 mismatch score

**Source**

LA Escobar and WQ Meeker Jr (1992), Assessing influence in regression analysis with censored data. *Biometrics* **48**, 507–528. Page 519.

**See Also**

[predict.survreg](#), [heart](#)

---

`strata`*Identify Stratification Variables*

---

**Description**

This is a special function used in the context of the Cox survival model. It identifies stratification variables when they appear on the right hand side of a formula.

**Usage**

```
strata(..., na.group=FALSE, shortlabel=FALSE, sep=', ')
```

**Arguments**

<code>...</code>	any number of variables. All must be the same length.
<code>na.group</code>	a logical variable, if TRUE, then missing values are treated as a distinct level of each variable.
<code>shortlabel</code>	if TRUE omit variable names from resulting factor labels
<code>sep</code>	the character used to separate groups, in the created label

**Details**

The result is identical to the `interaction` function, but for the labeling of the factors (`strata` is more verbose).

**Value**

a new factor, whose levels are all possible combinations of the factors supplied as arguments.

**See Also**

[coxph](#), [interaction](#)

**Examples**

```
a<-factor(rep(1:3,4))
b<-factor(rep(1:4,3))
levels(strata(a))
levels(strata(a,b,shortlabel=TRUE))

coxph(Surv(futime, fustat) ~ age + strata(rx), data=ovarian)
```

---

summary.aareg

*Summarize an aareg fit*

---

**Description**

Creates the overall test statistics for an Aalen additive regression model

**Usage**

```
## S3 method for class 'aareg':
summary(object, maxtime, test=c("aalen", "nrisk"), scale=1,...)
```

**Arguments**

<code>object</code>	the result of a call to the <code>aareg</code> function
<code>maxtime</code>	truncate the input to the model at time "maxtime"
<code>test</code>	the relative time weights that will be used to compute the test
<code>scale</code>	scales the coefficients. For some data sets, the coefficients of the Aalen model will be very small (10 <sup>-4</sup> ); this simply multiplies the printed values by a constant, say 1e6, to make the printout easier to read.
<code>...</code>	for future methods

**Details**

It is not uncommon for the very right-hand tail of the plot to have large outlying values, particularly for the standard error. The `maxtime` parameter can then be used to truncate the range so as to avoid these. This gives an updated value for the test statistics, without refitting the model.

**Value**

a list is returned with the following components

<code>table</code>	a matrix with rows for the intercept and each covariate, and columns giving a slope estimate, the test statistic, its standard error, the z-score and a p-value
<code>test</code>	the time weighting used for computing the test statistics
<code>test.statistic</code>	the vector of test statistics
<code>test.var</code>	the model based variance matrix for the test statistic
<code>test.var2</code>	optionally, a robust variance matrix for the test statistic
<code>chisq</code>	the overall test (ignoring the intercept term) for significance of any variable
<code>n</code>	a vector containing the number of observations, the number of unique death times used in the computation, and the total number of unique death times

**See Also**

`aareg`, `plot.aareg`

**Examples**

```
afit <- aareg(Surv(time, status) ~ age + sex + ph.ecog, data=lung,
             dfbeta=TRUE)
summary(afit)
## Not run:
      slope   test se(test) robust se      z      p
Intercept 5.05e-03   1.9   1.54   1.55  1.23 0.219000
      age  4.01e-05 108.0  109.00  106.00  1.02 0.307000
      sex -3.16e-03 -19.5   5.90   5.95 -3.28 0.001030
      ph.ecog 3.01e-03  33.2   9.18   9.17  3.62 0.000299

Chisq=22.84 on 3 df, p=4.4e-05; test weights=aalen

## End(Not run)

summary(afit, maxtime=600)
## Not run:
      slope   test se(test) robust se      z      p
Intercept 4.16e-03   2.13   1.48   1.47  1.450 0.146000
      age  2.82e-05  85.80  106.00  100.00  0.857 0.392000
      sex -2.54e-03 -20.60   5.61   5.63 -3.660 0.000256
      ph.ecog 2.47e-03  31.60   8.91   8.67  3.640 0.000271

Chisq=27.08 on 3 df, p=5.7e-06; test weights=aalen

## End(Not run)
```

summary.coxph

*Summary method for Cox models***Description**

Produces a summary of a fitted coxph model

**Usage**

```
## S3 method for class 'coxph':
summary(object, conf.int=0.95, scale=1,...)
```

**Arguments**

object	the result of a coxph fit
conf.int	level for computation of the confidence intervals. If set to FALSE no confidence intervals are printed
scale	vector of scale factors for the coefficients, defaults to 1. The confidence limits are for the risk change associated with one scale unit.
...	for future methods

**Value**

An object of class summary.coxph.

**See Also**

coxph, print.coxph

**Examples**

```
fit <- coxph(Surv(time, status) ~ age + sex, lung)
summary(fit)
## Not run:
Call:
coxph(formula = Surv(time, status) ~ age + sex, data = lung)

n= 228

      coef exp(coef) se(coef)      z      p
age  0.017      1.017  0.00922  1.85 0.0650
sex -0.513      0.599  0.16745 -3.06 0.0022

      exp(coef) exp(-coef) lower .95 upper .95
age      1.017      0.983   0.999   1.036
sex      0.599      1.670   0.431   0.831

Rsquare= 0.06 (max possible= 0.999 )
Likelihood ratio test= 14.1 on 2 df,  p=0.000857
Wald test              = 13.5 on 2 df,  p=0.00119
Score (logrank) test = 13.7 on 2 df,  p=0.00105

## End(Not run)
```

---

summary.survfit      *Summary of a Survival Curve*

---

### Description

Returns a list containing the survival curve, confidence limits for the curve, and other information.

### Usage

```
## S3 method for class 'survfit':
summary(object, times=, censored=FALSE, scale=1,
        extend=FALSE, rmean=getOption('survfit.rmean'), ...)
```

### Arguments

object	the result of a call to the <code>survfit</code> function.
times	vector of times; the returned matrix will contain 1 row for each time. This must be in increasing order and missing values are not allowed. If <code>censored=T</code> , the default <code>times</code> vector contains all the unique times in <code>fit</code> , otherwise the default <code>times</code> vector uses only the event (death) times.
censored	logical value: should the censoring times be included in the output? This is ignored if the <code>times</code> argument is present.
scale	numeric value to rescale the survival time, e.g., if the input data to <code>survfit</code> were in days, <code>scale = 365.25</code> would scale the output to years.
extend	logical value: if TRUE, prints information for all specified <code>times</code> , even if there are no subjects left at the end of the specified <code>times</code> . This is only valid if the <code>times</code> argument is present.
rmean	Show restricted mean: see <a href="#">print.summary.survfit</a> for details
...	for future methods

### Value

a list with the following components:

surv	the estimate of survival at time $t+0$ .
time	the timepoints on the curve.
n.risk	the number of subjects at risk at time $t-0$ (but see the comments on weights in the <code>survfit</code> help file).
n.event	if the <code>times</code> argument is missing, then this column is the number of events that occurred at time $t$ . Otherwise, it is the cumulative number of events that have occurred since the last time listed until time $t+0$ .
n.entered	This is present only for counting process survival data. If the <code>times</code> argument is missing, this column is the number of subjects that entered at time $t$ . Otherwise, it is the cumulative number of subjects that have entered since the last time listed until time $t$ .



<code>n.exit.censored</code>	if the <code>times</code> argument is missing, this column is the number of subjects that left without an event at time <code>t</code> . Otherwise, it is the cumulative number of subjects that have left without an event since the last time listed until time <code>t+0</code> . This is only present for counting process survival data.
<code>std.err</code>	the standard error of the survival value.
<code>conf.int</code>	level of confidence for the confidence intervals of survival.
<code>lower</code>	lower confidence limits for the curve.
<code>upper</code>	upper confidence limits for the curve.
<code>strata</code>	indicates stratification of curve estimation. If <code>strata</code> is not <code>NULL</code> , there are multiple curves in the result and the <code>surv</code> , <code>time</code> , <code>n.risk</code> , etc. vectors will contain multiple curves, pasted end to end. The levels of <code>strata</code> (a factor) are the labels for the curves.
<code>call</code>	the statement used to create the <code>fit</code> object.
<code>na.action</code>	same as for <code>fit</code> , if present.
<code>table</code>	table of information that is returned from <code>print.survfit</code> function.
<code>type</code>	type of data censoring. Passed through from the <code>fit</code> object.

**See Also**

[survfit](#), [print.summary.survfit](#)

**Examples**

```
summary(survfit(Surv(futime, fustat)~1, data=ovarian))
summary(survfit(Surv(futime, fustat)~rx, data=ovarian))
```

Surv

*Create a Survival Object***Description**

Create a survival object, usually used as a response variable in a model formula. Argument matching is special for this function, see Details below.

**Usage**

```
Surv(time, time2, event,
      type=c('right', 'left', 'interval', 'counting', 'interval2'),
      origin=0)
is.Surv(x)
```

**Arguments**

`time` for right censored data, this is the follow up time. For interval data, the first argument is the starting time for the interval.

event	The status indicator, normally 0=alive, 1=dead. Other choices are TRUE/FALSE (TRUE = death) or 1/2 (2=death). For interval censored data, the status indicator is 0=right censored, 1=event at time, 2=left censored, 3=interval censored. Although unusual, the event indicator can be omitted, in which case all subjects are assumed to have an event.
time2	ending time of the interval for interval censored or counting process data only. Intervals are assumed to be open on the left and closed on the right, (start, end]. For counting process data, event indicates whether an event occurred at the end of the interval.
type	character string specifying the type of censoring. Possible values are "right", "left", "counting", "interval", or "interval2". The default is "right" or "counting" depending on whether the time2 argument is absent or present, respectively.
origin	for counting process data, the hazard function origin. This option was intended to be used in conjunction with a model containing time dependent strata in order to align the subjects properly when they cross over from one strata to another, but it has rarely proven useful.
x	any R object.

## Details

Typical usages are

```
Surv(time, event)
Surv(time, time2, event, type= )
```

The time,time2 and event arguments are matched by position, not by name, so use, eg, Surv(time, dead) rather than Surv(time, event=dead)

In theory it is possible to represent interval censored data without a third column containing the explicit status. Exact, right censored, left censored and interval censored observation would be represented as intervals of [a,a], (a, infinity), (-infinity,b), and [a,b] respectively; each interval is a pair of time points within which the event is known to have occurred.

If type="interval2" then the representation given above is assumed, with NA taking the place of infinity. If type="interval" then event must be given. If event is 0, 1, or 2, the relevant information is assumed to be contained in time, the value in time2 is ignored, and the second column of the internal representation contains a placeholder value.

Presently, the only methods allowing interval censored data are the parametric models computed by survreg and survival curves computed by survfit; for both of these, the distinction between open and closed intervals is unimportant. The distinction is important for counting process data and the Cox model.

The function tries to distinguish between the use of 0/1 and 1/2 coding for left and right censored data using if (max(status)==2). If 1/2 coding is used and all the subjects are censored, it will guess wrong. In any questionable case it is safer to use logical coding, e.g., Surv(time, status==3) would indicate that a 3 is the code for an event.

Surv objects can be subscripted either as an object, e.g. x[1:3] using a single subscript; in which case the drop argument is ignored; or as a matrix, using two arguments. If the second subscript is missing and drop=F (the default), the result of the subscripting will be a Surv object, e.g., x[1:3, , drop=F], otherwise the result will be a matrix (or vector), in accordance with the default behavior for subscripting matrices.

**Value**

An object of class `Surv`. There are methods for `print`, `is.na`, and subscripting survival objects. `Surv` objects are implemented as a matrix of 2 or 3 columns.

In the case of `is.Surv`, a logical value `TRUE` if `x` inherits from class `"Surv"`, otherwise an `FALSE`.

**See Also**

`coxph`, `survfit`, `survreg`.

**Examples**

```
with(lung, Surv(time, status))
Surv(heart$start, heart$stop, heart$event)
```

---

`survConcordance`      *Compute a concordance measure.*

---

**Description**

This function computes the concordance between a right-censored survival time and a single continuous covariate

**Usage**

```
survConcordance(formula, data, weights, subset, na.action)
```

**Arguments**

`formula`            a formula with a survival time on the left and a single covariate on the right.  
`data`                a data frame  
`weights, subset, na.action`  
                      as for `coxph`

**Details**

Concordance is defined as  $\Pr(\text{agreement})$  for any two randomly chosen observations, where in this case agreement means that the observation with the shorter survival time of the two also has the larger risk score. The predictor (or risk score) will often be the result of a Cox model or other regression.

For continuous covariates concordance is equivalent to Kendall's tau, and for logistic regression is equivalent to the area under the ROC curve. A value of 1 signifies perfect agreement, .6-.7 a common result for survival data, .5 an agreement that is no better than chance, and .3-.4 the performance of some stock market analysts.

The computation involves all  $n(n-1)/2$  pairs of data points in the sample. For survival data, however, some of the pairs are incomparable. For instance a pair of times (5+, 8), the first being a censored value. We do not know whether the first survival time is greater than or less than the second. Among observations that are comparable, pairs may also be tied on survival time (but only if both are uncensored) or on the predictor. The final concordance is  $(\text{agree} + \text{tied}/2)/(\text{agree} + \text{disagree} + \text{tied})$ .

There is, unfortunately, one aspect of the formula above that is unclear. Should the count of ties include observations that are tied on survival time  $y$ , tied on the predictor  $x$ , or both? In 2 by 2 tables, Kendall's tau-b is equal to  $(\text{agree} - \text{disagree})/n$ , where  $n$  is the geometric mean of  $(\text{agree} + \text{disagree} + \text{tied.x})$  and  $(\text{agree} + \text{disagree} + \text{tied.y})$ . The Goodman-Kruskal Gamma statistic is  $(\text{agree} - \text{disagree})/(\text{agree} + \text{disagree})$ , ignoring ties. It ranges from -1 to +1 similar to a correlation coefficient.

In this program we count those observations which were tied on  $x$ , but not tied on  $y$  (survival time), as 'ties'. All of the components are returned in the result, however, so people can compute other combinations if interested. (If two observations have the same survival and the same  $x$ , they are counted in the tied.time category).

### Value

an object containing the concordance, followed by the number of pairs that agree, disagree, are tied, and are not comparable.

### See Also

summary.coxph

### Examples

```
survConcordance(Surv(time, status) ~age, data=lung)
## Not run:
  n= 228
Concordance= 0.5501899 , Gamma= 0.1034234
  agree disagree tied.x tied.time incomparable
  10717      8708      589         28         5836

## End(Not run)

options(na.action=na.exclude)
fit <- coxph(Surv(time, status) ~ ph.ecog + age + sex, lung)
survConcordance(Surv(time, status) ~predict(fit), lung)
## Not run:
  n=227 (1 observations deleted due to missing values)
Concordance= 0.6371102 , Gamma= 0.2759638
  agree disagree tied.x tied.time incomparable
  12544      7118      125         28         5836

## End(Not run)
```

---

survdiff

*Test Survival Curve Differences*

---

### Description

Tests if there is a difference between two or more survival curves using the  $G^p$  family of tests, or for a single curve against a known alternative.

### Usage

```
survdiff(formula, data, subset, na.action, rho=0)
```

**Arguments**

<code>formula</code>	a formula expression as for other survival models, of the form <code>Surv(time, status) ~ predictors</code> . For a one-sample test, the predictors must consist of a single <code>offset(sp)</code> term, where <code>sp</code> is a vector giving the survival probability of each subject. For a k-sample test, each unique combination of predictors defines a subgroup. A <code>strata</code> term may be used to produce a stratified test. To cause missing values in the predictors to be treated as a separate group, rather than being omitted, use the <code>strata</code> function with its <code>na.group=T</code> argument.
<code>data</code>	an optional data frame in which to interpret the variables occurring in the formula.
<code>subset</code>	expression indicating which subset of the rows of data should be used in the fit. This can be a logical vector (which is replicated to have length equal to the number of observations), a numeric vector indicating which observation numbers are to be included (or excluded if negative), or a character vector of row names to be included. All observations are included by default.
<code>na.action</code>	a missing-data filter function. This is applied to the <code>model.frame</code> after any subset argument has been used. Default is <code>options()\$na.action</code> .
<code>rho</code>	a scalar parameter that controls the type of test.

**Value**

a list with components:

<code>n</code>	the number of subjects in each group.
<code>obs</code>	the weighted observed number of events in each group. If there are strata, this will be a matrix with one column per stratum.
<code>exp</code>	the weighted expected number of events in each group. If there are strata, this will be a matrix with one column per stratum.
<code>chisq</code>	the chisquare statistic for a test of equality.
<code>var</code>	the variance matrix of the test.
<code>strata</code>	optionally, the number of subjects contained in each stratum.

**METHOD**

This function implements the G-rho family of Harrington and Fleming (1982), with weights on each death of  $S(t)^\rho$ , where  $S(t)$  is the Kaplan-Meier estimate of survival. With `rho = 0` this is the log-rank or Mantel-Haenszel test, and with `rho = 1` it is equivalent to the Peto & Peto modification of the Gehan-Wilcoxon test.

If the right hand side of the formula consists only of an offset term, then a one sample test is done. To cause missing values in the predictors to be treated as a separate group, rather than being omitted, use the `factor` function with its `exclude` argument.

**References**

Harrington, D. P. and Fleming, T. R. (1982). A class of rank test procedures for censored survival data. *Biometrika* **69**, 553-566.

**Examples**

```
## Two-sample test
survdif(Surv(futime, fustat) ~ rx, data=ovarian)

## Stratified 7-sample test

survdif(Surv(time, status) ~ pat.karno + strata(inst), data=lung)

## Expected survival for heart transplant patients based on
## US mortality tables
expect <- survexp(futime ~ ratetable(age=(accept.dt - birth.dt),
  sex=1, year=accept.dt, race="white"), jasa, cohort=FALSE,
  ratetable=survexp.usr)
## actual survival is much worse (no surprise)
survdif(Surv(jasa$futime, jasa$fustat) ~ offset(expect))
```

survexp

*Compute Expected Survival***Description**

Returns either the expected survival of a cohort of subjects, or the individual expected survival for each subject.

**Usage**

```
survexp(formula, data, weights, subset, na.action, times, cohort=TRUE,
  conditional=FALSE, ratetable=survexp.us, scale=1, npoints,
  se.fit, model=FALSE, x=FALSE, y=FALSE)
```

**Arguments**

formula	formula object. The response variable is a vector of follow-up times and is optional. The predictors consist of optional grouping variables separated by the + operator (as in <code>survfit</code> ), along with a <code>ratetable</code> term. The <code>ratetable</code> term matches each subject to his/her expected cohort.
data	data frame in which to interpret the variables named in the <code>formula</code> , <code>subset</code> and <code>weights</code> arguments.
weights	case weights.
subset	expression indicating a subset of the rows of <code>data</code> to be used in the fit.
na.action	function to filter missing data. This is applied to the model frame after <code>subset</code> has been applied. Default is <code>options()\$na.action</code> . A possible value for <code>na.action</code> is <code>na.omit</code> , which deletes observations that contain one or more missing values.
times	vector of follow-up times at which the resulting survival curve is evaluated. If absent, the result will be reported for each unique value of the vector of follow-up times supplied in <code>formula</code> .
cohort	logical value: if <code>FALSE</code> , each subject is treated as a subgroup of size 1. The default is <code>TRUE</code> .

<code>conditional</code>	logical value: if TRUE, the follow-up times supplied in <code>formula</code> are death times and conditional expected survival is computed. If FALSE, the follow-up times are potential censoring times. If follow-up times are missing in <code>formula</code> , this argument is ignored.
<code>ratetable</code>	a table of event rates, such as <code>survexp.uswhite</code> , or a fitted Cox model.
<code>scale</code>	numeric value to scale the results. If <code>ratetable</code> is in units/day, <code>scale = 365.25</code> causes the output to be reported in years.
<code>npoints</code>	number of points at which to calculate intermediate results, evenly spaced over the range of the follow-up times. The usual (exact) calculation is done at each unique follow-up time. For very large data sets specifying <code>npoints</code> can reduce the amount of memory and computation required. For a prediction from a Cox model <code>npoints</code> is ignored.
<code>se.fit</code>	compute the standard error of the predicted survival. The default is to compute standard errors whenever possible, which at this time is only for the Ederer method and a Cox model as the rate table.
<code>model, x, y</code>	flags to control what is returned. If any of these is true, then the model frame, the model matrix, and/or the vector of response times will be returned as components of the final result, with the same names as the flag arguments.

## Details

Individual expected survival is usually used in models or testing, to ‘correct’ for the age and sex composition of a group of subjects. For instance, assume that birth date, entry date into the study, sex and actual survival time are all known for a group of subjects. The `survexp.uswhite` population tables contain expected death rates based on calendar year, sex and age. Then

```
haz <- -log(survexp(death.time ~ ratetable(sex=sex, year=entry.dt,
                                         age=(birth.dt-entry.dt)), cohort=FALSE))
```

gives for each subject the total hazard experienced up to their observed death time or censoring time. This probability can be used as a rescaled time value in models:

```
glm(status ~ 1 + offset(log(haz)), family=poisson)
glm(status ~ x + offset(log(haz)), family=poisson)
```

In the first model, a test for `intercept=0` is the one sample log-rank test of whether the observed group of subjects has equivalent survival to the baseline population. The second model tests for an effect of variable `x` after adjustment for age and sex.

Cohort survival is used to produce an overall survival curve. This is then added to the Kaplan-Meier plot of the study group for visual comparison between these subjects and the population at large. There are three common methods of computing cohort survival. In the "exact method" of Ederer the cohort is not censored; this corresponds to having no response variable in the formula. Hakulinen recommends censoring the cohort at the anticipated censoring time of each patient, and Verheul recommends censoring the cohort at the actual observation time of each patient. The last of these is the conditional method. These are obtained by using the respective time values as the follow-up time or response in the formula.

## Value

if `cohort=TRUE` an object of class `survexp`, otherwise a vector of per-subject expected survival values. The former contains the number of subjects at risk and the expected survival for the cohort at each requested time.

## References

- Berry, G. (1983). The analysis of mortality by the subject-years method. *Biometrics*, 39:173-84.
- Ederer, F., Axtell, L. and Cutler, S. (1961). The relative survival rate: a statistical methodology. *Natl Cancer Inst Monogr*, 6:101-21.
- Hakulinen, T. (1982). Cancer survival corrected for heterogeneity in patient withdrawal. *Biometrics*, 38:933-942.
- Verheul, H., Dekker, E., Bossuyt, P., Moulijn, A. and Dunning, A. (1993). Background mortality in clinical survival studies. *Lancet*, 341: 872-875.

## See Also

[survfit](#), [pyears](#), [survexp.us](#), [survexp.fit](#).

## Examples

```
#
# Stanford heart transplant data
# Estimate of conditional survival
survexp(futime ~ ratetable(sex="male", year=accept.dt,
                          age=(accept.dt-birth.dt)), conditional=TRUE, data=jasa)
# Estimate of conditional survival stratified by prior surgery
survexp(futime ~ surgery + ratetable(sex="male", year=accept.dt,
                                     age=(accept.dt-birth.dt)), conditional=TRUE, data=jasa)

## Compare the survival curves for the Mayo PBC data to Cox model fit
##
pfit <-coxph(Surv(time,status>0) ~ trt + log(bili) + log(protime) + age +
            platelet, data=pbcc)
plot(survfit(Surv(time, status>0) ~ trt, data=pbcc))
lines(survexp(~ trt, ratetable=pfit, data=pbcc), col='purple')
```

---

survexp.fit

*Compute Expected Survival*

---

## Description

Compute expected survival times.

## Usage

```
survexp.fit(x, y, times, death, ratetable)
```

## Arguments

- |           |   |
|-----------|---|
| x         | a matrix. The first column contains the group, an integer value that divides the subjects into subsets. Remaining columns must match the dimensions of the ratetable, in the correct order. |
| y         | the follow up time for each subject.  |
| times     | the vector of times at which a result will be computed.   |
| death     | a logical value, if TRUE the conditional survival is computed, if FALSE the cohort survival is computed. See <a href="#">survexp</a> for more details.                                      |
| ratetable | a rate table, such as <a href="#">survexp.uswhite</a> .   |



**Details**

For conditional survival  $y$  must be the time of last follow-up or death for each subject. For cohort survival it must be the potential censoring time for each subject, ignoring death.

For an exact estimate `times` should be a superset of  $y$ , so that each subject at risk is at risk for the entire sub-interval of time. For a large data set, however, this can use an inordinate amount of storage and/or compute time. If the `times` spacing is more coarse than this, an actuarial approximation is used which should, however, be extremely accurate as long as all of the returned values are  $> .99$ .

For a subgroup of size 1 and `times`  $> y$ , the conditional method reduces to  $\exp(-h)$  where  $h$  is the expected cumulative hazard for the subject over his/her observation time. This is used to compute individual expected survival.

**Value**

A list containing the number of subjects and the expected survival(s) at each time point. If there are multiple groups, these will be matrices with one column per group.

**Warning**

Most users will call the higher level routine `survexp`. Consequently, this function has very few error checks on its input arguments.

**See Also**

[survexp](#), [survexp.us](#).

---

survfit

*Create survival curves*

---

**Description**

This function creates survival curves from either a formula (e.g. the Kaplan-Meier), a previously fitted Cox model, or a previously fitted accelerated failure time model.

**Usage**

```
survfit(formula, ...)
```

**Arguments**

<code>formula</code>	either a formula or a previously fitted model
<code>...</code>	other arguments to the specific method

**Details**

For details see the documentation for the appropriate method, i.e., `?survfit.formula` or `?survfit.coxph`.

**Value**

An object of class `survfit` containing one or more survival curves.

**Note**

Older releases of the code also allowed the specification for a single curve to omit the right hand of the formula, i.e.,  $\sim 1$ . Handling this case required some non-standard and fairly fragile manipulations, and this case is no longer supported.

**Author(s)**

Terry Therneau

**See Also**

`survfit.formula`, `survfit.coxph`, `survfit.object`, `print.survfit`,  
`plot.survfit`, `summary.survfit`

---

`survfit.coxph`

*Compute a Survival Curve from a Cox model*

---

**Description**

Computes the predicted survivor function for a Cox proportional hazards model.

**Usage**

```
## S3 method for class 'coxph':
survfit(formula, newdata,
        se.fit=TRUE, conf.int=.95,
        individual=FALSE,
        type, vartype,
        conf.type=c("log", "log-log", "plain", "none"), ...)
```

**Arguments**

<code>formula</code>	A <code>coxph</code> object.
<code>newdata</code>	a data frame with the same variable names as those that appear in the <code>coxph</code> formula. The curve(s) produced will be representative of a cohort whose covariates correspond to the values in <code>newdata</code> . Default is the mean of the covariates used in the <code>coxph</code> fit.
<code>individual</code>	a logical value indicating whether each row of <code>newdata</code> represents a distinct individual (FALSE, the default), or if each row of the data frame represents different time epochs for only one individual (TRUE). In the former case the result will have one curve for each row in <code>newdata</code> , in the latter only a single curve will be produced.
<code>conf.int</code>	the level for a two-sided confidence interval on the survival curve(s). Default is 0.95.
<code>se.fit</code>	a logical value indicating whether standard errors should be computed. Default is TRUE.

<code>type, vartype</code>	a character string specifying the type of survival curve. Possible values are "aalen" or "kaplan-meier" (only the first two characters are necessary). The default is "aalen". Earlier versions of <code>survfit</code> used <code>type="tsiatis"</code> to get the "aalen" estimator. For backward compatibility, this is still allowed.
<code>conf.type</code>	One of "none", "plain", "log" (the default), or "log-log". Only enough of the string to uniquely identify it is necessary. The first option causes confidence intervals not to be generated. The second causes the standard intervals $\text{curve} \pm k * \text{se}(\text{curve})$ , where $k$ is determined from <code>conf.int</code> . The log option calculates intervals based on the cumulative hazard or $\log(\text{survival})$ . The last option bases intervals on the log hazard or $\log(-\log(\text{survival}))$ .
<code>...</code>	for future methods

### Details

See [survfit](#) for more Details.

The estimates used are the Kalbfleisch-Prentice (Kalbfleisch and Prentice, 1980, p.86) and the Tsiatis/Link/Breslow, which reduce to the Kaplan-Meier and Fleming-Harrington estimates, respectively, when the weights are unity. When the parent data is a Cox model, there is an extra term in the variance of the curve, due to the variance of the coefficients and hence variance in the computed weights. Details of the Aalen estimator and its variance are found in Tsiatis (1981).

The two variants of the F-H estimate have to do with how ties are handled. If there were 3 deaths out of 10 at risk, then the first increments the hazard by  $3/10$  and the second by  $1/10 + 1/9 + 1/8$ . For the first method  $S(t) = \exp(H)$ , where  $H$  is the Nelson-Aalen cumulative hazard estimate, whereas the `fh2` method will give results  $S(t)$  results closer to the Kaplan-Meier. For curves created after a Cox model these correspond to the Breslow and Efron estimates, respectively, and the proper choice is made automatically.

### Value

an object of class "survfit". See `survfit.object` for details. Methods defined for `survfit` objects are `print`, `plot`, `lines`, and `points`.

### References

- Dorey, F. J. and Korn, E. L. (1987). Effective sample sizes for confidence intervals for survival probabilities. *Statistics in Medicine* **6**, 679-87.
- Fleming, T. H. and Harrington, D. P. (1984). Nonparametric estimation of the survival distribution in censored data. *Comm. in Statistics* **13**, 2469-86.
- Kalbfleisch, J. D. and Prentice, R. L. (1980). *The Statistical Analysis of Failure Time Data*. New York: Wiley.
- Link, C. L. (1984). Confidence intervals for the survival function using Cox's proportional hazards model with covariates. *Biometrics* **40**, 601-610.
- Tsiatis, A. (1981). A large sample study of the estimate for the integrated hazard function in Cox's regression model for survival data. *Annals of Statistics* **9**, 93-108.

### See Also

[print](#), [plot](#), [lines](#), [coxph](#), [Surv](#), [strata](#).

**Examples**

```

#fit a Kaplan-Meier and plot it
fit <- survfit(Surv(time, status) ~ x, data = aml)
plot(fit, lty = 2:3)
legend(100, .8, c("Maintained", "Nonmaintained"), lty = 2:3)

#fit a Cox proportional hazards model and plot the
#predicted survival for a 60 year old
fit <- coxph(Surv(futime, fustat) ~ age, data = ovarian)
plot(survfit(fit, newdata=data.frame(age=60)),
     xscale=365.25, xlab = "Years", ylab="Survival")

# Here is the data set from Turnbull
# There are no interval censored subjects, only left-censored (status=3),
# right-censored (status 0) and observed events (status 1)
#
#
#           Time
#           1   2   3   4
# Type of observation
#     death      12   6   2   3
#     losses      3   2   0   3
#     late entry  2   4   2   5
#
tdata <- data.frame(time =c(1,1,1,2,2,2,3,3,3,4,4,4),
                    status=rep(c(1,0,2),4),
                    n      =c(12,3,2,6,2,4,2,0,2,3,3,5))
fit <- survfit(Surv(time, time, status, type='interval') ~1,
               data=tdata, weight=n)

#
# Time to progression/death for patients with monoclonal gammopathy
# Competing risk curves (cumulative incidence)
fit1 <- survfit(Surv(stop, event=='progression') ~1, data=mgus1,
               subset=(start==0))
fit2 <- survfit(Surv(stop, status) ~1, data=mgus1,
               subset=(start==0), etype=event) #competing risks
# CI curves are always plotted from 0 upwards, rather than 1 down
plot(fit2, fun='event', xscale=365.25, xmax=7300, mark.time=FALSE,
     col=2:3, xlab="Years post diagnosis of MGUS")
lines(fit1, fun='event', xscale=365.25, xmax=7300, mark.time=FALSE,
      conf.int=FALSE)
text(10, .4, "Competing Risk: death", col=3)
text(16, .15, "Competing Risk: progression", col=2)
text(15, .30, "KM:prog")

```

survfit.formula

*Compute a Survival Curve for Censored Data***Description**

Computes an estimate of a survival curve for censored data using either the Kaplan-Meier or the Fleming-Harrington method. For competing risks data it computes the cumulative incidence curve.

**Usage**

```
## S3 method for class 'formula':
survfit(formula, data, weights, subset, na.action,
        etype, id, ...)
```

**Arguments**

- |           |  |
|-----------|--|
| formula   | a formula object, which must have a <code>Surv</code> object as the response on the left of the <code>~</code> operator and, if desired, terms separated by <code>+</code> operators on the right. One of the terms may be a <code>strata</code> object. For a single survival curve the right hand side should be <code>~ 1</code> .  |
| data      | a data frame in which to interpret the variables named in the formula, <code>subset</code> and <code>weights</code> arguments.   |
| weights   | The weights must be nonnegative and it is strongly recommended that they be strictly positive, since zero weights are ambiguous, compared to use of the <code>subset</code> argument.  |
| subset    | expression saying that only a subset of the rows of the data should be used in the fit.  |
| na.action | a missing-data filter function, applied to the model frame, after any <code>subset</code> argument has been used. Default is <code>options()\$na.action</code> .   |
| etype     | a variable giving the type of event. Presence of this variable signals the program to compute the cumulative incidence estimate. For each event <code>status==1</code> , the <code>etype</code> variable indicates the type of event. For a censored observation the value of <code>etype</code> is ignored - but do not set it to <code>NA</code> , since that will cause <code>na.action</code> to delete the observation.   |
| id        | identifies individual subjects, when a given person can have multiple lines of data. when used with the <code>etype</code> variable, this allows the computation of a cumulative prevalence estimate, i.e., the incidence over time.   |
| ...       | The following additional arguments are passed to internal functions called by <code>survfit</code> .<br><b>type</b> a character string specifying the type of survival curve. Possible values are "kaplan-meier", "fleming-harrington" or "fh2" if a formula is given. This is ignored for competing risks or when the Turnbull estimator is used.<br><b>error</b> a character string specifying the error. Possible values are "greenwood" for the Greenwood formula or "tsiatis" for the Tsiatis formula, (only the first character is necessary).<br><b>conf.type</b> One of "none", "plain", "log" (the default), or "log-log". Only enough of the string to uniquely identify it is necessary. The first option causes confidence intervals not to be generated. The second causes the standard intervals $curve \pm k * se(curve)$ , where <code>k</code> is determined from <code>conf.int</code> . The <code>log</code> option calculates intervals based on the cumulative hazard or $\log(\text{survival})$ . The last option bases intervals on the log hazard or $\log(-\log(\text{survival}))$ .<br><b>conf.lower</b> a character string to specify modified lower limits to the curve, the upper limit remains unchanged. Possible values are "usual" (unmodified), "peto", and "modified". The modified lower limit is based on an "effective n" argument. The confidence bands will agree with the usual calculation at each death time, but unlike the usual bands the confidence |

interval becomes wider at each censored observation. The extra width is obtained by multiplying the usual variance by a factor  $m/n$ , where  $n$  is the number currently at risk and  $m$  is the number at risk at the last death time. (The bands thus agree with the un-modified bands at each death time.) This is especially useful for survival curves with a long flat tail.

The Peto lower limit is based on the same "effective  $n$ " argument as the modified limit, but also replaces the usual Greenwood variance term with a simple approximation. It is known to be conservative.

**start.time** numeric value specifying a time to start calculating survival information. The resulting curve is the survival conditional on surviving to `start.time`.

**conf.int** the level for a two-sided confidence interval on the survival curve(s). Default is 0.95.

**se.fit** a logical value indicating whether standard errors should be computed. Default is TRUE.

## Details

The estimates used are the Kalbfleisch-Prentice (Kalbfleisch and Prentice, 1980, p.86) and the Tsiatis/Link/Breslow, which reduce to the Kaplan-Meier and Fleming-Harrington estimates, respectively, when the weights are unity.

The Greenwood formula for the variance is a sum of terms  $d/(n*(n-m))$ , where  $d$  is the number of deaths at a given time point,  $n$  is the sum of weights for all individuals still at risk at that time, and  $m$  is the sum of weights for the deaths at that time. The justification is based on a binomial argument when weights are all equal to one; extension to the weighted case is ad hoc. Tsiatis (1981) proposes a sum of terms  $d/(n*n)$ , based on a counting process argument which includes the weighted case.

The two variants of the F-H estimate have to do with how ties are handled. If there were 3 deaths out of 10 at risk, then the first increments the hazard by  $3/10$  and the second by  $1/10 + 1/9 + 1/8$ . For the first method  $S(t) = \exp(H)$ , where  $H$  is the Nelson-Aalen cumulative hazard estimate, whereas the `fn2` method will give results  $S(t)$  results closer to the Kaplan-Meier.

When the data set includes left censored or interval censored data (or both), then the EM approach of Turnbull is used to compute the overall curve. When the baseline method is the Kaplan-Meier, this is known to converge to the maximum likelihood estimate.

The cumulative incidence curve is an alternative to the Kaplan-Meier for competing risks data. For instance, in patients with MGUS, conversion to an overt plasma cell malignancy occurs at a nearly constant rate among those still alive. A Kaplan-Meier estimate, treating death due to other causes as censored, gives a 20 year cumulative rate of 33% for the 241 early patients of Kyle. This estimates the incidence of conversion, if other causes of death were removed.

The CI estimate, on the other hand, estimates the total number of conversions that will actually occur. Because the population is older, this is much smaller than the KM, 22% at 20 years for Kyle's data. If there were no censoring, then  $CI(t)$  could very simply be computed as total number of patients with progression by time  $t$  divided by the sample size  $n$ .

## Value

an object of class "survfit". See `survfit.object` for details. Methods defined for `survfit` objects are `print`, `plot`, `lines`, and `points`.

## References

Dorey, F. J. and Korn, E. L. (1987). Effective sample sizes for confidence intervals for survival probabilities. *Statistics in Medicine* **6**, 679-87.

Fleming, T. H. and Harrington, D. P. (1984). Nonparametric estimation of the survival distribution in censored data. *Comm. in Statistics* **13**, 2469-86.

Kablfeisch, J. D. and Prentice, R. L. (1980). *The Statistical Analysis of Failure Time Data*. New York:Wiley.

Kyle, R. A. (1997). Monoclonal gammopathy of undetermined significance and solitary plasmacytoma. Implications for progression to overt multiple myeloma}, *Hematology/Oncology Clinics N. Amer.* **11**, 71-87.

Link, C. L. (1984). Confidence intervals for the survival function using Cox's proportional hazards model with covariates. *Biometrics* **40**, 601-610.

Turnbull, B. W. (1974). Nonparametric estimation of a survivorship function with doubly censored data. *J Am Stat Assoc*, **69**, 169-173.

### See Also

[survfit.coxph](#) for survival curves from Cox models.

[print](#), [plot](#), [lines](#), [coxph](#), [Surv](#), [strata](#).

### Examples

```
#fit a Kaplan-Meier and plot it
fit <- survfit(Surv(time, status) ~ x, data = aml)
plot(fit, lty = 2:3)
legend(100, .8, c("Maintained", "Nonmaintained"), lty = 2:3)

#fit a Cox proportional hazards model and plot the
#predicted survival for a 60 year old
fit <- coxph(Surv(futime, fustat) ~ age, data = ovarian)
plot(survfit(fit, newdata=data.frame(age=60)),
      xscale=365.25, xlab = "Years", ylab="Survival")

# Here is the data set from Turnbull
# There are no interval censored subjects, only left-censored (status=3),
# right-censored (status 0) and observed events (status 1)
#
#
#           Time
#           1   2   3   4
# Type of observation
#       death    12   6   2   3
#       losses    3   2   0   3
#       late entry 2   4   2   5
#
tdata <- data.frame(time =c(1,1,1,2,2,2,3,3,3,4,4,4),
                    status=rep(c(1,0,2),4),
                    n      =c(12,3,2,6,2,4,2,0,2,3,3,5))
fit <- survfit(Surv(time, time, status, type='interval') ~1,
              data=tdata, weight=n)

#
# Time to progression/death for patients with monoclonal gammopathy
# Competing risk curves (cumulative incidence)
fit1 <- survfit(Surv(stop, event=='progression') ~1, data=mgus1,
               subset=(start==0))
fit2 <- survfit(Surv(stop, status) ~1, data=mgus1,
               subset=(start==0), etype=event) #competing risks
```

```
# CI curves are always plotted from 0 upwards, rather than 1 down
plot(fit2, fun='event', xscale=365.25, xmax=7300, mark.time=FALSE,
     col=2:3, xlab="Years post diagnosis of MGUS")
lines(fit1, fun='event', xscale=365.25, xmax=7300, mark.time=FALSE,
      conf.int=FALSE)
text(10, .4, "Competing Risk: death", col=3)
text(16, .15, "Competing Risk: progression", col=2)
text(15, .30, "KM:prog")
```

---

survfit.object      *Survival Curve Object*

---

## Description

This class of objects is returned by the `survfit` class of functions to represent a fitted survival curve.

Objects of this class have methods for the functions `print`, `summary`, `plot`, `points` and `lines`. The `print.survfit` method does more computation than is typical for a print method and is documented on a separate page. Class of objects that represent a fitted survival curve.

## Arguments

<code>n</code>	total number of subjects in each curve.
<code>time</code>	the time points at which the curve has a step.
<code>n.risk</code>	the number of subjects at risk at <code>t</code> .
<code>n.event</code>	the number of events that occur at time <code>t</code> .
<code>n.enter</code>	for counting process data only, the number of subjects that enter at time <code>t</code> .
<code>n.censor</code>	for counting process data only, the number of subjects who exit the risk set, without an event, at time <code>t</code> . (For right censored data, this number can be computed from the successive values of the number at risk).
<code>surv</code>	the estimate of survival at time <code>t+0</code> . This may be a vector or a matrix.
<code>std.err</code>	the standard error of the cumulative hazard or $-\log(\text{survival})$ .
<code>upper</code>	upper confidence limit for the survival curve.
<code>lower</code>	lower confidence limit for the survival curve.
<code>strata</code>	if there are multiple curves, this component gives the number of elements of the <code>time</code> etc. vectors corresponding to the first curve, the second curve, and so on. The names of the elements are labels for the curves.
<code>start.time</code>	the value specified for the <code>start.time</code> argument, if it was used in the call.
<code>n.all</code>	for counting process data, and any time that the <code>start.time</code> argument was used, this contains the total number of observations that were available. Not all may have been used in creating the curve, in which case this value will be larger than <code>n</code> above. of observations that were available
<code>conf.type</code>	the approximation used to compute the confidence limits.
<code>conf.int</code>	the level of the confidence limits, e.g. 90 or 95%.
<code>na.action</code>	the returned value from the <code>na.action</code> function, if any. It will be used in the printout of the curve, e.g., the number of observations deleted due to missing values.
<code>call</code>	an image of the call that produced the object.
<code>type</code>	type of survival censoring.



**Structure**

The following components must be included in a legitimate `survfit` object.

**Subscripts**

Survfit objects that contain multiple survival curves can be subscripted. This is most often used to plot a subset of the curves. Usually a single subscript will be used. In one particular case – survival curves for multiple covariate values, from a Cox model that includes a `strata` statement – there is a matrix of curves and 2 subscripts may be used. (In this case `summary.survfit` will also print the data as a matrix).

**See Also**

[plot.survfit](#), [summary.survfit](#), [print.survfit](#), [survfit](#).

---

survobrien

*O'Brien's Test for Association of a Single Variable with Survival*

---

**Description**

Peter O'Brien's test for association of a single variable with survival This test is proposed in Biometrics, June 1978.

**Usage**

```
survobrien(formula, data)
```

**Arguments**

<code>formula</code>	a valid formula for a cox model, without time dependent covariates.
<code>data</code>	a data frame.

**Value**

a new data frame. The original time and status variables are removed, and have been replaced with `start`, `stop`, and `event`. If a predictor variable is a factor or is protected with `I()`, it is retained as is. Other predictor variables have been replaced with time-dependent logit scores.

Because of the time dependent variables, the new data frame will have many more rows than the original data, approximately  $\#rows * \#deaths / 2$ .

**Method**

A time-dependent cox model can now be fit to the new data. The univariate statistic, as originally proposed, is equivalent to single variable score tests from the time-dependent model. This equivalence is the rationale for using the time dependent model as a multivariate extension of the original paper.

In O'Brien's method, the x variables are re-ranked at each death time. A simpler method, proposed by Prentice, ranks the data only once at the start. The results are usually similar.

## References

O'Brien, Peter, "A Nonparametric Test for Association with Censored Data", *Biometrics* 34: 243-250, 1978.

## See Also

[survdiff](#)

## Examples

```
xx <- survobrien(Surv(futime, fustat) ~ age + factor(rx) + I(ecog.ps),
  data=ovarian)
coxph(Surv(start, stop, event) ~ age, data=xx)
coxph(Surv(start, stop, event) ~ age + rx + ecog.ps, data=xx)
```

---

survreg

*Regression for a Parametric Survival Model*

---

## Description

Fit a parametric survival regression model. These are location-scale models for an arbitrary transform of the time variable; the most common cases use a log transformation, leading to accelerated failure time models.

## Usage

```
survreg(formula, data, weights, subset,
  na.action, dist="weibull", init=NULL, scale=0,
  control, parms=NULL, model=FALSE, x=FALSE,
  y=TRUE, robust=FALSE, score=FALSE, ...)
```

## Arguments

formula	a formula expression as for other regression models. The response is usually a survival object as returned by the <code>Surv</code> function. See the documentation for <code>Surv</code> , <code>lm</code> and <code>formula</code> for details.
data	a data frame in which to interpret the variables named in the <code>formula</code> , <code>weights</code> or the <code>subset</code> arguments.
weights	optional vector of case weights
subset	subset of the observations to be used in the fit
na.action	a missing-data filter function, applied to the <code>model.frame</code> , after any <code>subset</code> argument has been used. Default is <code>options()\$na.action</code> .
dist	assumed distribution for <code>y</code> variable. If the argument is a character string, then it is assumed to name an element from <code>survreg.distributions</code> . These include "weibull", "exponential", "gaussian", "logistic", "lognormal" and "loglogistic". Otherwise, it is assumed to be a user defined list conforming to the format described in <code>survreg.distributions</code> .

parms	a list of fixed parameters. For the t-distribution for instance this is the degrees of freedom; most of the distributions have no parameters.
init	optional vector of initial values for the parameters.
scale	optional fixed value for the scale. If set to $\leq 0$ then the scale is estimated.
control	a list of control values, in the format produced by <code>survreg.control</code> . The default value is <code>survreg.control()</code>
model, x, y	flags to control what is returned. If any of these is true, then the model frame, the model matrix, and/or the vector of response times will be returned as components of the final result, with the same names as the flag arguments.
score	return the score vector. (This is expected to be zero upon successful convergence.)
robust	Use robust 'sandwich' standard errors, based on independence of individuals if there is no <code>cluster()</code> term in the formula, based on independence of clusters if there is.
...	other arguments which will be passed to <code>survreg.control</code> .

**Value**

an object of class `survreg` is returned.

**See Also**

[survreg.object](#), [survreg.distributions](#), [pspline](#), [frailty](#), [ridge](#)

**Examples**

```
# Fit an exponential model: the two fits are the same
survreg(Surv(futime, fustat) ~ ecog.ps + rx, ovarian, dist='weibull',
        scale=1)
survreg(Surv(futime, fustat) ~ ecog.ps + rx, ovarian,
        dist="exponential")

#
# A model with different baseline survival shapes for two groups, i.e.,
# two different scales
survreg(Surv(time, status) ~ ph.ecog + age + strata(sex), lung)

# There are multiple ways to parameterize a Weibull distribution. The survreg
# function imbeds it in a general location-scale family, which is a
# different parameterization than the rweibull function, and often leads
# to confusion.
# survreg's scale = 1/(rweibull shape)
# survreg's intercept = log(rweibull scale)
# For the log-likelihood all parameterizations lead to the same value.
y <- rweibull(1000, shape=2, scale=5)
survreg(Surv(y)~1, dist="weibull")

# Economists fit a model called 'tobit regression', which is a standard
# linear regression with Gaussian errors, and left censored data.
tobinfit <- survreg(Surv(durable, durable>0, type='left') ~ age + quant,
                  data=tobin, dist='gaussian')
```

---

survreg.control      *Package options for survreg and coxph*

---

### Description

This functions checks and packages the fitting options for [survreg](#)

### Usage

```
survreg.control(maxiter=30, rel.tolerance=1e-09,  
toler.chol=1e-10, iter.max, debug=0, outer.max=10)
```

### Arguments

maxiter	maximum number of iterations
rel.tolerance	relative tolerance to declare convergence
toler.chol	Tolerance to declare Cholesky decomposition singular
iter.max	same as maxiter
debug	print debugging information
outer.max	maximum number of outer iterations for choosing penalty parameters

### Value

A list with the same elements as the input

### See Also

[survreg](#)

---

survreg.distributions  
*Parametric Survival Distributions*

---

### Description

List of distributions for accelerated failure models. These are location-scale families for some transformation of time. The entry describes the cdf  $F$  and density  $f$  of a canonical member of the family.

### Usage

```
survreg.distributions
```

### Format

There are two basic formats, the first defines a distribution de novo, the second defines a new distribution in terms of an old one.

name:	name of distribution
variance:	function(parms) returning the variance (currently unused)
init(x,weights,...):	Function returning an initial estimate of the mean and variance (used for initial values in the iteration)
density(x,parms):	Function returning a matrix with columns $F$ , $1 - F$ , $f$ , $f'/f$ , $f''/f$
quantile(p,parms):	Quantile function
scale:	Optional fixed value for the scale parameter
parms:	Vector of default values and names for any additional parameters
deviance(y,scale,parms):	Function returning the deviance for a saturated model; used only for deviance residuals.

and to define one distribution in terms of another

name:	name of distribution
dist:	name of parent distribution
trans:	transformation (eg log)
dtrans:	derivative of transformation
itrans:	inverse of transformation
scale:	Optional fixed value for scale parameter

## Details

There are four basic distributions: `extreme`, `gaussian`, `logistic` and `t`. The last three are parametrised in the same way as the distributions already present in R. The extreme value cdf is

$$F = 1 - e^{-e^t}.$$

When the logarithm of survival time has one of the first three distributions we obtain respectively `weibull`, `lognormal`, and `loglogistic`. The location-scale parameterization of a Weibull distribution found in `survreg` is not the same as the parameterization of `rweibull`.

The other predefined distributions are defined in terms of these. The exponential and rayleigh distributions are Weibull distributions with fixed scale of 1 and 0.5 respectively, and `loggaussian` is a synonym for `lognormal`.

For speed parts of the three most commonly used distributions are hardcoded in C; for this reason the elements of `survreg.distributions` with names of "Extreme value", "Logistic" and "Gaussian" should not be modified. (The order of these in the list is not important, recognition is by name.) As an alternative to modifying `survreg.distributions` a new distribution can be specified as a separate list. This is the preferred method of addition and is illustrated below.

## See Also

[survreg](#), [pweibull](#), [pnorm](#), [plogis](#), [pt](#), [survregDtest](#)

## Examples

```
# time transformation
survreg(Surv(time, status) ~ ph.ecog + sex, dist='weibull', data=lung)
# change the transformation to work in years
# intercept changes by log(365), everything else stays the same
```

```

my.weibull <- survreg.distributions$weibull
my.weibull$strans <- function(y) log(y/365)
my.weibull$itrans <- function(y) 365*exp(y)
survreg(Surv(time, status) ~ ph.ecog + sex, lung, dist=my.weibull)

# Weibull parametrisation
y<-rweibull(1000, shape=2, scale=5)
survreg(Surv(y)~1, dist="weibull")
# survreg parameters are scale=1/shape, intercept=log(scale)

# Cauchy fit
mycauchy <- list(name='Cauchy',
  init= function(x, weights, ...)
    c(median(x), mad(x)),
  density= function(x, parms) {
    temp <- 1/(1 + x^2)
    cbind(.5 + atan(temp)/pi, .5+ atan(-temp)/pi,
      temp/pi, -2 *x*temp, 2*temp^2*(4*x^2*temp -1))
  },
  quantile= function(p, parms) tan((p-.5)*pi),
  deviance= function(...) stop('deviance residuals not defined')
)
survreg(Surv(log(time), status) ~ ph.ecog + sex, lung, dist=mycauchy)

```

---

survreg.object

*Parametric Survival Model Object*


---

## Description

This class of objects is returned by the `survreg` function to represent a fitted parametric survival model. Objects of this class have methods for the functions `print`, `summary`, `predict`, and `residuals`.

## COMPONENTS

The following components must be included in a legitimate `survreg` object.

**coefficients** the coefficients of the `linear.predictors`, which multiply the columns of the model matrix. It does not include the estimate of error (sigma). The names of the coefficients are the names of the single-degree-of-freedom effects (the columns of the model matrix). If the model is over-determined there will be missing values in the coefficients corresponding to non-estimable coefficients.

**icoef** coefficients of the baseline model, which will contain the intercept and `log(scale)`, or multiple scale factors for a stratified model.

**var** the variance-covariance matrix for the parameters, including the `log(scale)` parameter(s).

**loglik** a vector of length 2, containing the log-likelihood for the baseline and full models.

**iter** the number of iterations required

**linear.predictors** the linear predictor for each subject.

**df** the degrees of freedom for the final model. For a penalized model this will be a vector with one element per term.

**scale** the scale factor(s), with length equal to the number of strata.

**idf** degrees of freedom for the initial model.

**means** a vector of the column means of the coefficient matrix.

**dist** the distribution used in the fit.

The object will also have the following components found in other model results (some are optional): `linear`, `predictors`, `weights`, `x`, `y`, `model`, `call`, `terms` and `formula`. See `lm`.

### See Also

[survreg](#), [lm](#)

---

survregDtest	<i>Verify a survreg distribution</i>
--------------	--------------------------------------

---

### Description

This routine is called by `survreg` to verify that a distribution object is valid.

### Usage

```
survregDtest(dlist, verbose = F)
```

### Arguments

<code>dlist</code>	the list describing a survival distribution
<code>verbose</code>	return a simple TRUE/FALSE from the test for validity (the default), or a verbose description of any flaws.

### Details

If the `survreg` function rejects your user-supplied distribution as invalid, this routine will tell you why it did so.

### Value

TRUE if the distribution object passes the tests, and either FALSE or a vector of character strings if not.

### Author(s)

Terry Therneau

### See Also

[survreg.distributions](#), [survreg](#)

**Examples**

```
# An invalid distribution (it should have "init =" on line 2)
# survreg would give an error message
mycauchy <- list(name='Cauchy',
  init<- function(x, weights, ...)
    c(median(x), mad(x)),
  density= function(x, parms) {
    temp <- 1/(1 + x^2)
    cbind(.5 + atan(temp)/pi, .5+ atan(-temp)/pi,
          temp/pi, -2 *x*temp, 2*temp^2*(4*x^2*temp -1))
  },
  quantile= function(p, parms) tan((p-.5)*pi),
  deviance= function(...) stop('deviance residuals not defined')
)

survregDtest(mycauchy, TRUE)
```

---

survSplit

*Split a survival data set at specified times*


---

**Description**

Given a survival data set and a set of specified cut times, split each record into multiple subrecords at each cut time. The new data set will be in ‘counting process’ format, with a start time, stop time, and event status for each record.

**Usage**

```
survSplit(data, cut, end, event, start, id = NULL, zero = 0,
  episode=NULL)
```

**Arguments**

data	data frame
cut	vector of timepoints to cut at
end	character string with name of event time variable
event	character string with name of censoring indicator
start	character string with name of start time variable (will be created if it does not exist)
id	character string with name of new id variable to create (optional)
zero	If <code>start</code> doesn't already exist, this is the time that the original records start. May be a vector or single value.
episode	character string with name of new episode variable (optional)

**Details**

The function also works when the original data are in counting-process format, but the `id` and `episode` options are of little use in this context.



**Value**

New, longer, data frame.

**See Also**

[Surv](#), [cut](#), [reshape](#)

**Examples**

```
aml3<-survSplit(aml,cut=c(5,10,50),end="time",start="start",
               event="status",episode="i")

summary(aml)
summary(aml3)

coxph(Surv(time,status)~x,data=aml)
## the same
coxph(Surv(start,time,status)~x,data=aml3)

aml4<-survSplit(aml3,cut=20,end="time",start="start", event="status")
coxph(Surv(start,time,status)~x,data=aml4)
```

---

tcut

*Factors for person-year calculations*

---

**Description**

Attaches categories for person-year calculations to a variable without losing the underlying continuous representation

**Usage**

```
tcut(x, breaks, labels, scale=1)
```

**Arguments**

x	numeric/date variable
breaks	breaks between categories, which are right-continuous
labels	labels for categories
scale	Multiply x and breaks by this.

**Value**

An object of class tcut

**See Also**

[cut](#), [pyears](#)

**Examples**

```

mdy.date <- function(m,d,y)
  as.Date(paste(ifelse(y<100, y+1900, y), m, d, sep='/'))
temp1 <- mdy.date(6,6,36)
temp2 <- mdy.date(6,6,55) # Now compare the results from person-years
#
temp.age <- tcut(temp2-temp1, floor(c(-1, (18:31 * 365.24))),
labels=c('0-18', paste(18:30, 19:31, sep='-')))
temp.yr <- tcut(temp2, mdy.date(1,1,1954:1965), labels=1954:1964)
temp.time <- 3700 #total days of fu
py1 <- pyears(temp.time ~ temp.age + temp.yr, scale=1) #output in days
py1

```

---

tobin

*Tobin's Tobit data*


---

**Description**

Economists fit a parametric censored data model called the 'tobit'. These data are from Tobin's original paper.

**Usage**

```
tobin
```

**Format**

A data frame with 20 observations on the following 3 variables.

**durable** Durable goods purchase

**age** Age in years

**quant** Liquidity ratio (x 1000)

**Source**

J Tobin (1958), Estimation of relationships for limited dependent variables. *Econometrica* **26**, 24–36.

**Examples**

```

tfit <- survreg(Surv(durable, durable>0, type='left') ~age + quant,
               data=tobin, dist='gaussian')

predict(tfit,type="response")

```

---

`untangle.specials` *Help Process the 'specials' Argument of the 'terms' Function.*

---

### Description

Given a `terms` structure and a desired special name, this returns an index appropriate for subscripting the `terms` structure and another appropriate for the data frame.

### Usage

```
untangle.specials(tt, special, order=1)
```

### Arguments

<code>tt</code>	a <code>terms</code> object.
<code>special</code>	the name of a special function, presumably used in the <code>terms</code> object.
<code>order</code>	the order of the desired terms. If set to 2, interactions with the special function will be included.

### Value

a list with two components:

<code>vars</code>	a vector of variable names, as would be found in the data frame, of the specials.
<code>terms</code>	a numeric vector, suitable for subscripting the <code>terms</code> structure, that indexes the terms in the expanded model formula which involve the special.

### Examples

```
formula<-Surv(tt,ss)~x+z*strata(id)
tms<-terms(formula,specials="strata")
## the specials attribute
attr(tms,"specials")
## main effects
untangle.specials(tms,"strata")
## and interactions
untangle.specials(tms,"strata",order=1:2)
```

---

`veteran`

*Veterans' Administration Lung Cancer study*

---

### Description

Randomised trial of two treatment regimens for lung cancer. This is a standard survival analysis data set.

### Usage

```
veteran
```

### Format

trt: 1=standard 2=test  
celltype: 1=squamous, 2=smallcell, 3=adeno, 4=large  
time: survival time  
status: censoring status  
karno: Karnofsky performance score (100=good)  
diagtime: months from diagnosis to randomisation  
age: in years  
prior: prior therapy 0=no, 1=yes

**Source**

D Kalbfleisch and RL Prentice (1980), *The Statistical Analysis of Failure Time Data*. Wiley, New York.



## Chapter 26

# The `tcltk` package

---

`tcltk-package`      *Tcl/Tk Interface*

---

### Description

Interface and language bindings to Tcl/Tk GUI elements.

### Details

This package provides access to the platform-independent Tcl scripting language and Tk GUI elements. See [TkWidgets](#) for a list of supported widgets, [TkWidgetcmds](#) for commands to work with them, and references in those files for more.

The Tcl/Tk documentation is in the system man pages.

For a complete list of functions, use `ls ("package:tcltk")`.

Note that Tk will not be initialized if there is no `DISPLAY` variable set, but Tcl can still be used. This is most useful to allow the loading of a package which depends on `tcltk` in a session that does not actually use it (e.g. during installation).

### Author(s)

R Development Core Team

Maintainer: R Core Team <[R-core@r-project.org](mailto:R-core@r-project.org)>

---

`TclInterface`      *Low-level Tcl/Tk Interface*

---

### Description

These functions and variables provide the basic glue between R and the Tcl interpreter and Tk GUI toolkit. Tk windows may be represented via R objects. Tcl variables can be accessed via objects of class `tclVar` and the C level interface to Tcl objects is accessed via objects of class `tclObj`.

**Usage**

```

.Tcl(...)
.Tcl.objv(objv)
.Tcl.args(...)
.Tcl.args.objv(...)
.Tcl.callback(...)
.Tk.ID(win)
.Tk.newwin(ID)
.Tk.subwin(parent)
.TkRoot

tkdestroy(win)
is.tkwin(x)

tclvalue(x)
tclvalue(x) <- value

tclVar(init="")
## S3 method for class 'tclVar':
as.character(x, ...)
## S3 method for class 'tclVar':
tclvalue(x)
## S3 replacement method for class 'tclVar':
tclvalue(x) <- value

tclArray()
## S3 method for class 'tclArray':
x[[...]]
## S3 replacement method for class 'tclArray':
x[[...]] <- value
## S3 method for class 'tclArray':
x$i
## S3 replacement method for class 'tclArray':
x$i <- value

## S3 method for class 'tclArray':
names(x)
## S3 method for class 'tclArray':
length(x)

tclObj(x)
tclObj(x) <- value
## S3 method for class 'tclVar':
tclObj(x)
## S3 replacement method for class 'tclVar':
tclObj(x) <- value

as.tclObj(x, drop=FALSE)
is.tclObj(x)

## S3 method for class 'tclObj':
as.character(x, ...)

```

```

## S3 method for class 'tclObj':
as.integer(x, ...)
## S3 method for class 'tclObj':
as.double(x, ...)
## S3 method for class 'tclObj':
as.logical(x, ...)
## S3 method for class 'tclObj':
as.raw(x, ...)
## S3 method for class 'tclObj':
tclvalue(x)

## Default S3 method:
tclvalue(x)
## Default S3 method:
tclvalue(x) <- value

addTclPath(path = ".")
tclRequire(package, warn = TRUE)

```

### Arguments

objv	a named vector of Tcl objects
win	a window structure
x	an object
i	character or (unquoted) name
drop	logical. Indicates whether a single-element vector should be made into a simple Tcl object or a list of length one
value	For <code>tclvalue</code> assignments, a character string. For <code>tclObj</code> assignments, an object of class <code>tclObj</code>
ID	a window ID
parent	a window which becomes the parent of the resulting window
path	path to a directory containing Tcl packages
package	a Tcl package name
warn	logical. Warn if not found?
...	Additional arguments. See below.
init	initialization value

### Details

Many of these functions are not intended for general use but are used internally by the commands that create and manipulate Tk widgets and Tcl objects. At the lowest level `.Tcl` sends a command as a text string to the Tcl interpreter and returns the result as an object of class `tclObj` (see below). A newer variant `.Tcl.objv` accepts arguments in the form of a named list of `tclObj` objects.

`.Tcl.args` converts an R argument list of `tag=value` pairs to the Tcl `-option value` style, thus enabling a simple translation between the two languages. To send a value with no preceding option flag to Tcl, just use an untagged argument. In the rare case one needs an option with no subsequent value `tag=NULL` can be used. Most values are just converted to character mode and



inserted in the command string, but window objects are passed using their ID string, and callbacks are passed via the result of `.Tcl.callback`. Tags are converted to option flags simply by prepending a `-`

`.Tcl.args.objv` serves a similar purpose as `.Tcl.args` but produces a list of `tclObj` objects suitable for passing to `.Tcl.objv`. The names of the list are converted to Tcl option style internally by `.Tcl.objv`.

Callbacks can be either *atomic callbacks* handled by `.Tcl.callback` or expressions. An expression is treated as a list of atomic callbacks, with the following exceptions: if an element is a name, it is first evaluated in the callers frame, and likewise if it is an explicit function definition; the `break` expression is translated directly to the Tcl counterpart. `.Tcl.callback` converts R functions and unevaluated calls to Tcl command strings. The argument must be either a function closure or an object of mode `"call"` followed by an environment. The return value in the first case is of the form `R_call 0x408b94d4` in which the hexadecimal number is the memory address of the function. In the second case it will be of the form `R_call_lang 0x8a95904 0x819bfd0`. For expressions, a sequence of similar items is generated, separated by semicolons. `.Tcl.args` takes special precautions to ensure that functions or calls will continue to exist at the specified address by assigning the callback into the relevant window environment (see below).

Tk windows are represented as objects of class `tkwin` which are lists containing a `ID` field and an `env` field which is an R environments, enclosed in the global environment. The value of the `ID` field is identical to the Tk window name. The `env` environment contains a `parent` variable and a `num.subwin` variable. If the window obtains sub-windows and callbacks, they are added as variables to the environment. `.TkRoot` is the top window with ID `."`; this window is not displayed in order to avoid ill effects of closing it via window manager controls. The `parent` variable is undefined for `.TkRoot`.

`.Tk.ID` extracts the ID of a window, `.Tk.newwin` creates a new window environment with a given ID and `.Tk.subwin` creates a new window which is a sub-window of a given parent window.

`tkdestroy` destroys a window and also removes the reference to a window from its parent.

`is.tkwin` can be used to test whether a given object is a window environment.

`tclVar` creates a new Tcl variable and initializes it to `init`. An R object of class `tclVar` is created to represent it. Using `as.character` on the object returns the Tcl variable name. Accessing the Tcl variable from R is done using the `tclvalue` function, which can also occur on the left-hand side of assignments. If `tclvalue` is passed an argument which is not a `tclVar` object, then it will assume that it is a character string explicitly naming global Tcl variable. Tcl variables created by `tclVar` are uniquely named and automatically unset by the garbage collector when the representing object is no longer in use.

`tclArray` creates a new Tcl array and initializes it to the empty array. An R object of class `tclArray` and inheriting from class `tclVar` is created to represent it. You can access elements of the Tcl array using indexing with `[]` or `$`, which also allow replacement forms. Notice that Tcl arrays are associative by nature and hence unordered; indexing with a numeric index `i` refers to the element with the *name* `as.character(i)`. Multiple indices are pasted together separated by commas to form a single name. You can query the length and the set of names in an array using methods for `length` and `names`, respectively; these cannot meaningfully be set so assignment forms exist only to print an error message.

It is possible to access Tcl's 'dual-ported' objects directly, thus avoiding parsing and deparsing of their string representation. This works by using objects of class `tclObj`. The string representation of such objects can be extracted (but not set) using `tclvalue` and conversion to vectors of mode `"character"`, `"double"`, `"integer"`, `"logical"`. Conversely, such vectors can be converted using `as.tclObj`. There is an ambiguity as to what should happen for length one vectors, controlled by the `drop` argument; there are cases where the distinction matters to Tcl, although

mostly it treats them equivalently. Notice that `tclvalue` and `as.character` differ on an object whose string representation has embedded spaces, the former is sometimes to be preferred, in particular when applied to the result of `tclread`, `tkgetOpenFile`, and similar functions. The `as.raw` method returns a raw vector or a list of raw vectors and can be used to return binary data from Tcl.

The object behind a `tclVar` object is extracted using `tclObj(x)` which also allows an assignment form, in which the right hand side of the assignment is automatically converted using `as.tclObj`. There is a `print` method for `tclObj` objects; it prints `<Tcl>` followed by the string representation of the object. Notice that `as.character` on a `tclVar` object is the *name* of the corresponding Tcl variable and not the value.

Tcl packages can be loaded with `tclRequire`; it may be necessary to add the directory where they are found to the Tcl search path with `addTclPath`. The return value is a class `"tclObj"` object if it succeeds, or `FALSE` if it fails (when a warning is issued).

### Note

Strings containing unbalanced braces are currently not handled well in many circumstances.

### See Also

[TkWidgets](#), [TkCommands](#), [TkWidgetcmds](#).

`capabilities("tcltk")` to see if Tcl/Tk support was compiled into this build of R.

### Examples

```
## Not run:
## These cannot be run by example() but should be OK when pasted
## into an interactive R session with the tcltk package loaded
.Tcl("format \"%s\n\" \"Hello, World!\")
f <- function()cat("HI!\n")
.Tcl.callback(f)
.Tcl.args(text="Push!", command=f) # NB: Different address

xyzy <- tclVar(7913)
tclvalue(xyzy)
tclvalue(xyzy) <- "foo"
as.character(xyzy)
tcl("set", as.character(xyzy))

top <- tktoplevel() # a Tk widget, see Tk-widgets
ls(envir=top$env, all=TRUE)
ls(envir=.TkRoot$env, all=TRUE) # .Tcl.args put a callback ref in here

## End(Not run)
```

---

tclServiceMode	<i>Allow Tcl events to be serviced or not</i>
----------------	---

---

### Description

This function controls or reports on the Tcl service mode, i.e. whether Tcl will respond to events.

**Usage**

```
tclServiceMode(on = NULL)
```

**Arguments**

`on` (logical) Whether event servicing is turned on.

**Details**

If called with `on == NULL` (the default), no change is made.

Note that this blocks all Tcl/Tk activity, including for widgets from other packages. It may be better to manage mapping of windows individually.

**Value**

The value of the Tcl service mode before the call.

**Examples**

```
## see demo(tkcanvas) for an example
## Not run:
  oldmode <- tclServiceMode(FALSE)
  # Do some work to create a nice picture.  Nothing will be displayed until...
  tclServiceMode(oldmode)

## End(Not run)
## another idea is to use tkwm.withdraw() ... tkwm.deiconify()
```

---

TkCommands

*Tk non-widget commands*

---

**Description**

These functions interface to Tk non-widget commands, such as the window manager interface commands and the geometry managers.

**Usage**

```
tcl(...)
tktitle(x)

tktitle(x) <- value

tkbell(...)
tkbind(...)
tkbindtags(...)
tkfocus(...)
tklower(...)
tkraise(...)

tkclipboard.append(...)
tkclipboard.clear(...)
```

```
tkevent.add(...)
tkevent.delete(...)
tkevent.generate(...)
tkevent.info(...)

tkfont.actual(...)
tkfont.configure(...)
tkfont.create(...)
tkfont.delete(...)
tkfont.families(...)
tkfont.measure(...)
tkfont.metrics(...)
tkfont.names(...)

tkgrab(...)
tkgrab.current(...)
tkgrab.release(...)
tkgrab.set(...)
tkgrab.status(...)

tkimage.cget(...)
tkimage.configure(...)
tkimage.create(...)
tkimage.names(...)

## NB: some widgets also have a selection.clear command, hence the "X".

tkXselection.clear(...)
tkXselection.get(...)
tkXselection.handle(...)
tkXselection.own(...)

tkwait.variable(...)
tkwait.visibility(...)
tkwait.window(...)

## winfo actually has a large number of subcommands, but it's rarely
## used, so use tkwinfo("atom", ...) etc. instead.

tkwinfo(...)

# Window manager interface

tkwm.aspect(...)
tkwm.client(...)
tkwm.colormapwindows(...)
tkwm.command(...)
tkwm.deiconify(...)
tkwm.focusmodel(...)
tkwm.frame(...)
tkwm.geometry(...)
```

```
tkwm.grid(...)
tkwm.group(...)
tkwm.iconbitmap(...)
tkwm.iconify(...)
tkwm.iconmask(...)
tkwm.iconname(...)
tkwm.iconposition(...)
tkwm.iconwindow(...)
tkwm.maxsize(...)
tkwm.minsize(...)
tkwm.overrideredirect(...)
tkwm.positionfrom(...)
tkwm.protocol(...)
tkwm.resizable(...)
tkwm.sizefrom(...)
tkwm.state(...)
tkwm.title(...)
tkwm.transient(...)
tkwm.withdraw(...)
```

### ### Geometry managers

```
tkgrid(...)
tkgrid.bbox(...)
tkgrid.columnconfigure(...)
tkgrid.configure(...)
tkgrid.forget(...)
tkgrid.info(...)
tkgrid.location(...)
tkgrid.propagate(...)
tkgrid.rowconfigure(...)
tkgrid.remove(...)
tkgrid.size(...)
tkgrid.slaves(...)
```

```
tkpack(...)
tkpack.configure(...)
tkpack.forget(...)
tkpack.info(...)
tkpack.propagate(...)
tkpack.slaves(...)
```

```
tkplace(...)
tkplace.configure(...)
tkplace.forget(...)
tkplace.info(...)
tkplace.slaves(...)
```

```
## Standard dialogs
tkgetOpenFile(...)
tkgetSaveFile(...)
```

```

tkchooseDirectory(...)
tkmessageBox(...)
tkdialog(...)
tkpopup(...)

## File handling functions
tclfile.tail(...)
tclfile.dir(...)
tclopen(...)
tclclose(...)
tclputs(...)
tclread(...)

```

### Arguments

x	A window object
value	For <code>tktitle</code> assignments, a character string.
...	Handled via <code>.Tcl.args</code>

### Details

`tcl` provides a generic interface to calling any Tk or Tcl command by simply running `.Tcl.args.objv` on the argument list and passing the result to `.Tcl.objv`. Most of the other commands simply call `tcl` with a particular first argument and sometimes also a second argument giving the subcommand.

`tktitle` and its assignment form provides an alternate interface to Tk's `wm title`

There are far too many of these commands to describe them and their arguments in full. Please refer to the Tcl/Tk documentation for details. With a few exceptions, the pattern is that Tk subcommands like `pack` `configure` are converted to function names like `tkpack.configure`, and Tcl subcommands are like `tclfile.dir`.

### See Also

[TclInterface](#), [TkWidgets](#), [TkWidgetcmds](#)

### Examples

```

## Not run:
## These cannot be run by examples() but should be OK when pasted
## into an interactive R session with the tcltk package loaded

tt <- tktoplevel()
tkpack(l1<-tklabel(tt,text="Heave"), l2<-tklabel(tt,text="Ho"))
tkpack.configure(l1, side="left")

## Try stretching the window and then

tkdestroy(tt)

## End(Not run)

```

---

`tkpager`*Page file using Tk text widget*

---

**Description**

This plugs into `file.show`, showing files in separate windows.

**Usage**

```
tkpager(file, header, title, delete.file)
```

**Arguments**

<code>file</code>	character vector containing the names of the files to be displayed
<code>header</code>	headers to use for each file
<code>title</code>	common title to use for the window(s). Pasted together with the header to form actual window title.
<code>delete.file</code>	logical. Should file(s) be deleted after display?

**Note**

The "`\b_`" string used for underlining is currently quietly removed. The font and background colour are currently hardcoded to Courier and gray90.

**See Also**

[file.show](#)

---

`tkProgressBar`*Progress Bars via Tk*

---

**Description**

Put up a Tk progress bar widget.

**Usage**

```
tkProgressBar(title = "R progress bar", label = "",
              min = 0, max = 1, initial = 0, width = 300)

getTkProgressBar(pb)
setTkProgressBar(pb, value, title = NULL, label = NULL)
## S3 method for class 'tkProgressBar':
close(con, ...)
```

## Arguments

<code>title, label</code>	character strings, giving the window title and the label on the dialog box respectively.
<code>min, max</code>	(finite) numeric values for the extremes of the progress bar.
<code>initial, value</code>	initial or new value for the progress bar.
<code>width</code>	the width of the progress bar in pixels: the dialog box will be 40 pixels wider (plus frame).
<code>pb, con</code>	an object of class "tkProgressBar".
<code>...</code>	for consistency with the generic.

## Details

`tkProgressBar` will display a widget containing a label and progress bar.

`setTkProgressBar` will update the value and for non-NULL values, the title and label (provided there was one when the widget was created). Missing (NA) and out-of-range values of `value` will be (silently) ignored.

The progress bar should be `closed` when finished with.

This will use the `ttk::progressbar` widget for Tk version 8.5 or later, otherwise R's copy of `BWidget's progressbar`.

## Value

For `tkProgressBar` an object of class "tkProgressBar".

For `getTkProgressBar` and `setTkProgressBar`, a length-one numeric vector giving the previous value (invisibly for `setTkProgressBar`).

## See Also

[txtProgressBar](#)

## Examples

```
pb <- tkProgressBar("test progress bar", "Some information in %",
                   0, 100, 50)
Sys.sleep(0.5)
u <- c(0, sort(runif(20, 0, 100)), 100)
for(i in u) {
  Sys.sleep(0.1)
  info <- sprintf("%d%% done", round(i))
  setTkProgressBar(pb, i, sprintf("test (%s)", info), info)
}
Sys.sleep(5)
close(pb)
```



---

tkStartGUI	<i>Tcl/Tk GUI startup</i>
------------	---------------------------

---

**Description**

Starts up the Tcl/Tk GUI

**Usage**

```
tkStartGUI()
```

**Details**

Starts a GUI console implemented via a Tk text widget. This should probably be called at most once per session. Also redefines the file pager (as used by `help()`) to be the Tk pager.

**Note**

`tkStartGUI()` saves its evaluation environment as `.GUIenv`. This means that the user interface elements can be accessed in order to extend the interface. The three main objects are named `Term`, `Menu`, and `Toolbar`, and the various submenus and callback functions can be seen with `ls(envir=.GUIenv)`.

**Author(s)**

Peter Dalgaard

---

TkWidgetcmds	<i>Tk widget commands</i>
--------------	---------------------------

---

**Description**

These functions interface to Tk widget commands.

**Usage**

```
tkactivate(widget, ...)  
tkadd(widget, ...)  
tkaddtag(widget, ...)  
tkbbox(widget, ...)  
tkcanvasx(widget, ...)  
tkcanvasy(widget, ...)  
tkcget(widget, ...)  
tkcompare(widget, ...)  
tkconfigure(widget, ...)  
tkcoords(widget, ...)  
tkcreate(widget, ...)  
tkcurselection(widget, ...)  
tkdchars(widget, ...)  
tkdebug(widget, ...)
```

```
tkdelete(widget, ...)
tkdelta(widget, ...)
tkdeselect(widget, ...)
tkdlineinfo(widget, ...)
tkdtag(widget, ...)
tkdump(widget, ...)
tkentrycget(widget, ...)
tkentryconfigure(widget, ...)
tkfind(widget, ...)
tkflash(widget, ...)
tkfraction(widget, ...)
tkget(widget, ...)
tkgettags(widget, ...)
tkicursor(widget, ...)
tkidentify(widget, ...)
tkindex(widget, ...)
tkinsert(widget, ...)
tkinvoke(widget, ...)
tkitembind(widget, ...)
tkitemcget(widget, ...)
tkitemconfigure(widget, ...)
tkitemfocus(widget, ...)
tkitemlower(widget, ...)
tkitemraise(widget, ...)
tkitemscale(widget, ...)
tkmark.gravity(widget, ...)
tkmark.names(widget, ...)
tkmark.next(widget, ...)
tkmark.previous(widget, ...)
tkmark.set(widget, ...)
tkmark.unset(widget, ...)
tkmove(widget, ...)
tknearest(widget, ...)
tkpost(widget, ...)
tkpostcascade(widget, ...)
tkpostscript(widget, ...)
tkscan.mark(widget, ...)
tkscan.dragto(widget, ...)
tksearch(widget, ...)
tksee(widget, ...)
tkselect(widget, ...)
tkselection.adjust(widget, ...)
tkselection.anchor(widget, ...)
tkselection.clear(widget, ...)
tkselection.from(widget, ...)
tkselection.includes(widget, ...)
tkselection.present(widget, ...)
tkselection.range(widget, ...)
tkselection.set(widget, ...)
tkselection.to(widget, ...)
tkset(widget, ...)
tksize(widget, ...)
```

```

tktoggle(widget, ...)
tktag.add(widget, ...)
tktag.bind(widget, ...)
tktag.cget(widget, ...)
tktag.configure(widget, ...)
tktag.delete(widget, ...)
tktag.lower(widget, ...)
tktag.names(widget, ...)
tktag.nextrange(widget, ...)
tktag.prevrange(widget, ...)
tktag.raise(widget, ...)
tktag.ranges(widget, ...)
tktag.remove(widget, ...)
tktype(widget, ...)
tkunpost(widget, ...)
tkwindow.cget(widget, ...)
tkwindow.configure(widget, ...)
tkwindow.create(widget, ...)
tkwindow.names(widget, ...)
tkxview(widget, ...)
tkxview.moveto(widget, ...)
tkxview.scroll(widget, ...)
tkyposition(widget, ...)
tkyview(widget, ...)
tkyview.moveto(widget, ...)
tkyview.scroll(widget, ...)

```

### Arguments

widget	The widget this applies to
...	Handled via <code>.Tcl.args</code>

### Details

There are far too many of these commands to describe them and their arguments in full. Please refer to the Tcl/Tk documentation for details. Except for a few exceptions, the pattern is that Tcl widget commands possibly with subcommands like `.a.b selection clear` are converted to function names like `tkselection.clear` and the widget is given as the first argument.

### See Also

[TclInterface](#), [TkWidgets](#), [TkCommands](#)

### Examples

```

## Not run:
## These cannot be run by examples() but should be OK when pasted
## into an interactive R session with the tcltk package loaded

tt <- tktoplevel()
tkpack(txt.w <- tktext(tt))
tkinsert(txt.w, "0.0", "plot(1:10)")

# callback function

```

```
eval.txt <- function()  
  eval(parse(text=tclvalue(tkget(txt.w, "0.0", "end"))))  
tkpack(but.w <- tkbutton(tt,text="Submit", command=eval.txt))  
  
## Try pressing the button, edit the text and when finished:  
  
tkdestroy(tt)  
  
## End(Not run)
```

---

TkWidgets

*Tk widgets*

---

## Description

Create Tk widgets and associated R objects.

## Usage

```
tkwidget(parent, type, ...)  
  
tkbutton(parent, ...)  
tkcanvas(parent, ...)  
tkcheckbutton(parent, ...)  
tkentry(parent, ...)  
ttkentry(parent, ...)  
tkframe(parent, ...)  
tklabel(parent, ...)  
tklistbox(parent, ...)  
tkmenu(parent, ...)  
tkmenubutton(parent, ...)  
tkmessage(parent, ...)  
tkradiobutton(parent, ...)  
tkscale(parent, ...)  
tkscrollbar(parent, ...)  
tktext(parent, ...)  
tktoplevel(parent = .TkRoot, ...)  
  
ttkbutton(parent, ...)  
ttkcheckbutton(parent, ...)  
ttkcombobox(parent, ...)  
ttkframe(parent, ...)  
ttkimage(parent, ...)  
ttklabel(parent, ...)  
ttklabelframe(parent, ...)  
ttkmenubutton(parent, ...)  
ttknotebook(parent, ...)  
ttkpanedwindow(parent, ...)  
ttkprogressbar(parent, ...)  
ttkradiobutton(parent, ...)  
ttkscrollbar(parent, ...)
```

```
ttkseparator(parent, ...)
ttksizegrip(parent, ...)
ttktreeview(parent, ...)
```

### Arguments

parent	Parent of widget window.
type	string describing the type of widget desired.
...	handled via <code>.Tcl.args</code> .

### Details

These functions create Tk widgets. `tkwidget` creates a widget of a given type, the others simply call `tkwidget` with the respective `type` argument.

The functions starting `ttk` are for the themed widget set for Tk 8.5 or later. A tutorial can be found at <http://www.tkdocks.com>.

It is not possible to describe the widgets and their arguments in full. Please refer to the Tcl/Tk documentation.

### See Also

[TclInterface](#), [TkCommands](#), [TkWidgetcmds](#)

### Examples

```
## Not run:
## These cannot be run by examples() but should be OK when pasted
## into an interactive R session with the tcltk package loaded

tt <- tktoplevel()
label.widget <- tklabel(tt, text="Hello, World!")
button.widget <- tkbutton(tt, text="Push",
                          command=function() cat ("OW!\n"))
tkpack(label.widget, button.widget) # geometry manager
                                   # see Tk-commands

## Push the button and then...

tkdestroy(tt)

## test for themed widgets
if(as.character(tcl("info", "tclversion")) >= "8.5") {
  # make use of themed widgets
  # list themes
  as.character(tcl("ttk::style", "theme", "names"))
  # select a theme -- here pre-XP windows
  tcl("ttk::style", "theme use", "winnative")
} else {
  # use Tk 8.0 widgets
}

## End(Not run)
```

---

tk\_choose.dir      *Choose a Folder Interactively*

---

**Description**

Use a Tk widget to choose a directory interactively.

**Usage**

```
tk_choose.dir(default = "", caption = "Select directory")
```

**Arguments**

default	which directory to show initially.
caption	the caption on the selection dialog.

**Value**

A length-one character vector, character NA if 'Cancel' was selected.

**See Also**

[tk\\_choose.files](#)

**Examples**

```
## Not run:
tk_choose.dir(getwd(), "Choose a suitable folder")

## End(Not run)
```

---

tk\_choose.files      *Choose a List of Files Interactively*

---

**Description**

Use a Tk file dialog to choose a list of zero or more files interactively.

**Usage**

```
tk_choose.files(default = "", caption = "Select files",
                multi = TRUE, filters = NULL, index = 1)
```

**Arguments**

default	which filename to show initially.
caption	the caption on the file selection dialog.
multi	whether to allow multiple files to be selected.
filters	two-column character matrix of filename filters.
index	unused.

**Details**

Unlike `file.choose`, `tk_choose.files` will always attempt to return a character vector giving a list of files. If the user cancels the dialog, then zero files are returned, whereas `file.choose` would signal an error.

The format of `filters` can be seen from the example. File patterns are specified via extensions, with "\*" meaning any file, and "" any file without an extension (a filename not containing a period). (Other forms may work on specific platforms.) Note that the way to have multiple extensions for one file type is to have multiple rows with the same name in the first column, and that whether the extensions are named in file chooser widget is platform-specific. **The format may change before release.**

**Value**

A character vector giving zero or more file paths.

**Note**

A bug in Tk 8.5.0–8.5.4 prevented multiple selections being used.

**See Also**

`file.choose`, `tk_choose.dir`

**Examples**

```
Filters <- matrix(c("R code", ".R", "R code", ".s",
                  "Text", ".txt", "All files", "*"),
                4, 2, byrow = TRUE)
Filters
if(interactive()) tk_choose.files(filter = Filters)
```

---

tk\_messageBox

*Tk Message Box*


---

**Description**

An implementation of a generic message box using Tk

**Usage**

```
tk_messageBox(type = c("ok", "okcancel", "yesno", "yesnocancel",
                      "retrycancel", "aburtretrycancel"),
             message, caption = "", default = "", ...)
```

**Arguments**

<code>type</code>	character. The type of dialog box. It will have the buttons implied by its name.
<code>message</code>	character. The information field of the dialog box.
<code>caption</code>	the caption on the widget displayed.
<code>default</code>	character. The name of the button to be used as the default.
<code>...</code>	additional named arguments to be passed to the Tk function of this name. An example is <code>icon="warning"</code> .

**Value**

A character string giving the name of the button pressed.

**See Also**

[tkmessageBox](#) for a 'raw' interface.

---

tk\_select.list      *Select Items from a List*

---

**Description**

Select item(s) from a character vector using a Tk listbox.

**Usage**

```
tk_select.list(choices, preselect = NULL, multiple = FALSE, title = NULL)
```

**Arguments**

choices	a character vector of items.
preselect	a character vector, or NULL. If non-null and if the string(s) appear in the list, the item(s) are selected initially.
multiple	logical: can more than one item be selected?
title	optional character string for window title, or NULL for no title.

**Details**

This is a version of [select.list](#) implemented as a Tk list box plus OK and Cancel buttons. There will be a scrollbar if the list is too long to fit comfortably on the screen.

The dialog box is *modal*, so a selection must be made or cancelled before the R session can proceed. As from R 2.10.1 double-clicking on an item is equivalent to selecting it and then clicking OK.

If Tk is version 8.5 or later, themed widgets will be used.

**Value**

A character vector of selected items. If `multiple` is false and no item was selected (or Cancel was used), "" is returned. If `multiple` is true and no item was selected (or Cancel was used) then a character vector of length 0 is returned.

**See Also**

[select.list](#) (a text version except on Windows and the Mac OS X GUI), [menu](#) (whose `graphics=TRUE` mode uses this on most Unix-alikes).





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